

GenCore version 5.1.6
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main search, using sw model

February 20, 2004, 16:47:50 ; Search time 38.5367 Seconds
(without alignments)
4378.325 Million cell updates/sec

S-10-090-827-15

599
MAAGCLIALTLTLEOSLLIG.....PDVCFDNNVLEDYTDGGVS 1063

T.O.S.I.TM62

Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues

its satisfying chosen parameters:

length: 0

ing: 20000000

Minimum Match 0%

Maximum Match 100%

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A. Genesepc_19Junc03.*

1.	:	/SIDS1/cgcdata/geneseq/geneseqp-emb1/AAL1980.DAT.*
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24.	:	/SIDS1/cgcdata/geneseq/geneseqp-emb1/AAL2003.DAT.*

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

§	very	match	Length	DB	ID	Description
00.0	0	1063	22	AAU01034	Human secreted sol	
00.0	0	1063	22	AA662258	Porcine calcium ch	
00.0	0	1091	16	AAK71011	Human neuronal cal	
00.0	0	1091	19	AAW63145	Human calcium chan	
00.0	0	1091	21	AA810576	Human calcium chan	
00.0	0	1091	22	AAU01035	Human secreted sol	
00.0	0	1091	22	AA662259	Porcine calcium ch	
00.0	0	1091	23	AAE24789	Human calcium chan	
99.9	9	1091	19	AAK37879	Human calcium chan	

10	5593	99.9	1091	14	AAR333553	Sequence
11	5579.5	99.7	1110	16	AAW633148	Human cal
12	5559.5	99.3	1086	16	AAR71013	Human cal
13	5559.5	99.3	1086	21	AAW633153	Human cal
14	5559.5	99.3	1086	21	AA310587	Human cal
15	5559.5	99.3	1086	23	AA324799	Human cal
16	5542.5	99.0	1084	16	AAW71015	Human cal
17	5542.5	99.0	1084	16	AAW633155	Human cal
18	5542.5	99.0	1084	21	AA310589	Human cal
19	5542.5	99.0	1084	23	AA324801	Human cal
20	5532	98.8	1063	22	AAU01030	Pig secret
21	5532	98.8	1063	22	AA362254	Porcine c
22	5532	98.8	1069	22	AAU01031	Pig secret
23	5532	98.8	1069	22	AA362255	Porcine c
24	5532	98.8	1091	22	AAU01027	Porcine c
25	5532	98.8	1091	22	AA362251	Human nei
26	5523	98.6	1103	16	AAR71012	Human cal
27	5523	98.6	1103	19	AAW633151	Human cal
28	5523	98.6	1103	21	AA310586	Human cal
29	5523	98.6	1103	23	AA324798	Human cal
30	5503	98.3	1079	19	AAW633154	Human cal
31	5503	98.3	1079	21	AA310588	Human cal
32	5503	98.3	1079	23	AA324800	Human cal
33	5497	98.2	1079	16	AAR71014	Human nei
34	5443	97.2	1036	22	AAU01033	Human sec
35	5443	97.2	1036	22	AA362257	Porcine c
36	5385.5	96.2	1106	18	AAW37712	Rabbit s
37	5385.5	96.2	1106	18	AAW18389	Rabbit c
38	5385.5	96.2	1106	21	AAW77545	Rabbit s
39	5380	96.1	1036	22	AAU01029	Pig secret
40	5380	96.1	1036	22	AA362253	Porcine c
41	5344.5	95.8	1106	16	AA373056	Rabbit s
42	5346	95.5	1018	22	AAU01032	Human sec
43	5346	95.5	1018	22	AA362256	Porcine c
44	5288	94.4	1018	22	AAU01028	Pig secret
45	5288	94.4	1018	22	AA362252	Porcine c

ALIGNMENTS

RESULT 1	
AAU01034	AAU01034 standard; Protein; 1063 AA.
ID	
XX	
XX	AAU01034;
XX	
XX	AC
XX	AC
XX	04-JUL-2001 (first entry)
DE	
XX	Human secreted soluble alpha2delta calcium channel subunit #14]
XX	
KW	Human; secreted calcium channel alpha2delta subunit; alpha2delta;
KW	alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel
KW	gabapentin; scintillation proximity assay; SPA; nickel flashplate
KW	filter binding assay; wheat germ lectin flashplate assay.
XX	
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OS	Homo sapiens.
XX	
PN	WO200119870-A2.
XX	
PD	22-MAR-2001.
XX	
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PF	18-SEP-2000; 2000WO-EP09137.
XX	
PR	16-SEP-1999; 99US-0397550.
XX	
PA	(WARN) WARNER LAMBERT CO.
XX	
PI	Brown JP, Bertelli F;
XX	
XX	WPI; 2001-235262/24.
DR	N-PSDB; AAS01425.
XX	
XX	

nel alpha2delta subunits, useful in e.g. SPA assays, assays, Nickel Flashplate assays, Filter binding assays or actin Flashplate assays -

ge 137-140; 160pp; English.

sequence represents human secreted calcium channel subunit #14 which is soluble and retains the functional ics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated 2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins, their affinity for radioactively labelled gabapentin. The subunit is 1 of the components of the heteromultimeric calcium channel (VDC) complexes present in neuronal and tissues including heart and skeletal muscle. Numerous as of the human calcium channel alpha2delta subunits AU01024 and AU01032-AU01038) and 5 soluble forms of the calcium channel alpha2delta subunits (AU01027-AU01031) are the secreted soluble alpha2delta subunit may be used in assays. lation proximity assay (SPA), flashplate, nickel flashplate, ng or wheat germ lectin flashplate assays to detect or binding or interaction of a ligand (e.g. gabapentin, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine, xerme and/or L-Phenylalanine) of a calcium channel subunit.

1063 AA;

100.0%; Score 5599; DB 22; Length 1063;

ilarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Conservative 0;

AGCCLALTLFQSLGIPSEPPFSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

AGCCLALTLFQSLGIPSEPPFSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60

KYQDYVTEPNNAQVLEIAARDIEKLLNRSKALVSLAEAEKVQAHQWRDPSN 120

KYQDYVTEPNNAQVLEIAARDIEKLLNRSKALVSLAEAEKVQAHQWRDPSN 120

VYVNAKDDLPEKNSPGRQIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180

VYVNAKDDLPEKNSPGRQIKPVFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180

LNWTSALDVEFKKREDDPSLLWVFGSAGLARYYPASPWVNSRTPNKIDLYDVR 240

LNWTSALDVEFKKREDDPSLLWVFGSAGLARYYPASPWVNSRTPNKIDLYDVR 240

WYTOGAASPKDMLTLVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVSFNSNAQ 300

WYTOGAASPKDMLTLVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVSFNSNAQ 300

CFQHLVQANVRNKKVLDVANNITAKGTDYKGFSPAFQOLLNYSRANCKIIML 360

CFQHLVQANVRNKKVLDVANNITAKGTDYKGFSPAFQOLLNYSRANCKIIML 360

DGGERAQEIPFNKNDKKVRFVSGQHNYERGPQWMAKCNKGYIPIPSIGAIR 420

DGGERAQEIPFNKNDKKVRFVSGQHNYERGPQWMAKCNKGYIPIPSIGAIR 420

TQEYLDVLRPMVLGAKQVQNTNVDLDELGLVITGLTPFNITGQFENKTNLK 480

TQEYLDVLRPMVLGAKQVQNTNVDLDELGLVITGLTPFNITGQFENKTNLK 480

QLILGVMGVDSLEDKRLTPRTCPNGYYFAIDPNGVLLHPNLQPNKPSQBPVTL 540

QLILGVMGVDSLEDKRLTPRTCPNGYYFAIDPNGVLLHPNLQPNKPSQBPVTL 540

LDALENDIKVEIRNKMIDSGSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600

LDALENDIKVEIRNKMIDSGSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600

NLPTVSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFTIAPROYCNDLKI 660

NLPTVSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFTIAPROYCNDLKI 660

601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFTIAPROYCNDLKI 660

661 SDNNTFELLNMFNEFIDRKTPNPNPSCNADLINRVLLDAGFTNQLVNTYWSKQKNI 661

661 SDNNTFELLNMFNEFIDRKTPNPNPSCNADLINRVLLDAGFTNQLVNTYWSKQKNI 661

721 FVVTGGITRIVYKAGENQENPETTEDSFYKESLNDNVDVFTAPYFNKSGPG 721

721 FVVTGGITRIVYKAGENQENPETTEDSFYKESLNDNVDVFTAPYFNKSGPG 721

781 MVSXAVEIYQGLLKPAVVGKIDVNSWIENFTKTSIRDPACGVPDCCKNSD 781

781 MVSXAVEIYQGLLKPAVVGKIDVNSWIENFTKTSIRDPACGVPDCCKNSD 781

841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSSLRHLVNI SVAFNKSVDYQSVCEP 841

841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSSLRHLVNI SVAFNKSVDYQSVCEP 841

901 GAGHSAYVPSVADILQIGWATAAANSILQOFLLSLTFFPELLRAVEMEDDDFT 901

901 GAGHSAYVPSVADILQIGWATAAANSILQOFLLSLTFFPELLRAVEMEDDDFT 901

961 SCITEQTYQYFFDNDKSKFSFVGLDCGNCRSRI FHGKLMNTNLI FIMVESKGTCP 961

961 SCITEQTYQYFFDNDKSKFSFVGLDCGNCRSRI FHGKLMNTNLI FIMVESKGTCP 961

1021 QAEQTSQYQYFFDNDKSKFSFVGLDCGNCRSRI FHGKLMNTNLI FIMVESKGTCP 1021

1021 QAEQTSQYQYFFDNDKSKFSFVGLDCGNCRSRI FHGKLMNTNLI FIMVESKGTCP 1021

RESULT 2

AAB62258

ID AAB62258 standard; Protein; 1063 AA.

AC AAB62258;

DT 11-JUN-2001 (first entry)

Porcine calcium channel alpha2delta subunit.

Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co nervous system disorder, pain; epilepsy; anxiety; pig.

Sus scrofa.

WO200120336-A2.

22-MAR-2001.

18-SEP-2000; 2000WO-EP09136.

16-SEP-1999; 99US-0397549.

(WARN) WARNER LAMBERT CO.

Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N

WPI; 2001-257902/26.

N-PSDB; AAF57562.

Competitive binding assay for screening ligands which bind a ce cortical voltage-dependent calcium channel alpha2delta-1 subun where the ligands identified are useful for treating disorders nervous system, including pain -

Claim 8; Page 135-139; 158pp; English.

The invention relates to a new method for screening ligands wh cerebral cortical voltage-dependent calcium channel alpha2delta preferably alpha2delta-1 subunit. The method comprises contacti secreted soluble recombinant alpha2delta-1 subunit with a ligan

XX	AAB10576;	
XX	22-DEC-2000 (first entry)	
XX	Human calcium channel alpha-2 subunit protein.	
XX	Human; calcium channel; calcium channel subunit; diagnosis;	
XX	Lambert Eaton Syndrome; calcium channel subunit alpha-2.	
XX	Homo sapiens.	
XX	US6096514-A.	
XX	01-AUG-2000.	
XX	25-MAY-1995; 95US-0450562.	
XX	04-APR-1988; 88US-0176899.	
XX	02-FEB-1990; 90US-0482384.	
XX	08-NOV-1990; 90US-0603751.	
XX	30-NOV-1990; 90US-0620250.	
XX	15-AUG-1991; 91US-0745206.	
XX	10-APR-1992; 92US-0868354.	
XX	13-JUL-1993; 92US-0914231.	
XX	11-AUG-1993; 93US-0105536.	
XX	05-NOV-1993; 93US-0149097.	
XX	07-FEB-1994; 94US-0193078.	
XX	04-APR-1994; 94US-0223305.	
XX	11-AUG-1994; 94US-0290012.	
XX	23-SEP-1994; 94US-0311363.	
XX	28-SEP-1994; 94US-0314083.	
XX	07-NOV-1994; 94US-0336257.	
XX	13-MAR-1995; 95US-0404950.	
XX	(SIBI-) SIBIA NEUROSCIENCES INC.	
XX	Ellis SB, Williams ME, McCue AF, Harpold MM;	
XX	WPI; 2000-548230/50.	
XX	N-PSDB; AAA71707.	
XX	Human calcium channel beta subunit polynucleotides, useful for	
XX	producing recombinant eukaryotic cells and for diagnosing Lambert	
XX	Syndrome	
XX	Example IV, Column 135-144; 153pp; English.	
XX	This invention describes a novel isolated DNA molecule (I) compo	
XX	sequence encoding a beta3-1 subunit of a human calcium channel.	
XX	Nucleic acid probes comprising 14-30 contiguous nucleotides of	
XX	beta 3 subunit encoding DNA are useful for isolation and cloning	
XX	calcium channel subunit-encoding DNA. Recombinant eukaryotic cel	
XX	express heterologous calcium channel are useful for identifying	
XX	that modulate calcium channel activity and in assays for identifi	
XX	agonists and antagonists of calcium channel activity in humans.	
XX	calcium channel subunit or eukaryotic cells expressing the chan	
XX	useful for diagnosing Lambert Eaton Syndrome (LES) in a human.	
XX	sequence represents the human calcium channel alpha-2 subunit w	
XX	described in the method of the invention.	
XX	Sequence 1091 AA;	
XX	Query Match 100.0%; Score 5599; DB 21; Length 1091;	
XX	Best Local Similarity 100.0%; Pred. No. 0;	
XX	Matches 1063; Conservative 0; Mismatches 0; Indels 0;	
QY	1 MAAGCIALTLTLFQSLLIGPSEPPFSAVTKSWDKMQEDLVTLAKTASGV	
DB	1 MAAGCIALTLTLFQSLLIGPSEPPFSAVTKSWDKMQEDLVTLAKTASGV	
QY	61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAQAHQW	

YQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKQAAHQRWEDFASN 120
 YNAKDDLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
 YNAKDDLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
 NWTSDALDEVFKONREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
 NWTSDALDEVFKONREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
 YIOGAASPKOMLILVDVSGVSGLTLLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 YIOGAASPKOMLILVDVSGVSGLTLLKIRTSVSEMLETSDDDFVNVSFNSNAQD 300
 FOHLVQANVRNKVLDKAVNNITAGITDYKKGFSFAFEOLLNVNVRANCKNKLML 360
 FOHLVQANVRNKVLDKAVNNITAGITDYKKGFSFAFEOLLNVNVRANCKNKLML 360
 GGERAQEIEFNKYNKKVRVFRFSVQGHYERGPQIMACENKGYIYEIPSGAIR 420
 GGERAQEIEFNKYNKKVRVFRFSVQGHYERGPQIMACENKGYIYEIPSGAIR 420
 QEYLDVLRPMVLADGAKAQVNTNVDLDALEGLVITGTLPVENITQGFENKTNLK 480
 QEYLDVLRPMVLADGAKAQVNTNVDLDALEGLVITGTLPVENITQGFENKTNLK 480
 ILVGMGVDSVLEDKRLTPRTLLCPNGYYPALDPNGVYVLLHPNLQPKNPKSQEPVIL 540
 ILVGMGVDSVLEDKRLTPRTLLCPNGYYPALDPNGVYVLLHPNLQPKNPKSQEPVIL 540
 DAELENDIKVEIRNKMDIGSEKFTFLVKSQDERVIDKGNRTYTWTVPNGTDSL 600
 DAELENDIKVEIRNKMDIGSEKFTFLVKSQDERVIDKGNRTYTWTVPNGTDSL 600
 LPTSYFYIKAKLRETTQARSKGKMKDSTLKPDPNFEESGYTFIAPRDYCNLDKI 660
 LPTSYFYIKAKLRETTQARSKGKMKDSTLKPDPNFEESGYTFIAPRDYCNLDKI 660
 NTEFLANFNEFIDRKTNNPCNADLINRVLLDAGFTNELVQNTWASKQNKIKGVKAR 720
 NTEFLANFNEFIDRKTNNPCNADLINRVLLDAGFTNELVQNTWASKQNKIKGVKAR 720
 TDGGITRYYPKEAGENWQENPETYEDSFYKESLDNDNVFTAPYFNKSGPGAYESGI 780
 TDGGITRYYPKEAGENWQENPETYEDSFYKESLDNDNVFTAPYFNKSGPGAYESGI 780
 KAVRIYIOGKLIKPAVYGIKIDVNSWIENFTKTSIRDPKAGPVCCKKNSDVMDCVI 840
 KAVRIYIOGKLIKPAVYGIKIDVNSWIENFTKTSIRDPKAGPVCCKKNSDVMDCVI 840
 QGFLIMANHDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSXYDQSVCEFGAAPKQ 900
 QGFLIMANHDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSXYDQSVCEFGAAPKQ 900
 HRSAYVPSVADILQIGWATAAANSILOQFLSLTFFPRLLAEVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGWATAAANSILOQFLSLTFFPRLLAEVEMEDDDFTASLSKQ 960
 TEQTYQFFDNDKSPGVLDCGNCRI FHGEKLMNTNLI FIMVSKSGTCCPCTRLLI 1020
 TEQTYQFFDNDKSPGVLDCGNCRI FHGEKLMNTNLI FIMVSKSGTCCPCTRLLI 1020

undard; Protein; 1091 AA.

DT 04-JUL-2001 (first entry)
 XX Human secreted soluble alpha2delta calcium channel subunit #15 p
 DE Human; secreted calcium channel alpha2delta subunit; alpha2delta
 XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;
 KW gabapentin; scintillation proximity assay; SPA; nickel flashplat
 KW filter binding assay; wheat germ lectin flashplate assay.
 XX Homo sapiens.
 OS

XX WO200119870-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09137.

XX 16-SEP-1999; 99US-0397550.

XX (WARN) WARNER LAMBERT CO.

XX Brown JP, Bertelli F;

XX WPI; 2001-235262/24.

XX N-PSDB; AAS01426.

XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 PT Flashplate assays, Nickel Flashplate assays, Filter binding ass
 PT Wheat Germ Lectin Flashplate assays -
 XX Claim 30; Page 141-144; 160pp; English.

XX The present sequence represents human secreted calcium channel
 CC alpha2delta subunit #15 which is soluble and retains the funcitc
 CC characteristics of the full length or wild type alpha2delta subu
 CC (AAU01025) from which it is derived. The invention relates to tr
 CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble pr
 CC which retain their affinity for radioactively labelled gabapenti
 CC alpha2delta subunit is 1 of the components of the heteromultimer
 CC voltage-dependent calcium channel (VDCC) complexes present in ne
 CC and non-neuronal tissues including heart and skeletal muscle. N
 CC soluble forms of the human calcium channel alpha2delta subunits
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of
 CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031)
 CC described. The secreted soluble alpha2delta subunit may be used
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel fla
 CC filter binding or wheat germ lectin flashplate assays to detect
 CC measure the binding or interaction of a ligand (e.g. gabapentin,
 CC L-Norleucine, L-Allo-isoleucine, L-methionine, L-Leucine, L-Iso
 CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
 CC alpha2delta subunit.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 22; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1063; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MAAGCLIALTLTIFQSLIGPSSEEPSPSAVTIKSWDKMQEDLVTLAKTASGV
 Db 1 MAAGCLIALTLTIFQSLIGPSSEEPSPSAVTIKSWDKMQEDLVTLAKTASGV

Qy 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKQAAHQR
 Db 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKQAAHQR

Qy 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEC
 Db 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEC

Qy 181 NELNWTSDALDEVFKONREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKID
 Db 181 NELNWTSDALDEVFKONREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKID

IQGAASPKDMLILVDVSGVSGLTALKLIRTSVSEMLETSLDDDFNVASFNSAQD 300
 IQGAASPKDMLILVDVSGVSGLTALKLIRTSVSEMLETSLDDDFNVASFNSAQD 300
 QHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCNKIIML 360
 QHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCNKIIML 360
 GEERAQELFNKYNKDKKVRVRFVSVOGHNVYERGPIQWMAKCNKGYIPEISGAIR 420
 GEERAQELFNKYNKDKKVRVRFVSVOGHNVYERGPIQWMAKCNKGYIPEISGAIR 420
 EYLDVLRGPMVLADGKAKQVQWNTVYLDALGLVITGLTFVFNITGQFENKTNLK 480
 EYLDVLRGPMVLADGKAKQVQWNTVYLDALGLVITGLTFVFNITGQFENKTNLK 480
 LGVMGVDSLSBDIKRLTPRFTLCPNGYYFAIDPNQVLLHPNLQPNKPSQEPVTL 540
 LGVMGVDSLSBDIKRLTPRFTLCPNGYYFAIDPNQVLLHPNLQPNKPSQEPVTL 540
 AELNDIKVEIRNMKIDGESGKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 AELNDIKVEIRNMKIDGESGKTRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 PTYGFYIYKAKLEETITQARSKGKWKDSETLKPDNFEEGYTFIAPRDYCNLKI 660
 PTYGFYIYKAKLEETITQARSKGKWKDSETLKPDNFEEGYTFIAPRDYCNLKI 660
 TEFLNFNEFDTRKTPNPNPCNADLINRVLDAGFTNELVQVNSKQKNIKGVKAR 720
 TEFLNFNEFDTRKTPNPNPCNADLINRVLDAGFTNELVQVNSKQKNIKGVKAR 720
 TGGITRVYPKAGENQWQNPETYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 TGGITRVYPKAGENQWQNPETYDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 JAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
 JAVEIYIQGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
 XGPLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SYVAFNKSVDYQSVCEPGAAPKQ 900
 XGPLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SYVAFNKSVDYQSVCEPGAAPKQ 900
 IRSAYVPSVADIIQIGWATAAASIIQQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 IRSAYVPSVADIIQIGWATAAASIIQQFLLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 TQTOYFFDNDSSKFSFGLDCGNCRIFFHGEKLMNTNLIPIFIMVESKGTCPDTRLLI 1020
 TQTOYFFDNDSSKFSFGLDCGNCRIFFHGEKLMNTNLIPIFIMVESKGTCPDTRLLI 1020
 JTSDBGNPDGMVQPRYKGPVDFDNNVLEDYTDCCGVS 1063
 JTSDBGNPDGMVQPRYKGPVDFDNNVLEDYTDCCGVS 1063

idard; Protein; 1091 AA.

(first entry)

ium channel alpha2delta subunit.

nel alpha2delta subunit; alpha2delta-1; cerebral cortex;
 em disorder; pain; epilepsy; anxiety; pig.

PN WO200120336-A2.
 XX 22-MAR-2001.
 XX 18-SEP-2000; 2000MO-EP09136.
 XX 16-SEP-1999; 99US-0397549.
 XX (WARN) WARNER LAMBERT CO.
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS.
 XX WPI; 2001-257902/26.
 XX N-PSDB; AAP57563.
 XX Competitive binding assay for screening ligands which bind a cer
 XX tical voltage-dependent calcium channel alpha2-delta-1 subunit
 XX where the ligands identified are useful for treating disorders o
 XX nervous system, including pain -
 XX Claim 7; Page 139-142; 158pp; English.
 XX The invention relates to a new method for screening ligands whi
 XX cerebrol cortical voltage-dependent calcium channel alpha2delta
 XX preferably alpha2delta-1 subunit. The method comprises contactin
 XX secreted soluble recombinant alpha2delta-1 subunit with a ligand
 XX interest and a labelled compound which binds the subunit, follow
 XX measuring the level of binding of the labelled compound to alpha
 XX subunit. The method is useful for screening ligands, preferably
 XX biologically active products that modulate a nervous system func
 XX which bind a cerebrol cortical voltage-dependent calcium channel
 XX alpha2delta-1 subunit. The ligands identified by the method are
 XX for treating disorders of the nervous system, including pain, ep
 XX and anxiety. The present sequence represents a porcine calcium c
 XX alpha2delta subunit.
 XX Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 22; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1063; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLIALTLTFLQSLIGPSSEPPSPSAVTIKSWVDKQEDLVTLAKTAGSVN
 DB 1 MAAGCLIALTLTFLQSLIGPSSEPPSPSAVTIKSWVDKQEDLVTLAKTAGSVN
 QY 61 YEKYQDLYTVENPNARQLVEIAARDIEKLSNRKALVSLAEAKVQAAHQWRE
 DB 61 YEKYQDLYTVENPNARQLVEIAARDIEKLSNRKALVSLAEAKVQAAHQWRE
 QY 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHIFTDIYEG
 DB 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHIFTDIYEG
 QY 181 NELNWTLSALDEVFKKRRDEPSLLMQVFGSATGLARYYPASPWNRSRPNKIDL
 DB 181 NELNWTLSALDEVFKKRRDEPSLLMQVFGSATGLARYYPASPWNRSRPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTALKLIRTSVSEMLETSLDDDFNVASFN
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTALKLIRTSVSEMLETSLDDDFNVASFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCN
 DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFEQLLNNVSRANCN
 QY 361 FTDGGEERAQELFNKYNKDKKVRVRFVSVOGHNVYERGPIQWMAKCNKGYIPEIS
 DB 361 FTDGGEERAQELFNKYNKDKKVRVRFVSVOGHNVYERGPIQWMAKCNKGYIPEIS
 QY 421 INTQEYLDVLRGPMVLADGKAKQVQWNTVYLDALGLVITGLTFVFNITGQFEN
 DB 421 INTQEYLDVLRGPMVLADGKAKQVQWNTVYLDALGLVITGLTFVFNITGQFEN

ILGVMGVDSLEDEKRLTPRTLLCPNGYVFAIDPENGVLHPNLPKNPKSQBPVTL 540
 ILGVMGVDSLEDEKRLTPRTLLCPNGYVFAIDPENGVLHPNLPKNPKSQBPVTL 540
 DAELENDIKVEIRNKMIDGESGKTRTLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 DAELENDIKVEIRNKMIDGESGKTRTLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 LPTYSFYIKAKLETTIQAARKKGMKDSITLKPDMFEESGYTFIAPROYCNDLKI 660
 LPTYSFYIKAKLETTIQAARKKGMKDSITLKPDMFEESGYTFIAPROYCNDLKI 660
 NTEFLNFNEFIDKTPNPNPCNADLINRVLLDAGFTNELVQWWSQKNIKGVYKAR 720
 NTEFLNFNEFIDKTPNPNPCNADLINRVLLDAGFTNELVQWWSQKNIKGVYKAR 720
 TDGGITRYVPKEAGENWQENPETYEDSPYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780
 TDGGITRYVPKEAGENWQENPETYEDSPYKRSNDNDNYVFTAPYFNKSGPGAYESGI 780
 KAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVCDCKRNSDVMDCVI 840
 QGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSXDYQSVCEPGAAPKQ 900
 QGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSXDYQSVCEPGAAPKQ 900
 HRSAYVPSVADITQIGWATAAASILQOFLLSLTPPRLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADITQIGWATAAASILQOFLLSLTPPRLLEAVEMEDDDFTASLSKQ 960
 TEOTQYFFDNDKSPGVLDCGNCRSRI FHGEKLMNTNLI FTWVSKGTCPCDTRLLI 1020
 TEOTQYFFDNDKSPGVLDCGNCRSRI FHGEKLMNTNLI FTWVSKGTCPCDTRLLI 1020
 QTSQGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
 QTSQGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063

undard; Protein; 1091 AA.

(first entry)

um channel alpha 2b subunit protein.

um channel protein; therapeutic; autoimmune disease;
 Lambert Eaton Syndrome; alpha 2b subunit.

95US-0450272.

89WO-0501408.

90US-0603751.

92US-0914231.

90US-0482384.

90US-0620250.

91US-0745206.

92WO-0506903.

93US-0105536.

93US-0149097.

94US-0193078.

23-SEP-1994; 94US-0311363.
 07-NOV-1994; 94US-0336257.
 15-FEB-1995; 95US-0404354.
 XX (MERI) MERCK & CO INC.
 PA Harpold MM, Ellis SB, Williams ME, McCue AF;
 PI N-PSDB; AAD39959.
 DR WPI; 2002-470318/50.
 DR N-PSDB; AAD39959.
 XX Eukaryotic cells expressing a functional heterologous human calc
 PT channel and encoding nucleic acid isolated from human cerebellum
 PT drug design and to diagnose Lambert Eaton Syndrome -
 XX Disclosure; Column 137-144; 154pp; English.
 XX The present invention relates to novel human calcium channel prc
 CC and polynucleotides encoding such proteins. The invention also i
 CC to eukaryotic cells expressing a functional heterologous human c
 CC channel alpha 1, alpha 2, beta and gamma subunits. The eukaryoti
 CC are useful for screening for potential calcium channel antagonis
 CC agonists to select compounds that have potential as disease or t
 CC specific therapeutic agents. The subunits may be used in diagno
 CC assays for the autoimmune disease Lambert Eaton Syndrome. The pr
 CC sequence is human calcium channel alpha 2b subunit protein.
 XX Sequence 1091 AA;

Query Match 100.0%; Score 5599; DB 23; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1063; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MAAGCLLALTLTIFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGV
 Db 1 MAAGCLLALTLTIFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGV
 Qy 61 YEKYQDLYTVEPNARQVIAARDIEKLLSNRSKALVSLALEAEKQVAAHOMRI
 Db 61 YEKYQDLYTVEPNARQVIAARDIEKLLSNRSKALVSLALEAEKQVAAHOMRI
 Qy 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROI SYQHAHVHIPTDIYEK
 Db 121 EVVYNAKDDLDPEKNDSEPGSRIKPVFIEDANFGROI SYQHAHVHIPTDIYEK
 Qy 181 NELNWTSALEDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTENKIDI
 Db 181 NELNWTSALEDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTENKIDI
 Qy 241 RPWYIQGAASPQDMILIVDSVSGSVSGITLKLIRTSVSEMLETSLDDDFVNVASPI
 Db 241 RPWYIQGAASPQDMILIVDSVSGSVSGITLKLIRTSVSEMLETSLDDDFVNVASPI
 Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSAFEQLNNTVNSRANCI
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSAFEQLNNTVNSRANCI
 Qy 361 FTDCGEERAQEI FNKYNKDKKRVFRFSVQHNHYERGP IQMMACENKGYEYIEP
 Db 361 FTDCGEERAQEI FNKYNKDKKRVFRFSVQHNHYERGP IQMMACENKGYEYIEP
 Qy 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFEN
 Db 421 INTOEYLDVLGRPMVLADGKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFEN
 Qy 481 NQLILGVMGVDVSLDIKRLTPRTLLCPNGYVFAIDPENGVLHPNLPKNPKSQ
 Db 481 NQLILGVMGVDVSLDIKRLTPRTLLCPNGYVFAIDPENGVLHPNLPKNPKSQ
 Qy 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSQDERVIDKGNRTYTWTPVNM
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKTRTLVKSQDERVIDKGNRTYTWTPVNM

PTYSFYIKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
 PTYSFYIKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYCNDLKI 660
 TEFLINFEFIDRKTTPNNPSCNADLINRVLLDAGFTNVLQVYNSKQNIKGVKAR 720
 TEFLINFEFIDRKTTPNNPSCNADLINRVLLDAGFTNVLQVYNSKQNIKGVKAR 720
 TGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSPGAYESGI 780
 TGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSPGAYESGI 780
 JAVEIYIQGLKLPAAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
 JAVEIYIQGLKLPAAVVGKIDVNSWIEFTKTSIRDPKAGPVCDCRNSDVMDCVI 840
 JQFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SYAFNKSIDYQSVCEPGAAPKQ 900
 JQFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SYAFNKSIDYQSVCEPGAAPKQ 900
 RSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
 RSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLEAVEMEDDDFTASLSKQ 960
 TQTOYFFDNDSKSFSGVLDGCGNCSRI FHGEKLMNTNLIFIMVBSKGTCPCDTRLII 1020
 TQTOYFFDNDSKSFSGVLDGCGNCSRI FHGEKLMNTNLIFIMVBSKGTCPCDTRLII 1020
 YTSQGNPCDMVKQRYRKGPDVCFDNNVLEDTDCGGVS 1063
 YTSQGNPCDMVKQRYRKGPDVCFDNNVLEDTDCGGVS 1063

idard; Protein; 1091 AA.

(first entry)

a channel a2d subunit.

tel; human; central nervous system disorder;
 1 syndrome; diagnosis; therapy.

97WO-US16146.

96US-0713118.

ICAN HOME PROD CORP.

rancio R, Shuey DJ;

7325/18.
 9060.

human neuronal calcium channel subunit(s) - useful for
 and treatment of central nervous system disorders, e.g.
 n syndrome

Fig 2; 89pp; English.

tide comprises the a2d subunit of the human neuronal
 nel. cDNA clones (see AAW29059-61) encoding the a1b
 AAW37878), the a2d subunit and a b3 subunit (see AAW37880)
 olated. These have been inserted into expression

CC vectors and are stably expressed in transformed cell lines. The
 CC transformed cells show omega-conotoxin GVIA binding activity,
 CC and omega-conotoxin GVIA toxin induced potassium-stimulated
 CC calcium uptake, indicating that the proteins expressed by the
 CC clones are capable of forming a functioning calcium channel.
 CC Nucleic acids encoding the 3 subunits, as well as vectors, host
 CC cells and methods of isolating nucleic acids encoding related
 CC calcium channels are disclosed. Fusion proteins incorporating
 CC subunit proteins, antibodies, and assays for identifying agents
 CC that modulate calcium channel activity are also provided. Such
 CC agents can be used to treat certain central nervous system
 CC disorders by altering calcium channel activity. Methods of
 CC diagnosing diseases associated with particular calcium channels,
 CC such as Lambert-Eaton syndrome, are disclosed.

XX Sequence 1091 AA;

Query Match 99.9%; Score 5595; DB 19; Length 1091;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 1; Indels 0;

QY 1 MAAGCLLALTTLTFLQSLLIGPSSEPPFSAVTIKSWVDKMQEDLVLTAKTASGVN
 Db 1 MAAGCLLALTTLTFLQSLLIGPSSEPPFSAVTIKSWVDKMQEDLVLTAKTASGVN
 QY 61 YEKYQDLTYTVEPNNAQVETIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
 Db 61 YEKYQDLTYTVEPNNAQVETIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
 QY 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
 Db 121 EYVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
 QY 181 NELNMTSALDEVFKKNREDDPSILLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 Db 181 NELNMTSALDEVFKKNREDDPSILLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTIRTSVSEMLETISDDDFVNVASFN
 Db 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTIRTSVSEMLETISDDDFVNVASFN
 QY 301 VSCFQHLVQANVRNKKVADAVNNITAKGITDYKKGFSFAFQOLLNINVSANCN
 Db 301 VSCFQHLVQANVRNKKVADAVNNITAKGITDYKKGFSFAFQOLLNINVSANCN
 QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQHNRYERGP IQMACENKGYIYEIPS
 Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQHNRYERGP IQMACENKGYIYEIPS
 QY 421 INTQEYLDVLRPMVLGAKAKQVQWNTNVLDALELGLVITGTLPVFNITGQFEN
 Db 421 INTQEYLDVLRPMVLGAKAKQVQWNTNVLDALELGLVITGTLPVFNITGQFEN
 QY 481 NQILGVMGVDVLSLEDIKRLTPRTFLCPNGYYPFAIDPNGYVLLHPLNLPKNPKSC
 Db 481 NQILGVMGVDVLSLEDIKRLTPRTFLCPNGYYPFAIDPNGYVLLHPLNLPKNPKSC
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNG
 Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPYVSFYIYKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYIC
 Db 601 ALVLPYVSFYIYKAKLEETITQARSKGKMDSETLKPDNFEESGYTFIAPRDYIC
 QY 661 SDNNTFLLNFNEFIDRKTTPNNPSCNADLINRVLLDAGFTNVLQVYNSKQNIK
 Db 661 SDNNTFLLNFNEFIDRKTTPNNPSCNADLINRVLLDAGFTNVLQVYNSKQNIK
 QY 721 FVYTDGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSGPGP
 Db 721 FVYTDGGITRVYPKEAGENWQENPETEYDSFYKRSIDNDNVYFTAPYFNKSGPGP

KAVEIYQGLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840
 KAVEIYQGLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840
 GGFLLMANHDDYTQIGRFFGEIDPDLNRHLVNI SVYAFNKSVDYQSVCEPAAAPKQ 900
 GGFLLMANHDDYTQIGRFFGEIDPDLNRHLVNI SVYAFNKSVDYQSVCEPAAAPKQ 900
 HRSAYVSVADILQIGWATAAANSILOOFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
 HRSAYVSVADILQIGWATAAANSILOOFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
 TEQTYQFFDNDSKFSFVLDGNCNSRI FHGEKLMNTNLI FIMVSKGTCPCDTRLLI 1020
 TEQTYQFFDNDSKFSFVLDGNCNSRI FHGEKLMNTNLI FIMVSKGTCPCDTRLLI 1020
 QTSQGNPCDMVKQPRYKGPDPVCPDNNVLEDDYTDGCGVS 1063
 QTSQGNPCDMVKQPRYKGPDPVCPDNNVLEDDYTDGCGVS 1063

ndard; Protein; 1091 AA.

(updated)
 (first entry)

the alpha 2 human calcium channel subunit.

um channel subunit; diagnosis; agonist; antagonist;
 n syndrome.

;

..

; 92WO-US06903.

; 91US-0745206.

; 92US-0868354.

(INST BIOTECHNOLOGY IND ASSOC.

; Ellis SB, Feldman DH, Harpold MM, McCue AF;

33936/11.
 37821.

; specific human calcium channel sub-units - used for
 calcium channel agonists and antagonists and
 Lambert Eaton syndrome

Page 134-138; 150pp; English.

; a human neuronal calcium channel alpha 2 subunit was
 am a human genomic DNA library probed under low and high
 conditions with a fragment of DNA encoding the rabbit
 scle calcium channel alpha 2 subunit. The fragment
 cletides having a sequence corresponding to the
 sequence between nucleotides 43 and 272 inclusive of
 skeletal muscle calcium channel alpha 2 subunit cDNA.
 s identified splice variants of the human calcium alpha
 ranscript. In particularly preferred embodiments, the
 g the alpha 2 subunit is produced by alternative
 of a primary transcript that includes DNA encoding the
 set forth in AAR3353 and the DNA of AAQ37823 inserted
 leotides 1624 and 1625 of AAQ37821.

CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1091 AA;
 Query Match 99.9%; Score 5593; DB 14; Length 1091;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1062; Conservative 0; Mismatches 1; Indels 0;
 QY 1 MAAGC LALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGV
 DB 1 MAAGC LALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGV
 QY 61 YEKYQDLYTVENPNARQLVEIAARDIEKLSNRSKALVSLAEAEKQAAHQRRI
 DB 61 YEKYQDLYTVENPNARQLVEIAARDIEKLSNRSKALVSLAEAEKQAAHQRRI
 QY 121 EVVYNAKDLDEPKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIYEK
 DB 121 EVVYNAKDLDEPKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIYEK
 QY 181 NELNWT SALDEVFKQNRREEDPSLLMQVFGSATGLARYYPASPWVDSNRTNPKIDI
 DB 181 NELNWT SALDEVFKQNRREEDPSLLMQVFGSATGLARYYPASPWVDSNRTNPKIDI
 QY 241 RPWYIQGAASPOMLILVDVSGSVSGLTLLKIRTSVSEMLETSLDDDFVNVASFI
 DB 241 RPWYIQGAASPOMLILVDVSGSVSGLTLLKIRTSVSEMLETSLDDDFVNVASFI
 QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQQLNTNVSRANCI
 DB 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQQLNTNVSRANCI
 QY 361 FTDGGEERAQEI FNKYNKDKKVRVFRFSVQGNHYERGP IOMMACENKGYEYIEIP
 DB 361 FTDGGEERAQEI FNKYNKDKKVRVFRFSVQGNHYERGP IOMMACENKGYEYIEIP
 QY 421 INTOEYLDVLGRPMVLADGKAKQVQNTNVYLDALGLVITGTLPVFNITQGFEEI
 DB 421 INTOEYLDVLGRPMVLADGKAKQVQNTNVYLDALGLVITGTLPVFNITQGFEEI
 QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLQPKNPKSI
 DB 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYFFAIDPNGYVLLHPNLQPKNPKSI
 QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYVTTVPVN
 DB 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYVTTVPVN
 QY 601 ALVLPYTSFYIYKAKLBETITQARKSKGKMDKSETLKPDPNFEESGYTFIAPRDY
 DB 601 ALVLPYTSFYIYKAKLBETITQARKSKGKMDKSETLKPDPNFEESGYTFIAPRDY
 QY 661 SDNNTFELNFEFTDRKTPNNPCNADLINRVLLDAGFTNELYQVYWSKQKNI
 DB 661 SDNNTFELNFEFTDRKTPNNPCNADLINRVLLDAGFTNELYQVYWSKQKNI
 QY 721 FVWTDGGITRVYPKEAGENWOENPETYEDSFYKSLDNDNVYVTFAPYFNKSGPG
 DB 721 FVWTDGGITRVYPKEAGENWOENPETYEDSFYKSLDNDNVYVTFAPYFNKSGPG
 QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSD
 DB 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSD
 QY 841 LDDGGFLLMANHDDYTQIGRFFGEIDPDLNRHLVNI SVYAFNKSVDYQSVCEP
 DB 841 LDDGGFLLMANHDDYTQIGRFFGEIDPDLNRHLVNI SVYAFNKSVDYQSVCEP
 QY 901 GAGHRSAYVSVADILQIGWATAAANSILOOFLLSLTFPRLLLEAVEMEDDDFT
 DB 901 GAGHRSAYVSVADILQIGWATAAANSILOOFLLSLTFPRLLLEAVEMEDDDFT
 QY 961 SCITEQTYQFFDNDSKFSFVLDGNCNSRI FHGEKLMNTNLI FIMVSKGTCPC

|||||TQYFFNDKSFVGLDGCNCSIFHGEKLMNTLIFIMVESKGTCPDTRLLI 1020
 |||||TSDGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGVS 1063
 |||||TSDGNPCDMVKQPRYKGPVCFDNNVLEDTDCGGVS 1063

idard; Protein; 1110 AA.

(updated)
 (first entry)

n channel alpha-2 subunit.

ait; human; calcium channel; assay; detection;
 tion; Lambert Eaton Syndrome; LES; diagnosis.

95US-0455543.

94US-0223305.
 88US-0176899.
 89WO-US01408.
 90US-0482384.
 90US-0603751.
 90US-0620250.
 91US-0745206.

A NEUROSCIENCES INC.

Ellis SB, Feldman DH, Harpold MM, McCue AF;
 6192/39.
 2694.

human calcium channel alpha 1B subunit protein -
 ecombinant production of the channel for screening of
 rs, and diagnosis of Lambert Eaton Syndrome

Columns 131-138; 166pp; English.

sequence represents the alpha-2 subunit of a human calcium
 cium channels are membrane-spanning, multi-subunit proteins
 ontrolled entry of calcium ions into cells. This leads
 ation events required for muscle contraction. The recombinant
 n expressed with nucleic acids encoding the complete calcium
 be used in assays for the detection and characterisation of
 at modulate the channel. The DNA encoding the subunits can
 vely spliced when transcribed, giving more than one form of
 from the same transcript, each having slightly different
 In addition, the reactivity of the alpha 1 subunit with IgG
 om the serum of an individual with Lambert Eaton Syndrome
 used as a diagnostic for the disease.
 25-MAR-2003 to correct PR field.)

110 AA;
 .larity 99.7%; Score 5579.5; DB 19; Length 1110;
 .Conservative 98.2%; Pred.No. 0; Mismatches 0; Indels 19; Gaps 1;

AGCLLALTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

1 MAAGCLLALTTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVN
 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEG
 121 EYVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEG
 181 NELNWTSALEDVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 181 NELNWTSALEDVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETSLDDDDFVNVSFN
 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETSLDDDDFVNVSFN
 301 VSCFQHLVQANVRNKKVLDKADANNITAKGITYKKGFSPAFQOLLNINYSRANCN
 301 VSCFQHLVQANVRNKKVLDKADANNITAKGITYKKGFSPAFQOLLNINYSRANCN
 361 FTDGGEERAQELFNKYNKDKKVRVFRFVSQGHYBERGPIQWMACENKGYIYELPS
 361 FTDGGEERAQELFNKYNKDKKVRVFRFVSQGHYBERGPIQWMACENKGYIYELPS
 421 INTOEYLDVLGRPMVLADKAKQVQNTVYLDLELGLVITGTLPVFNITGQFEN
 421 INTOEYLDVLGRPMVLADKAKQVQNTVYLDLELGLVITGTLPVFNITGQFEN
 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNLOPK-----
 481 NQLILGVMGVDVLSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLNLOPKPIGVG
 531 -----NPKSOEPVTLDFDAELENDIKVEIRNMKIDGESGEKTRFLVKSC
 541 LRKRPNIQNPKSOEPVTLDFDAELENDIKVEIRNMKIDGESGEKTRFLVKSC
 582 DKGNRVTWTVPVNGTDYSLALVLTPTYSFYIKAKLBETITQARSKKGKMKDSETI
 601 DKGNRVTWTVPVNGTDYSLALVLTPTYSFYIKAKLBETITQARSKKGKMKDSETI
 642 EESGYTFIAPRDYCNDLKISDNNTEFLNFEHIDRKTNNPSCNADLINRVLLI
 661 EESGYTFIAPRDYCNDLKISDNNTEFLNFEHIDRKTNNPSCNADLINRVLLI
 702 ELVQNYWSKOKNKGKARFVVTDDGGITRVYPKEAGENWQENPETYEDSFYKRSI
 721 ELVQNYWSKOKNKGKARFVVTDDGGITRVYPKEAGENWQENPETYEDSFYKRSI
 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLKPAVVGIKIDVNSWIENFTKQ
 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLKPAVVGIKIDVNSWIENFTKQ
 822 CAGPVCCKNSDVMDCVILDDGFFLMAHDDYTQNGIFRFFGEIDPSLRHLV
 841 CAGPVCCKNSDVMDCVILDDGFFLMAHDDYTQNGIFRFFGEIDPSLRHLV
 882 FNKSYDYQSVCEPQAPKQAGHRSVVPVSADILQIGWATAAASILQOFLLS
 901 FNKSYDYQSVCEPQAPKQAGHRSVVPVSADILQIGWATAAASILQOFLLS
 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKSFSGVLDGCNCSRIFHGEKI
 961 LLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKSFSGVLDGCNCSRIFHGEKI
 1002 IFIMVESKGTCPDTRLLIQAOTSDGNPCDMVKQPRYKGPVCFDNNVLEDT
 1021 IFIMVESKGTCPDTRLLIQAOTSDGNPCDMVKQPRYKGPVCFDNNVLEDT
 1062 VS 1063
 |||

1082

ndard; Protein; 1086 AA.

(updated)
(first entry)

al calcium channel subunit alpha 2c.

nel subunit; antagonist; agonist; diagnosis;
n Syndrome.

94WO-US09230.

93US-0105536.

93US-0149097.

: INST BIOTECHNOLOGY IND ASSOC.

illeespie A, Harpold MM, Mecue AF, Williams MB;

0900/12.

4667.

human calcium channel sub-unit(s) - used for
rods. for studying calcium channels, e.g. for
ionists and antagonists

Page 237-242; 285pp; English.

al alpha 2 coding sequence (AAQ84664) transcript is
ly processed in skeletal muscle, aorta, and CNS in
:resp. to nt 1595-1942 of AAQ84664 in each of the
e alternatively spliced variant transcripts that differ
nce or absence of one to three different portions of
There are three sequences involved (see AAQ84664 FT
; PT), sequence 1, sequence 2 and sequence 3. The five
ding transcripts from the different tissues include
mbinations of the three sequences, except for one of
transcripts expressed in aorta which lacks all three
the five alpha 2 forms identified are (1) a form that
ice 3 called alpha 2a, expressed in skeletal muscle
; lacks sequence 1 called alpha 2b, expressed in CNS
; lacks sequences 1 and 2 called alpha 2c, expressed in
ie that lacks sequences 1, 2 and 3 called alpha 2d,
1 aorta and (5) one that lacks sequences 1 and 3
a 2e. The DNA and AA sequences of alpha 2a - alpha 2e
h in AAQ84666-Q84669 and AAR71012-R71015 respectively.
25-MAR-2003 to correct FN field.)

1086 AA;

99.3%; Score 5559.5; DB 16; Length 1086;

ilarity 99.5%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 5; Gaps 1;

AGCLLALTTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60

AGCLLALTTLFQSLIGPSSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60

KYQDLYTEPNNAARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120

Db 61 YEKYQDLYTEPNNAARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRE
Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIRKPVFIEDANFGRIQISYQHAHVHIPTDIYEG
Db 121 EVVYNAKDDLDPEKNDSEPGSQRIRKPVFIEDANFGRIQISYQHAHVHIPTDIYEG
Qy 181 NELNWTSAODEVPKCKNREEDPSLLMQVFGSATGLARIYYPASPWVDSRTPNKIDL
Db 181 NELNWTSAODEVPKCKNREEDPSLLMQVFGSATGLARIYYPASPWVDSRTPNKIDL
Qy 241 RPYIIOGAASPKDMLILVDVSGSVGLTLKLIIRTSVSEMLETLSDDDDFVNVASFN
Db 241 RPYIIOGAASPKDMLILVDVSGSVGLTLKLIIRTSVSEMLETLSDDDDFVNVASFN
Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKGFSAFQELLYNYSRANCK
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKGFSAFQELLYNYSRANCK
Qy 361 FTDGGERAQEI FNKNYKDKKVRFPFVSVQHNHYERGPIOMMACENKGYIYEIPE
Db 361 FTDGGERAQEI FNKNYKDKKVRFPFVSVQHNHYERGPIOMMACENKGYIYEIPE
Qy 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVLDALELGLVITGTLFVFNITGQFEN
Db 421 INTQEYLDVLGRPMVLADGKAKOVQNTNVLDALELGLVITGTLFVFNITGQFEN
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIFAIIDPNGVYLLHPNLOPNKPKS(
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYIFAIIDPNGVYLLHPNLOPK-----
Qy 541 DFLDAELENDIKVEIRNKNMIDGESGKFTPLVKSQDERYIDKGNRTYTTPVVK
Db 536 DFLDAELENDIKVEIRNKNMIDGESGKFTPLVKSQDERYIDKGNRTYTTPVVK
Qy 601 ALVLPYTSFYVIRAKLEETITQARSKIGKMKDSETLKPDNPFESGYTFIAPRDY(
Db 596 ALVLPYTSFYVIRAKLEETITQARSKIGKMKDSETLKPDNPFESGYTFIAPRDY(
Qy 661 SDNNTFLLNPFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
Db 656 SDNNTFLLNPFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
Qy 721 FVWTDGGITRVYPKEAGENQENPETYEDSFYKESLNDNDVFTAPYFNKSGPG(
Db 716 FVWTDGGITRVYPKEAGENQENPETYEDSFYKESLNDNDVFTAPYFNKSGPG(
Qy 781 MYSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSD
Db 776 MYSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSD
Qy 841 LDDGGFLLMANHDDYTQIGRPFGEIDPSLMRHLVNIISVAFNKSVDYQSVCEP
Db 836 LDDGGFLLMANHDDYTQIGRPFGEIDPSLMRHLVNIISVAFNKSVDYQSVCEP
Qy 901 GAGHRSVPSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFT.
Db 896 GAGHRSVPSVADILQIGMWATAAASILQOFLLSLTFPRLLEAVEMEDDDFT.
Qy 961 SCITEQITQYFFDNDKSPSGVLDGCGNCSRIIPHGEKLMNTNLIIFIMVESKGTCPCI
Db 956 SCITEQITQYFFDNDKSPSGVLDGCGNCSRIIPHGEKLMNTNLIIFIMVESKGTCPCI
Qy 1021 QAEQTSQDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
Db 1016 QAEQTSQDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1058

RESULT 13

AAW63153

ID AAW63153 standard; Protein; 1086 AA.

XX

AC AAW63153;

XX

(updated)
(first entry)

1 channel alpha-2c subunit.

ic; human; calcium channel; assay; detection;
:ion; Lambert Eaton Syndrome; LES; diagnosis.

95US-0455543.

94US-0223305.

88US-0176899.

89MO-US01408.

90US-0482384.

90US-0603751.

90US-0620250.

91US-0745206.

A NEUROSCIENCES INC.

Ellis SB, Feldman DH, Harpold MM, McCue AF;

6192/39.
2702.

human calcium channel alpha 1B sub-unit protein -
eombinant production of the channel for screening of
rs, and diagnosis of Lambert Eaton Syndrome

umns 293-300; 166pp; English.

sequence represents the alpha-2c subunit of a human calcium
cium channels are membrane-spanning, multi-subunit proteins
ontrolled entry of calcium ions into cells. This leads
ation events required for muscle contraction. The recombinant
n expressed with nucleic acids encoding the complete calcium
be used in assays for the detection and characterization of
at modulate the channel. The DNA encoding the subunits can
vely spliced when transcribed, giving more than one form of
from the same transcript, each having slightly different
In addition, the reactivity of the alpha 1 subunit with IgG
om the serum of an individual with Lambert Eaton Syndrome
used as a diagnostic for the disease.
25-MAR-2003 to correct PR field.)

086 AA;

99.3%; Score 5559.5; DB 19; Length 1086;

larity 99.5%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 5; Gaps 1;

GCLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKQEDLVTAKTAGYNQLVDI 60

GCLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKQEDLVTAKTAGYNQLVDI 60

QYDLTVTPNNARQIVEAARDIEKLNRSKALVSLALEAKVQAQHWEDFASN 120

QYDLTVTPNNARQIVEAARDIEKLNRSKALVSLALEAKVQAQHWEDFASN 120

YYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYSYQHAHVHPTDIYEGSTIVL 180

YYNAKDDLDPEKNDSEPSQRIKPVFIEDANFGROIYSYQHAHVHPTDIYEGSTIVL 180

ANWTSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASFWVDNSRTPNKIDLYDVR 240

ANWTSALDEVFKKKNREEDPSLLMQVFGSATGLARYYPASFWVDNSRTPNKIDLYDVR 240

241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLRISVSSEMLETLSDDDFVNVSFN
241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLRISVSSEMLETLSDDDFVNVSFN
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYKKGFSAFQOLLNYSRANCN
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYKKGFSAFQOLLNYSRANCN
361 FTDGGERAQEIFNKYNKKVKVRFPSVQGHYERGPQWMAKCNKGYEYIIPS
361 FTDGGERAQEIFNKYNKKVKVRFPSVQGHYERGPQWMAKCNKGYEYIIPS
421 INTQEYLDVLGRPMVLADKAKQVQWNTVYLDALGLVITGLTPVFNITQGFEN
421 INTQEYLDVLGRPMVLADKAKQVQWNTVYLDALGLVITGLTPVFNITQGFEN
481 NQLILGVNGVDVSLIEDIKELTPRFTLCPNGYYPADIPNGVYLLHPLNPKPKSQ
481 NQLILGVNGVDVSLIEDIKELTPRFTLCPNGYYPADIPNGVYLLHPLNPKPKSQ
541 DFLDASLENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
536 DFLDASLENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
601 ALVLPYSPFYIKAKLEETITQARSKKGMKQSETLKPDNFESGTYTPIAPRDYC
596 ALVLPYSPFYIKAKLEETITQARSKKGMKQSETLKPDNFESGTYTPIAPRDYC
661 SDNNTFLLNFNEFIDRKTPNPNPCNADLNRVLLDAGFTNELVQVWSKQKNIK
656 SDNNTFLLNFNEFIDRKTPNPNPCNADLNRVLLDAGFTNELVQVWSKQKNIK
721 FVYTDGGITRVYKPEAGENWQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPG
716 FVYTDGGITRVYKPEAGENWQENPETEYDSFYKRSILDNDNYVFTAPYFNKSGPG
781 MVSKEAVIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRPCAGPVCDCKRNSDI
776 MVSKEAVIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRPCAGPVCDCKRNSDI
841 LDGGLFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSXDYQSVCEPC
836 LDGGLFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSXDYQSVCEPC
901 GAGHSAYVPSVADIIQIGWATAAASIIQQFLLSLTPRLLLEAVEMEDDDFTI
896 GAGHSAYVPSVADIIQIGWATAAASIIQQFLLSLTPRLLLEAVEMEDDDFTI
961 SCITEQTYQYFFDNDKSPSGVLDCGNCSTRIFHGEKLMNTNLIIFIMVSKGTCPC
956 SCITEQTYQYFFDNDKSPSGVLDCGNCSTRIFHGEKLMNTNLIIFIMVSKGTCPC
1021 QAEQTSQGNPCDMVKQPRYKGPVDCFDNNVLEDYDTCGVS 1063
1016 QAEQTSQGNPCDMVKQPRYKGPVDCFDNNVLEDYDTCGVS 1058

RESULT 14

AAB10587

ID AAB10587 standard; Protein; 1086 AA.

XX AAB10587;

XX AC

XX 22-DEC-2000 (first entry)

XX Human calcium channel alpha-2c subunit protein.

XX Human; calcium channel; calcium channel subunit; diagnosis;

XX Lambert Eaton Syndrome; calcium channel subunit alpha-2c.

XX Homo sapiens.

XX

95US-0450562.

88US-0176899.
90US-0482384.
90US-0603751.
90US-0620250.
91US-0745206.
92US-0868354.
92US-0914231.
93US-0105536.
93US-0149097.
94US-0193078.
94US-0223305.
94US-0290012.
94US-0311363.
94US-0314083.
94US-0336257.
95US-0404950.

A NEUROSCIENCES INC.

illiams ME, McCue AF, Harpold WM;

8230/50.

1725.

m channel beta subunit polynucleotides, useful for
combinant eukaryotic cells and for diagnosing Lambert Eaton

Column 237-244; 153pp; English.

on describes a novel isolated DNA molecule (I) comprising a
oding a beta3-1 subunit of a human calcium channel.
probes comprising 14-30 contiguous nucleotides of
it encoding DNA are useful for isolation and cloning of
nel subunit-encoding DNA. Recombinant eukaryotic cells that
ologous calcium channel are useful for identifying compounds
e calcium channel activity and in assays for identifying
antagonists of calcium channel activity in humans. Human
nel subunit or eukaryotic cells expressing the channel are
diagnosing Lambert Eaton Syndrome (LES) in a human. This
resents the human calcium channel alpha-2c subunit which is
the method of the invention.

.086 AA;

.larity 99.3%; Score 5559.5; DB 21; Length 1086;

Conservative 0; Mismatches 0; Indels 5; Gaps 1;

AGLLALTTLFQSLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSNQVLVDI 60
|||
AGLLALTTLFQSLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSNQVLVDI 60
|||
CYODLYTVPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120
|||
CYODLYTVPNNARQLVEIAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120
|||
YYNAKDDLPKNDSPGSRQIKPVFIEDANFGROIYQAAVHPITDIYEGSTIVL 180
|||
YYNAKDDLPKNDSPGSRQIKPVFIEDANFGROIYQAAVHPITDIYEGSTIVL 180
|||
LWNTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASFPWVDNSRTPNKIDLYDVR 240
|||
LWNTSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASFPWVDNSRTPNKIDLYDVR 240
|||
WYIQGAASPKDMLILVDVSGVSLTLKLTIRTSVSEMLETLSDDDFVNVAASFN 300
|||

Db 241 RPWYIQGAASPKDMLILVDVSGVSLTLKLTIRTSVSEMLETLSDDDFVNVAASFN
Qy 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCN
Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCN
Qy 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGQHNRYERGP IQMMA CENKGYEYIIPS
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSGQHNRYERGP IQMMA CENKGYEYIIPS
Qy 421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLGLVITGLTPVFNITGQFEN
Db 421 INTQEVLDVLRPMVLGAKAKOVQNTVYLDALGLGLVITGLTPVFNITGQFEN
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPLNLPKNPKSQ
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPLNLPKNPKSQ
Qy 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
Db 536 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNG
Qy 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKQSETLKPDNFESGVTFFIAPDYC
Db 596 ALVLPYTSFYIYKAKLEETITQARSKKGMKQSETLKPDNFESGVTFFIAPDYC
Qy 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYVWSKQKNIK
Db 656 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYVWSKQKNIK
Qy 721 FVYTDGGITRVYKPEAGENQENPEYEDSFYKRSILDNDNMYVETAPYFNKSGPGF
Db 716 FVYTDGGITRVYKPEAGENQENPEYEDSFYKRSILDNDNMYVETAPYFNKSGPGF
Qy 781 MVSXAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDP CAGPVDCCKRNSDY
Db 776 MVSXAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDP CAGPVDCCKRNSDY
Qy 841 LDGGFLLMANHDDYTNQIGRFFGEIDPDLMRHLVNI SVYAFNKSVDYQSVCEPC
Db 836 LDGGFLLMANHDDYTNQIGRFFGEIDPDLMRHLVNI SVYAFNKSVDYQSVCEPC
Qy 901 GAGHRSAYVPSVADILQIGHWATAAAWSILQOFLLSLTFPRLLLEAVEMEDDDFTI
Db 896 GAGHRSAYVPSVADILQIGHWATAAAWSILQOFLLSLTFPRLLLEAVEMEDDDFTI
Qy 961 SCITEQTYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTMLIFIMVSKGTCPCI
Db 956 SCITEQTYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTMLIFIMVSKGTCPCI
Qy 1021 QAEQTSQGNPNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1063
Db 1016 QAEQTSQGNPNPCDMVKQPRYKRGPDVCFDNNVLEDYTDCCGVS 1058
RESULT 15
AAE24799
ID AAE24799 standard; Protein; 1086 AA.
XX
AC AAE24799;
XX
DT 22-OCT-2002 (first entry)
XX
DE Human calcium channel alpha 2c subunit protein.
XX
KW Human; calcium channel protein; therapeutic; autoimmune disease.
KW diagnosis; Lambert Eaton Syndrome; alpha 2c subunit.
XX Homo sapiens.
XX OS
XX US6387696-B1.
XX PN
XX 14-MAY-2002.
PD

95US-0450272.
89WO-US01408.
90US-0603751.
92US-0914231.
90US-0482384.
90US-0620250.
91US-0745206.
92WO-US06903.
93US-0105536.
93US-0149097.
94US-0193078.
94US-0311363.
94US-0336257.
95US-0404354.
& CO INC.
Ellis SB, Williams ME, McCue AF;
318/50.
977.
lles expressing a functional heterologous human calcium
ncoding nucleic acid isolated from human cerebellum for
nd to diagnose Lambert Eaton Syndrome -
olumn 237-246; 154pp; English.
nvention relates to novel human calcium channel proteins
otides encoding such proteins. The invention also relates
cells expressing a functional heterologous human calcium
1, alpha 2, beta and gamma subunits. The eukaryotic cells
r screening for potential calcium channel antagonists or
elect compounds that have potential as disease or tissue-
apetic agents. The subunits may be used in diagnostic
e autoimmune disease Lambert Eaton Syndrome. The present
uman calcium channel alpha 2c subunit protein.
86 AA;
99.3%; Score 5559.5; DB 23; Length 1086;
arity 99.5%; Pred. No. 0;
onservative 0; Mismatches 0; Indels 5; Gaps 1;
KLLALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
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FQHLVQANVNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
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3GERAQEI FNKNYKOKKVVRFPSVQHNVERGPQIOMMACENKGYIYIIPSGAIR 420

QY 421 INTQEYLDVLGRPMVLADKAKOVQWNTNVYLDALGLVITGLPVFNITGQFENK
DB 421 INTQEYLDVLGRPMVLADKAKOVQWNTNVYLDALGLVITGLPVFNITGQFENK
QY 481 NQILGVGMVDVSLSDIKRLTPRFTLCPNGYYPFAIDPNGVYLLHPNLQPKPKSQE
DB 481 NQILGVGMVDVSLSDIKRLTPRFTLCPNGYYPFAIDPNGVYLLHPNLQPKPKSQE
QY 541 DFLDAELENDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTVYTWTPVNGI
DB 536 DFLDAELENDIKVEIRNMIDGESGKERTLVKSQDERYIDKGNRTVYTWTPVNGI
QY 601 ALVLPYTSFYIYIKAKLEETITQARSKKGKMDSETLKPDPNFEESGYTFIAPRDYCN
DB 596 ALVLPYTSFYIYIKAKLEETITQARSKKGKMDSETLKPDPNFEESGYTFIAPRDYCN
QY 661 SDNTEFLNPFNEFIDRKTNNPSCNADLNRVLLDAGFTNELVQNYWSKOKNIK
DB 656 SDNTEFLNPFNEFIDRKTNNPSCNADLNRVLLDAGFTNELVQNYWSKOKNIK
QY 721 FVVTDDGGITRVYKPEAGENWOENPETYEDSFYKRSNDNDNVFTAPYFNKSGPGCA
DB 716 FVVTDDGGITRVYKPEAGENWOENPETYEDSFYKRSNDNDNVFTAPYFNKSGPGCA
QY 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGPVCDCRNSDVA
DB 776 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGPVCDCRNSDVA
QY 841 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSIVAFNKSIDYQSVCEPG
DB 836 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNSIVAFNKSIDYQSVCEPG
QY 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLLEAVEMEDDDFTAI
DB 896 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLLEAVEMEDDDFTAI
QY 961 SCITEQTOYFFDNDKSPSGVLDGNCSCSRIFHGEKLMNTNLIIFIMVESKGTCPCD
DB 956 SCITEQTOYFFDNDKSPSGVLDGNCSCSRIFHGEKLMNTNLIIFIMVESKGTCPCD
QY 1021 QAEQTSDDGNPCDMVKQPRYKGPVCFDNNVLEDYTDGCVS 1063
DB 1016 QAEQTSDDGNPCDMVKQPRYKGPVCFDNNVLEDYTDGCVS 1058

Search completed: February 20, 2004, 16:55:19
Job time : 42.5367 secs

GenCore version 5.1.6
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tein search, using sw model

February 20, 2004, 16:47:50 ; Search time 36.9054 Seconds
(without alignments)
4378.325 Million cell updates/sec

JS-10-090-827-13

3346

1 MAAGCLIALTLFQSLIG.....TNLIFIMVESKGTCPDTRL 1018

3LOSUM62

Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues

uits satisfying chosen parameters: 1107863

angth: 0

angth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

A. Genesec 19Jun03.*

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24: /SIDSI/gcgdata/genesec/genesecp-emb1/AA2003.DAT.*

is the number of results predicted by chance to have a
per than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
100.0	1018	22	AAU01032	Human secreted sol
100.0	1018	22	AAAB62256	Porcine calcium ch
100.0	1036	22	AAAU01033	Human secreted sol
100.0	1036	22	AAAB62257	Porcine calcium ch
100.0	1063	22	AAU01034	Human secreted sol
100.0	1063	22	AAAB62258	Porcine calcium ch
100.0	1091	16	AAAR71011	Human neuronal cal
100.0	1091	19	AAAW63145	Human calcium chan
100.0	1091	21	AAAB10576	Human calcium chan

	10	5346	100.0	1091	22	AAU01035	Human se
11	5346	100.0	1091	22	AAAB62259	Porcine	
12	5346	100.0	1091	23	AAE24789	Human ca	
13	5342	99.9	1091	19	AAAB7879	Human ca	
14	5340	99.9	1091	14	AAAR3553	Sequence	
15	5326.5	99.6	1110	19	AAAW63148	Human ca	
16	5306.5	99.3	1086	16	AAAR71013	Human ne	
17	5306.5	99.3	1086	19	AAAW63153	Human ca	
18	5306.5	99.3	1086	21	AAAB10587	Human ca	
19	5306.5	99.3	1086	23	AAE24799	Human ca	
20	5289.5	98.9	1084	16	AAAR71015	Human ne	
21	5289.5	98.9	1084	19	AAAW63155	Human ca	
22	5289.5	98.9	1084	21	AAAB10589	Human ca	
23	5289.5	98.9	1084	23	AAE24801	Human ca	
24	5288	98.9	1018	22	AAU01028	Pig secr	
25	5288	98.9	1018	22	AAAB62252	Porcine	
26	5288	98.9	1036	22	AAU01029	Pig secr	
27	5288	98.9	1036	22	AAAB62253	Porcine	
28	5288	98.9	1063	22	AAU01030	Pig secr	
29	5288	98.9	1063	22	AAAB62254	Porcine	
30	5288	98.9	1069	22	AAU01031	Pig secr	
31	5288	98.9	1069	22	AAAB62255	Porcine	
32	5288	98.9	1091	22	AAU01027	Pig secr	
33	5288	98.9	1091	22	AAAB62251	Porcine	
34	5270	98.6	1103	16	AAAR71012	Human ne	
35	5270	98.6	1103	19	AAAW63151	Human ca	
36	5270	98.6	1103	21	AAAB10586	Human ca	
37	5270	98.6	1103	23	AAE24798	Human ca	
38	5250	98.2	1079	19	AAAW63154	Human ca	
39	5250	98.2	1079	21	AAAB10588	Human ca	
40	5250	98.2	1079	23	AAAB62250	Human ca	
41	5244	98.1	1079	16	AAAR71014	Human ne	
42	5137.5	96.1	1106	18	AAAW37712	Rabbit s	
43	5137.5	96.1	1106	18	AAAW18389	Rabbit c	
44	5137.5	96.1	1106	21	AAAY7545	Rabbit s	
45	5116.5	95.7	1106	16	AAAR73056	Rabbit s	

ALIGNMENTS

RESULT 1
AAU01032
ID AAU01032 standard; Protein; 1018 AA.
XX AAU01032;
XX AC AAU01032;
XX DT 04-JUL-2001 (first entry)
XX Human secreted soluble alpha2delta calcium channel subunit #12 ;
XX Human; secreted calcium channel alpha2delta subunit; alpha2delt
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel
KW gabapentin; scintillation proximity assay; SPA; nickel flashpla
KW filter binding assay; wheat germ lectin flashplate assay.
XX Homo sapiens.
XX WO2000119870-A2.
XX 22-MAR-2001.
XX 18-SEP-2000; 2000WO-EP09137.
XX 16-SEP-1999; 99US-0397550.
XX (WARN) WARNER LAMBERT CO.
XX Brown JP, Bertelli P;
XX WPI; 2001-235262/24.
XX N-PSDB; AAS01423.
XX

inel alpha2delta subunits, useful in e.g. SPA assays, assays, Nickel Flashplate assays, Filter binding assays or actin Flashplate assays -

age 130-133; 160pp; English.

sequence represents human secreted calcium channel subunit #12 which is soluble and retains the functional sites of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated 2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins and their affinity for radioactively labelled gabapentin. The subunit is 1 of the components of the heteromultimeric calcium channel (VCC) complexes present in neuronal tissues including heart and skeletal muscle. Numerous is of the human calcium channel alpha2delta subunits AU01024 and AU01032-AAU01038) and 5 soluble forms of the calcium channel alpha2delta subunits (AAU01027-AAU01031) are the secreted soluble alpha2delta subunit may be used in assays (lution proximity assay (SPA), flashplate, nickel flashplate, using or wheat germ lectin flashplate assays to detect or binding or interaction of a ligand (e.g. gabapentin, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine, serine and/or L-phenylalanine) of a calcium channel subunit.

1018 AA;

100.0%; Score 5346; DB 22; Length 1018;

100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGCLLALTTLFOSLLIGPSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

AGCLLALTTLFOSLLIGPSEPPFPSPAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

CYQDLVTVEPNNARQLVIAARDIEKLLNSRKALVSLALEAEKVQAAHQRDPSN 120

CYQDLVTVEPNNARQLVIAARDIEKLLNSRKALVSLALEAEKVQAAHQRDPSN 120

AYTNAKDDLPEKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHPTDIYEGSTVL 180

AYTNAKDDLPEKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHPTDIYEGSTVL 180

ANWTSALDEVKKNREDPSSLVQVGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240

ANWTSALDEVKKNREDPSSLVQVGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240

AYTQGAASPDKMLILVDVSGVSGLTTLKLRITSVSEMLETLSDDDDFVNVASFN 300

AYTQGAASPDKMLILVDVSGVSGLTTLKLRITSVSEMLETLSDDDDFVNVASFN 300

FOHLVQANVRNKKVLKDAVNNITAKGITDYKGFSPAFQQLNYSRANCKIIML 360

FOHLVQANVRNKKVLKDAVNNITAKGITDYKGFSPAFQQLNYSRANCKIIML 360

OGGEERAQEIFNKYNKDKKVRVFRFSVGOHNYERGPIONMACENKGYEIPSIGAIR 420

OGGEERAQEIFNKYNKDKKVRVFRFSVGOHNYERGPIONMACENKGYEIPSIGAIR 420

FOEYLDVLRPMVLGAKAKOVQWNTVYLDALBELGLVITGLPVTNITQGFENKTLK 480

FOEYLDVLRPMVLGAKAKOVQWNTVYLDALBELGLVITGLPVTNITQGFENKTLK 480

LILGVMGVDSLEDIKELTFRFTLCPNGYFADIPNGYVLLHPNLPKNPSQBPVTL 540

LILGVMGVDSLEDIKELTFRFTLCPNGYFADIPNGYVLLHPNLPKNPSQBPVTL 540

LDLAELNDIKVEIRNKNMIDGESKFTPLVKSQDERYIDKGNRTYTWTPVNGDYSL 600

LDLAELNDIKVEIRNKNMIDGESKFTPLVKSQDERYIDKGNRTYTWTPVNGDYSL 600

VLPTYSFYIYKAKLEETITQARSKKGMKQSETLKPDNPFESGYTFIAPRDYCN 660

601 ALVLPYTSFYIYKAKLEETITQARSKKGMKQSETLKPDNPFESGYTFIAPRDY(Db
661 SDNNTFELNPFNFIIDRKTNNPNSCNADLNRLVLLDAGFTNELLVONTWSQKNII Qy
661 SDNNTFELNPFNFIIDRKTNNPNSCNADLNRLVLLDAGFTNELLVONTWSQKNII Db
721 FVVTGSGITRVYPRKAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGI Qy
721 FVVTGSGITRVYPRKAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGI Db
781 MVSXAVIYIYQGLKLPVAVGIIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDI Qy
781 MVSXAVIYIYQGLKLPVAVGIIKIDVNSWIENFTKTSIRDPGAGPVCDCKRNSDI Db
841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPK Qy
841 LDDGGFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPK Db
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901 GAGHRSAYVPSVADILQIGMWATAAAWSILQQFLLSITFPRLLEAVEMEDDDFTY Db
961 SCITEQTYQYFPDNDKSKFSVGLDCGNCSTRIFPHGKLMNTNLI FTWVSKGTCPC Qy
961 SCITEQTYQYFPDNDKSKFSVGLDCGNCSTRIFPHGKLMNTNLI FTWVSKGTCPC Db

RESULT 2

AAB62256

ID AAB62256 standard; Protein; 1018 AA.

XX AAB62256;

DT 11-JUN-2001 (first entry)

XX Porcine calcium channel alpha2delta subunit.

XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co:
XX nervous system disorder; pain; epilepsy; anxiety; pig.

XX Sus scrofa.

XX WO200120336-A2.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000MO-EP09136.

XX 16-SEP-1999; 99US-0397549.

XX (WARN-) WARNER LAMBERT CO.

XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N.
XX WPI; 2001-257902/26.

XX N-PSDB; AAF57560.

XX Competitive binding assay for screening ligands which bind a ce:
XX cortical voltage-dependent calcium channel alpha2delta-1 subun:
XX where the ligands identified are useful for treating disorders
XX nervous system, including pain -

XX Claim 8; Page 129-132; 150pp; English.

XX The invention relates to a new method for screening ligands wh
XX cerebral cortical voltage-dependent calcium channel alpha2delta
XX preferably alpha2delta-1 subunit. The method comprises contacti
XX secreted soluble recombinant alpha2delta-1 subunit with a ligam
XX interest and a labelled compound which binds the subunit, follo
XX measuring the level of binding of the labelled compound to alph
XX subunit. The method is useful for screening ligands, preferably
XX biologically active products that modulate a nervous system fun

cerebral cortical voltage-dependent calcium channel
 1 subunit. The ligands identified by the method are useful
 disorders of the nervous system, including pain, epilepsy
 The present sequence represents a porcine calcium channel
 subunit.

018 AA;

100.0%; Score 5346; DB 22; Length 1018;
 larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SCLLALTLTFLQSLLIGSSSEPPSPSAVTIKSWDKQEDLVTLAKTAGVGNQLVDI 60
 SCLLALTLTFLQSLLIGSSSEPPSPSAVTIKSWDKQEDLVTLAKTAGVGNQLVDI 60
 YQDLTYVEPNARQLVIAARDIEKLISNRKALVSLALEAEKVAQAAHQWREDPASN 120
 YQDLTYVEPNARQLVIAARDIEKLISNRKALVSLALEAEKVAQAAHQWREDPASN 120
 YNAKDDLDPEKNDSEFGSQRIKPVFIEDANFGRQISYQHAHVHPTDIIYEGSTIVL 180
 YNAKDDLDPEKNDSEFGSQRIKPVFIEDANFGRQISYQHAHVHPTDIIYEGSTIVL 180
 NWTSDLVDFKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTNPKIDLYDVR 240
 NWTSDLVDFKKNREEDPSLLQVFGSATGLARYYPASPMVDNSRTNPKIDLYDVR 240
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 GGERAQBIFNKYNKDKKVRPRFSVQHNTERGPIOMMACENKGYIYEPSIGAIR 420
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 QEYLDVLRGPMVLADGAKAKQVQWNTNVYLDALDELGLVITGTLPVFNITGQENKTNLK 480
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 ILGVMGVDSVLEDKRLTPFTLCPNGYFAIDPENGVLVLLHPLNLPKNPKSQEPVTL 540
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 DAELENDIKVEIRNKMIDGESGKFTLTKVQSDERIVDKGNRTYTPVNGTDYSL 600
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 LPTYSFYIKAKLEBETITQARKSGKMKDSETLKPDNFESGYTFIAPRDYCNLDKI 660
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 NTEFLNFEFIDRKTNNPNSCNADLNRLVLLDAGTNELVQYNSQKIKGVKAR 720
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901 GAGERSAYVESVADIILQIGWATAAANSILQQLLSLTFFRLLLEAVEMEDDDFTY
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 961 SCITEQTQFFDNDKSKFSVGLDCGNCRIFFHGEKLMNTNLIFIMVESKGTCPCI

RESULT 3
 AAU01033
 ID AAU01033 standard; Protein; 1036 AA.
 AC AAU01033;
 XX 04-JUL-2001 (first entry)
 XX Human secreted soluble alpha2delta calcium channel subunit #13
 XX Human; secreted calcium channel alpha2delta subunit; alpha2delta
 XX alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;
 XX gabapentin; scintillation proximity assay; SPA; nickel flashplat
 XX filter binding assay; wheat germ lectin flashplate assay.
 OS Homo sapiens.
 XX WO200119870-A2.
 PN 22-MAR-2001.
 PD 18-SEP-2000; 2000WO-EP09137.
 PP 16-SEP-1999; 99US-0397550.
 PR (WARN) WARNER LAMBERT CO.
 PA Brown JP, Bertelli F;
 PI WPI; 2001-235262/24.
 DR N-PSDB; AAS01424.
 XX Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
 Flashplate assays, Nickel Flashplate assays, Filter binding ass
 Wheat Germ Lectin Flashplate assays -
 Claim 31; Page 134-137; 160pp; English.
 The present sequence represents human secreted calcium channel
 alpha2delta subunit #13 which is soluble and retains the func
 characteristics of the full length or wild type alpha2delta sub
 (AAU01025) from which it is derived. The invention relates to t
 alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble pr
 which retain their affinity for radioactively labelled gabapenti
 alpha2delta subunit is 1 of the components of the heteromultimer
 voltage-dependent calcium channel (VDCC) complexes present in ne
 and non-neuronal tissues including heart and skeletal muscle. Nu
 soluble forms of the human calcium channel alpha2delta subunits
 (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of
 porcine calcium channel alpha2delta subunits (AAU01027-AAU01031)
 described. The secreted soluble alpha2delta subunit may be used
 e.g. scintillation proximity assay (SPA), flashplate, nickel fla
 filter binding or wheat germ lectin flashplate assays to detect
 measure the binding or interaction of a ligand (e.g. gabapentin,
 L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Iso
 L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
 alpha2delta subunit.

XX Sequence 1036 AA;
 Query Match 100.0%; Score 5346; DB 22; Length 1036;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0;

1 MAAGCULLALTTLTFLQSLLIGPSSEPPSPSAVTIKSWDKQEDLVTLAKTAGSVN

[illegible]

undard; Protein; 1036 AA.

11-JUN-2001 (first entry)
Porcine calcium channel alpha2delta subunit.
Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co
nervous system disorder; pain; epilepsy; anxiety; pig.
Sug eerofa.
WO200120336-A2.
22-MAR-2001.
18-SEP-2000; 2000WO-EP09136.
16-SEP-1999; 99US-0397549.
(WARN) WARNER LAMBERT CO.
Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N
WPI; 2001-257902/26.
N-PSDE; AAF57561.
Competitive binding assay for screening ligands which bind a ce:
cortical voltage-dependent calcium channel alpha2-delta-1 subun:
where the ligands identified are useful for treating disorders (:
nervous system, including pain -
Claim 8; Page 132-135; 158pp; English.
The invention relates to a new method for screening ligands wh:
cerebral cortical voltage-dependent calcium channel alpha2delta
preferably alpha2delta-1 subunit. The method comprises contacti
secreted soluble recombinant alpha2delta-1 subunit with a ligam
interest and a labelled compound which binds the subunit, follo
measuring the level of binding of the labelled compound to alph
subunit. The method is useful for screening ligands, preferably
biologically active products that modulate a nervous system fun
which bind a cerebral cortical voltage-dependent calcium channe
alpha2delta-1 subunit. The ligands identified by the method are
for treating disorders of the nervous system, including pain, e
and anxiety. The present sequence represents a porcine calcium (:
alpha2delta subunit.
Sequence 1036 AA;

Query Match	100.0%;	Score 5346;	DB 22;	Length 1036;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1019;	Conservative 0;	Mismatches 0;	Indels 0;	
Qy	1	MAAGCCLLALTLT	FOSELLIGPSEPPFSSAVTIKSWDKMQEDVTLAKTASGV	
Db	1	MAAGCCLLALTLT	FOSELLIGPSEPPFSSAVTIKSWDKMQEDVTLAKTASGV	
Qy	61	YEKYQDLYTV	VEPNNAQLVEI	IAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRI
Db	61	YEKYQDLYTV	VEPNNAQLVEI	IAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRI
Qy	121	EVVYNAKD	LDPEKNDSFPGSR	IKPVFIEDANFGRQISYOHAAVHIPTDIYEK
Db	121	EVVYNAKD	LDPEKNDSFPGSR	IKPVFIEDANFGRQISYOHAAVHIPTDIYEK
Qy	181	NELNWT	SALDEVFKKNREDDPSLL	MQVFGSATGLARYYPASPWDNSRTPNKIDI
Db	181	NELNWT	SALDEVFKKNREDDPSLL	MQVFGSATGLARYYPASPWDNSRTPNKIDI
Qy	241	RPWYI	OGAASPDKMLIL	VDVSGVSGSLTKLIRTSVSEMLTSLSDDDPVNVASF
Db	241	RPWYI	OGAASPDKMLIL	VDVSGVSGSLTKLIRTSVSEMLTSLSDDDPVNVASF
Qy	301	VSCFOHLV	OAENVRNKKVLKDA	VNNITAKGITDYKKGFSPAPELLNLYNVSRANC

FOHLVQANVENKVKLDVANNITAKGITDYKGFSAFEQLLNNVSRANCNIIIML 360
 3GERAQEIIFNKYNKDKKVRFRFSVQHNVERGPIQWMACENKGYIYEIPSGAIR 420
 3GERAQEIIFNKYNKDKKVRFRFSVQHNVERGPIQWMACENKGYIYEIPSGAIR 420
 3EYLDVLRPMVLADGAKQVQWNTVYLDLALGLVITGTLPVFNITGQFENKTNLK 480
 3EYLDVLRPMVLADGAKQVQWNTVYLDLALGLVITGTLPVFNITGQFENKTNLK 480
 ILGVMGVDVLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSQBFTVL 540
 ILGVMGVDVLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSQBFTVL 540
 DAELENDIKVEIRNMKIDGESGKFTFLVKSQDERVIDKGNRTYTTPVNGTDYSL 600
 DAELENDIKVEIRNMKIDGESGKFTFLVKSQDERVIDKGNRTYTTPVNGTDYSL 600
 LPTYSPFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFIAPRDYCNLDKI 660
 LPTYSPFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFIAPRDYCNLDKI 660
 NTFELNPFNFIIDKTPNPNPSCNADLINRVLLDAGFTNELVQYNSKQNKIKGYKAR 720
 NTFELNPFNFIIDKTPNPNPSCNADLINRVLLDAGFTNELVQYNSKQNKIKGYKAR 720
 IDGGITRVYKPEAGENQENPETVEDSFYKRSILDNDNYVTAPYFNKSGPGAYESGI 780
 IDGGITRVYKPEAGENQENPETVEDSFYKRSILDNDNYVTAPYFNKSGPGAYESGI 780
 KAVEIYIQGKLLKPAVYGIKIDVNSWIENTFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVYGIKIDVNSWIENTFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 3GFLLMANHDDYTNQIGRFFGEIDPFLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 3GFLLMANHDDYTNQIGRFFGEIDPFLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 3RSAYVPSVADIIQIGHWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 3RSAYVPSVADIIQIGHWATAAASIIQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 TEQTQYFFDNDKSFSGVLDGNCGRIFPHGKLMNTNLIIFIMVESKTCPCDTRL 1018
 TEQTQYFFDNDKSFSGVLDGNCGRIFPHGKLMNTNLIIFIMVESKTCPCDTRL 1018

ndard; Protein; 1063 AA.

(first entry)

ed soluble alphas2delta calcium channel subunit #14 protein.

ted calcium channel alphas2delta subunit; alphas2delta-2;
 3; alphas2delta-4; voltage-dependent calcium channel; VDCC;
 scintillation proximity assay; SPA; nickel flashplate assay;
 ng assay; wheat germ lectin flashplate assay.

A2.

2000WO-EP09137.

99US-0397550.

PA (WARN) WARNER LAMBERT CO.
 XX Brown JP, Bertelli F;
 XX WPI: 2001-235262/24.
 DR N-PSDB; AA801425.
 DR
 XX Calcium channel alphas2delta subunits, useful in e.g. SPA assays,
 PT Flashplate assays, Nickel Flashplate assays, Filter binding ass
 PT Wheat Germ Lectin Flashplate assays -
 XX
 PS Claim 31; Page 137-140; 160pp; English.
 XX
 CC The present sequence represents human secreted calcium channel
 CC alphas2delta subunit #14 which is soluble and retains the functio
 CC characteristics of the full length or wild type alphas2delta subu
 CC (AAU01025) from which it is derived. The invention relates to tr
 CC alphas2delta-2, alphas2delta-3 or alphas2delta-4 subunit soluble pr
 CC which retain their affinity for radioactively labelled gabapenti
 CC alphas2delta subunit is 1 of the components of the heteromultimer
 CC voltage-dependent calcium channel (VDCC) complexes present in ne
 CC and non-neuronal tissues including heart and skeletal muscle. Nu
 CC soluble forms of the human calcium channel alphas2delta subunits
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of
 CC porcine calcium channel alphas2delta subunits (AAU01027-AAU01031)
 CC described. The secreted soluble alphas2delta subunit may be used
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel fla
 CC filter binding or wheat germ lectin flashplate assays to detect
 CC measure the binding or interaction of a ligand (e.g. gabapentin,
 CC L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isol
 CC L-valine, Spermine and/or L-Phenylalanine) of a calcium channel
 CC alphas2delta subunit.

XX Sequence 1063 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1063;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTLTIFQSLILIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVN
 DB 1 MAAGCLLALTLTIFQSLILIGPSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGVN
 QY 61 YEKYQDLTYTVEPNARQVLEIAARDIEKLLSNRSKALVSIALAEKVAQAHOHRE
 DB 61 YEKYQDLTYTVEPNARQVLEIAARDIEKLLSNRSKALVSIALAEKVAQAHOHRE
 QY 121 EVVYNAKDDLDPEKNDSPGSGORIKPVFTEDANFGROI SYQHAHVHIPTDIYEG
 DB 121 EVVYNAKDDLDPEKNDSPGSGORIKPVFTEDANFGROI SYQHAHVHIPTDIYEG
 QY 181 NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDSNRTFNKIDI
 DB 181 NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDSNRTFNKIDI
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETLSDDDDFNVASFN
 DB 241 RPWYIQGAASPKDMLILVDVSGVSGLTCLKLIRTSVSEMLETLSDDDDFNVASFN
 QY 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKGFSAFEQLLNNVSRANCN
 DB 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKGFSAFEQLLNNVSRANCN
 QY 361 FTDGGEERAQEIFNKYNKDKKVRFRFSVQHNVERGPIQWMACENKGYIYEIP
 DB 361 FTDGGEERAQEIFNKYNKDKKVRFRFSVQHNVERGPIQWMACENKGYIYEIP
 QY 421 INTQEYLDVLRPMVLADGAKQVQWNTVYLDLALGLVITGTLPVFNITGQFEN
 DB 421 INTQEYLDVLRPMVLADGAKQVQWNTVYLDLALGLVITGTLPVFNITGQFEN
 QY 481 NQLILGVMGVDVLEDIKRLTPFTLCPNGYFAIDPNGYVLLHPNLOPKNPKSQ

ILGVMGVDVSLIEDIKRLTPRTLCNGYFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540
 DAELNDIKVIRNMKIDGSEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600
 DAELNDIKVIRNMKIDGSEKTFRTLVKSQDERYIDKGNRTYTTPVNGTDYSL 600
 LPTYSFYIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDYCNLKI 660
 LPTYSFYIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDYCNLKI 660
 NTEFLANFNEIDRKTNNPCNADLINRVLLDAGFTNELYVNSKQKNIKGVKAR 720
 NTEFLANFNEIDRKTNNPCNADLINRVLLDAGFTNELYVNSKQKNIKGVKAR 720
 TDGGITRVYPKEAGENQENPETVEDSFYKSLDNDNVFTAPYFNKSGPGAYESGI 780
 TDGGITRVYPKEAGENQENPETVEDSFYKSLDNDNVFTAPYFNKSGPGAYESGI 780
 KAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCCKRNSDVMDCVI 840
 GGFLLMANHDDYTNOIGRFFGEIOPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
 GGFLLMANHDDYTNOIGRFFGEIOPSLMRHLVNSVYAFNKSVDYQSVCEPGAAPKQ 900
 HRSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFFRLLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFFRLLLEAVEMEDDDFTASLSKQ 960
 TEOTQYFFDNDKSPSGVLDGNCRSRIIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1018
 TEOTQYFFDNDKSPSGVLDGNCRSRIIFHGEKLMNTNLIIFIMVESKGTGCPDTRL 1018

standard; Protein; 1063 AA.

(first entry)

ium channel alpha2delta subunit.

nel alpha2delta subunit; alpha2delta-1; cerebral cortex;
 em disorder; pain; epilepsy; anxiety; pig.

32.

2000WO-EP09136.

99US-0397549.

IBR LAMBERT CO.

Brown JP, Dissanayake V, Suman-Chauban N, Gee NS;

7902/26.

7562.

binding assay for screening ligands which bind a cerebral
 tage-dependent calcium channel alpha2-delta-1 subunit,
 gands identified are useful for treating disorders of the
 .em, including pain -

re 135-139; 158pp; English.

on relates to a new method for screening ligands which bind a

CC cerebral cortical voltage-dependent calcium channel alpha2delta
 CC preferably alpha2delta-1 subunit. The method comprises contactir
 CC secreted soluble recombinant alpha2delta-1 subunit with a ligand
 CC interest and a labelled compound which binds the subunit, follow
 CC measuring the level of binding of the labelled compound to alpha
 CC subunit. The method is useful for screening ligands, preferably
 CC biologically active products that modulate a nervous system func
 CC which bind a cerebral cortical voltage-dependent calcium channel
 CC alpha2delta-1 subunit. The ligands identified by the method are
 CC for treating disorders of the nervous system, including pain, ef
 CC and anxiety. The present sequence represents a porcine calcium c
 CC alpha2delta subunit.
 XX

SQ Sequence 1063 AA;

Query Match 100.0%; Score 5346; DB 22; Length 1063;
 Best Local Similarity 100.0%; Pred No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGV
 DB 1 MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGV
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRSKALVSLALEAKVQAAHORE
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLSNRSKALVSLALEAKVQAAHORE
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEC
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEC
 QY 181 NELNWTALDEVFKGNREDEPSSLQWVFGSATGLARYYPASPWVDNRSRTNPKIDI
 DB 181 NELNWTALDEVFKGNREDEPSSLQWVFGSATGLARYYPASPWVDNRSRTNPKIDI
 QY 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLIRTSVSEMLETISDDDFVNVASF
 DB 241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLIRTSVSEMLETISDDDFVNVASF
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLNTNVSRANC
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLNTNVSRANC
 QY 361 FTDGGEERAQEIIFNKYNKDKKVRVFRFVSGQHNYERGPQIMMACENKGYTYEIP
 DB 361 FTDGGEERAQEIIFNKYNKDKKVRVFRFVSGQHNYERGPQIMMACENKGYTYEIP
 QY 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVYLDALGLGLVITGLPVFNITGQFER
 DB 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVYLDALGLGLVITGLPVFNITGQFER
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRTLCNGYFAIDPNGYVLLHPNLQPKNPKS
 DB 481 NQLILGVMGVDVSLIEDIKRLTPRTLCNGYFAIDPNGYVLLHPNLQPKNPKS
 QY 541 DFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTTPVNC
 DB 541 DFDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTTPVNC
 QY 601 ALVLPYTSFYIYIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDY
 DB 601 ALVLPYTSFYIYIKAKLEETITQARSKKGMKDSSTLKPDPNPEESGYTFIAPRDY
 QY 661 SDNNTEFLANFNEIDRKTNNPCNADLINRVLLDAGFTNELYVNSKQKNIK
 DB 661 SDNNTEFLANFNEIDRKTNNPCNADLINRVLLDAGFTNELYVNSKQKNIK
 QY 721 FVVTGIGITRVYPKEAGENQENPETVEDSFYKSLDNDNVFTAPYFNKSGPGF
 DB 721 FVVTGIGITRVYPKEAGENQENPETVEDSFYKSLDNDNVFTAPYFNKSGPGF
 QY 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCCKRNSD

2000WO-EP09137.
 99US-0397550.
 IER LAMBERT CO.
 Bertelli F;
 15262/24.
 11426.
 mel alpha2delta subunits, useful in e.g. SPA assays,
 assays, Nickel Flashplate assays, Filter binding assays or
 actin Flashplate assays -
 age 141-144; 160pp; English.
 sequence represents human secreted calcium channel
 subunit #15 which is soluble and retains the functional
 ics of the full length or wild type alpha2delta subunit
 from which it is derived. The invention relates to truncated
 -2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins
 i their affinity for radioactively labelled gabapentin. The
 subunit is 1 of the components of the heteromultimeric
 ndent calcium channel (VCC) complexes present in neuronal
 onal tissues including heart and skeletal muscle. Numerous
 is of the human calcium channel alpha2delta subunits
 u01024 and AAU01032-AAU01038) and 5 soluble forms of the
 um channel alpha2delta subunits (AAU01027-AAU01031) are
 The secreted soluble alpha2delta subunit may be used in assays
 .ation proximity assay (SPA), flashplate, nickel flashplate,
 ng or wheat germ lectin flashplate assays to detect or
 binding or interaction of a ligand (e.g. gabapentin,
 ;, L-Allo-isoleucine, L-methionine, L-leucine, L-isoleucine,
 ermine and/or L-Phenylalanine) of a calcium channel
 subunit.
 .091 AA;
 100.0%; Score 5346; DB 22; Length 1091;
 .larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AGCLLATLTTLFOSLLIGPSSEPPSPSANTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
 AGCLLATLTTLFOSLLIGPSSEPPSPSANTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
 YQDLYTVFPNNARQLVEIARADIEKLSNRSKALVSLALEAKVQAAHQWREDFASN 120
 YQDLYTVFPNNARQLVEIARADIEKLSNRSKALVSLALEAKVQAAHQWREDFASN 120
 YTNAKDDLDPEKNDSEPSQRIPKPFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
 YTNAKDDLDPEKNDSEPSQRIPKPFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
 ANTSALDEVKKNREEDPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240
 ANTSALDEVKKNREEDPSLLMQVFGSATGLARYYPASPVNDNSRTPNKIDLYDVR 240
 WYQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
 WYQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLSDDDDFVNVASFNNAQD 300
 FQHLVQANVRNKKVLDKAVNNITAKGIDTYKGFSPFAFEPOLLNVNVRANCKIIML 360
 FQHLVQANVRNKKVLDKAVNNITAKGIDTYKGFSPFAFEPOLLNVNVRANCKIIML 360
 XGGEERAQEIFNKYNKDKKVRFRFVSQVGHYERGPQWACENKGYIYFISGAIR 420
 XGGEERAQEIFNKYNKDKKVRFRFVSQVGHYERGPQWACENKGYIYFISGAIR 420

421 INTQEYLDVLGRPMVLGADKAKQVQWNTNVYLDALGLVITGTLPVENITQCFE
 421 INTQEYLDVLGRPMVLGADKAKQVQWNTNVYLDALGLVITGTLPVENITQCFE
 481 NQLILGVMGVDVLSLEDIKRLTPRTLCPNGYYFAIDPNGVYLLHPNLQPKPKS
 481 NQLILGVMGVDVLSLEDIKRLTPRTLCPNGYYFAIDPNGVYLLHPNLQPKPKS
 541 DFLDAELENDIKVEIRNKMIDGSEKTFRTLKSKQDERYIDKGNRTYVTPVVK
 541 DFLDAELENDIKVEIRNKMIDGSEKTFRTLKSKQDERYIDKGNRTYVTPVVK
 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRDY
 601 ALVLPTYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGYTFIAPRDY
 661 SDNTEFLILNPFEDIRKTPNPNPCNADLINRVLLDAGFTNELLVQNTWSKQKNI
 661 SDNTEFLILNPFEDIRKTPNPNPCNADLINRVLLDAGFTNELLVQNTWSKQKNI
 721 FVVTDDGGITRVYPKEAGENWQENPETVEDSFYKRSNDNDYVFTAPYFNKSGPG
 721 FVVTDDGGITRVYPKEAGENWQENPETVEDSFYKRSNDNDYVFTAPYFNKSGPG
 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVDCCKNSD
 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVDCCKNSD
 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSIMRHLVNI SVYAFNKS YDYQSVCEK
 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSIMRHLVNI SVYAFNKS YDYQSVCEK
 901 GAGHRSAYVSVADILQIGWMTAAASIIQQFLLSLTFFPRLLEAVEMEDDDFT
 901 GAGHRSAYVSVADILQIGWMTAAASIIQQFLLSLTFFPRLLEAVEMEDDDFT
 961 SCITEQTYFFDNDKSFSGVLDCGNCRIPIHGEKLANMTMLIFIMVPSKGTCPCI
 961 SCITEQTYFFDNDKSFSGVLDCGNCRIPIHGEKLANMTMLIFIMVPSKGTCPCI
 RESULT 11
 ID AAB62259 standard; Protein; 1091 AA.
 AC AAB62259;
 DT 11-JUN-2001 (first entry)
 DE Porcine calcium channel alpha2delta subunit.
 XX Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co
 XX nervous system disorder; pain; epilepsy; anxiety; pig.
 OS Sus scrofa.
 XX WO200120336-A2.
 XX 22-MAR-2001.
 XX 18-SEP-2000; 2000WO-EP09136.
 XX 16-SEP-1999; 99US-0397549.
 PA (WARN) WARNER LAMBERT CO.
 XX Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N
 DR WPI; 2001-257902/26.
 XX N-PSDB; AAF57563.
 PT Competitive binding assay for screening ligands which bind a cal
 PT cortical voltage-dependent calcium channel alpha2delta-1 subuni

ands identified are useful for treating disorders of the n, including pain -

139-142; 158pp; English.

relates to a new method for screening ligands which bind a ical voltage-dependent calcium channel alpha2delta subunit, pha2delta-1 subunit. The method comprises contacting a ble recombinant alpha2delta-1 subunit with a ligand of a labelled compound which binds the subunit, followed by level of binding of the labelled compound to alpha2delta-1 method is useful for screening ligands, preferably active products that modulate a nervous system function, cerebral cortical voltage-dependent calcium channel subunit. The ligands identified by the method are useful disorders of the nervous system, including pain, epilepsy The present sequence represents a porcine calcium channel ubunit.

91 AA;

100.0%; Score 5346; DB 22; Length 1091;

arity 100.0%; Pred. No. 0;

onservative 0; Mismatches 0; Indels 0; Gaps 0;

CLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

CLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

QDLTYVEPNARQOLVEIARQIEKLSNRKALVSLALEAKVQAAHQWRDPASN 120

QDLTYVEPNARQOLVEIARQIEKLSNRKALVSLALEAKVQAAHQWRDPASN 120

YNKXDDLPEKNDSPGQRKIPFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180

YNKXDDLPEKNDSPGQRKIPFIEDANFGRQISYQAAVHIPTDIYEGSTIVL 180

WTSALDEVFKKREEDPSLLQVFGSATGLARYYPASPWVNSRTPNKILDYVRR 240

WTSALDEVFKKREEDPSLLQVFGSATGLARYYPASPWVNSRTPNKILDYVRR 240

TQGAASPKDMLILVDVSSVGLTLKLRITSVSEMLETLSDDDFVNVAFSNSAQD 300

TQGAASPKDMLILVDVSSVGLTLKLRITSVSEMLETLSDDDFVNVAFSNSAQD 300

QHLVQANVRNKKVLKDAVNNTAKGIDYKGFSPAFQQLNLYNVRANCKNIIML 360

QHLVQANVRNKKVLKDAVNNTAKGIDYKGFSPAFQQLNLYNVRANCKNIIML 360

QGERAQEIFNKYNKDKKVRFRFSYGOHNYERGPQWMACENKGYIYIPSGAIR 420

QGERAQEIFNKYNKDKKVRFRFSYGOHNYERGPQWMACENKGYIYIPSGAIR 420

REYLDVGRPMVLGAKQVQNTVYLDALEGLVITGTLVPFNITGOFENKTNLK 480

REYLDVGRPMVLGAKQVQNTVYLDALEGLVITGTLVPFNITGOFENKTNLK 480

LGVMGVDSLEDIKRLTFRFTLCPNGYFADDPNGYVLLHPLNLPKPKSPEPVTI 540

LGVMGVDSLEDIKRLTFRFTLCPNGYFADDPNGYVLLHPLNLPKPKSPEPVTI 540

AELENDIKVEIRNKMIDGESBKTFTLVKSQDERIYIDKGNRTYTWTPVNGTDYSL 600

AELENDIKVEIRNKMIDGESBKTFTLVKSQDERIYIDKGNRTYTWTPVNGTDYSL 600

PTYSFYIYKAKLEETITQARSKKGKQKQSETLKPONFESGYTFTIAPRDYCNLDKI 660

PTYSFYIYKAKLEETITQARSKKGKQKQSETLKPONFESGYTFTIAPRDYCNLDKI 660

VTFLNFEFIDRKTNNPNSCNADLINRVLDDAGFTNVLQVYNSKQNKIKGVKAR 720

VTFLNFEFIDRKTNNPNSCNADLINRVLDDAGFTNVLQVYNSKQNKIKGVKAR 720

Qy 721 FVVTGGITRVYPKEAGENWOENPETTEDSYKRSKSLDNDNTVFTAPYFNKSGPGAI

Db 721 FVVTGGITRVYPKEAGENWOENPETTEDSYKRSKSLDNDNTVFTAPYFNKSGPGAI

Qy 781 MVSXAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGPVCDCCKNSDVA

Db 781 MVSXAVEIYIOGKLLKPAVVGIKIDVNSWIEFTKTSIRDPCAGPVCDCCKNSDVA

Qy 841 LDDGGFLMANHDDYTNQIGRFCEIDPISLMRHLVNSIVYAFNKSVDYQSVCEPGI

Db 841 LDDGGFLMANHDDYTNQIGRFCEIDPISLMRHLVNSIVYAFNKSVDYQSVCEPGI

Qy 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTAS

Db 901 GAGHSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTAS

Qy 961 SCITEQTQYFFDNDKSPSGVLDGNCNSRIEFGKLMNTNLIIFIMVESKGTCPCDI

Db 961 SCITEQTQYFFDNDKSPSGVLDGNCNSRIEFGKLMNTNLIIFIMVESKGTCPCDI

RESULT 12

AAE24789

ID AAE24789 standard; Protein; 1091 AA.

XX AAE24789;

XX 22-OCT-2002 (first entry)

XX Human calcium channel alpha 2b subunit protein.

XX Human; calcium channel protein; therapeutic; autoimmune disease; diagnosis; Lambert Eaton Syndrome; alpha 2b subunit.

XX Homo sapiens.

XX US6387696-B1.

XX 14-MAY-2002.

XX 25-MAY-1995; 95US-0450272.

XX 04-APR-1989; 89WO-US01408.

XX 08-NOV-1990; 90US-0603751.

XX 13-JUL-1992; 92US-0914231.

XX 02-FEB-1990; 90US-0482384.

XX 30-NOV-1990; 90US-0620250.

XX 15-AUG-1991; 91US-0745206.

XX 14-AUG-1992; 92WO-US06903.

XX 11-AUG-1993; 93US-0105536.

XX 05-NOV-1993; 93US-0149097.

XX 07-FEB-1994; 94US-0193078.

XX 23-SEP-1994; 94US-0311363.

XX 07-NOV-1994; 94US-0336257.

XX 15-FEB-1995; 95US-0404354.

XX (MERI) MERCK & CO INC.

XX Harpold MM, Ellis SB, Williams ME, McCue AF;

XX WPI; 2002-470318/50.

XX N-PSDB; AAD39959.

XX Eukaryotic cells expressing a functional heterologous human calc channel and encoding nucleic acid isolated from human cerebellum drug design and to diagnose Lambert Eaton Syndrome -

XX Disclosure; Column 137-144, 154pp; English.

XX The present invention relates to novel human calcium channel prot and polynucleotides encoding such proteins. The invention also r to eukaryotic cells expressing a functional heterologous human ci channel alpha 1, alpha 2, beta and gamma subunits. The eukaryoti

or screening for potential calcium channel antagonists or select compounds that have potential as disease or tissue-repactive agents. The subunits may be used in diagnostic he autoimmune disease Lambert Eaton Syndrome. The present human calcium channel alpha 2b subunit protein.

091 AA;

larity 100.0%; Score 5346; DB 23; Length 1091;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GCLIALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60

GCLIALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

YQDLTYTPNNARQLVEIARDIEKLNSKALVSIALAEKQVAAHQWREDFASN 120

Db 901 GAGHSAYVPSVADILQIGWATAAAWSILQOFLLSLTPRLLEAVEMEDDDFTF
QY 961 SCITEQTOYFFNDSSKSGVLDGNCNCSRIHFGEKLMNTNLIIFIMVESKGTCPCI
Db 961 SCITEQTOYFFNDSSKSGVLDGNCNCSRIHFGEKLMNTNLIIFIMVESKGTCPCI

RESULT 13

AAW37879

ID AAW37879 standard; Protein; 1091 AA.

XX AAW37879;

DT 28-AUG-1998 (first entry)

XX Human calcium channel a2d subunit.

XX Calcium channel; human; central nervous system disorder;

XX Lambert-Eaton syndrome; diagnosis; therapy.

XX Homo sapiens.

XX WO9811131-A2.

XX 19-MAR-1998.

XX 11-SEP-1997; 97WO-US16146.

XX 16-SEP-1996; 96US-0713118.

XX (AMHP) AMERICAN HOME PROD CORP.

XX Chen ARS, Franco R, Shuey DJ;

XX WPI; 1998-207325/18.

XX N-PSDB; AAV29060.

XX DNA encoding human neuronal calcium channel subunit(s) - useful

XX diagnosis of and treatment of central nervous system disorders,

XX Lambert-Eaton syndrome

XX Disclosure; Fig 2; 89pp; English.

XX This polypeptide comprises the a2d subunit of the human neuronal calcium channel. cDNA clones (see AAV29059-61) encoding the a1b subunit (see AAW37878), the a2d subunit and a b3 subunit (see AA have been isolated. These have been inserted into expression vectors and are stably expressed in transformed cell lines. The transformed cells show omega-conotoxin GVIA binding activity, and omega-conotoxin GVIA toxin sensitive potassium-stimulated calcium uptake, indicating that the proteins expressed by the clones are capable of forming a functioning calcium channel. Nucleic acids encoding the 3 subunits, as well as vectors, host cells and methods of isolating nucleic acids encoding related calcium channels are disclosed. Fusion proteins incorporating t subunit proteins, antibodies, and assays for identifying agents that modulate calcium channel activity are also provided. Such agents can be used to treat certain central nervous system disorders by altering calcium channel activity. Methods of diagnosing diseases associated with particular calcium channels, such as Lambert-Eaton syndrome, are disclosed.

XX Sequence 1091 AA;

Query Match 99.9%; Score 5342; DB 19; Length 1091;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1017; Conservative 0; Mismatches 1; Indels 0;

QY 1 MAAGCCLALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVGN

Db 1 MAAGCCLALTLTLFQSLILIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVGN

QDLTVFPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHOMREDFASN 120
 QDLTVFPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHOMREDFASN 120
 QDLTVFPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHOMREDFASN 120
 YNAKDDLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
 YNAKDDLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
 YNAKDDLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEGSTIVL 180
 WTSALDEVFKKNDREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDLYDVR 240
 WTSALDEVFKKNDREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDLYDVR 240
 WTSALDEVFKKNDREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDLYDVR 240
 TQGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300
 TQGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300
 TQGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVASFNSNAQD 300
 QHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNINVSFRANCNKIIML 360
 QHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNINVSFRANCNKIIML 360
 QHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNINVSFRANCNKIIML 360
 KGEERAOEIPFNKYNKKVRFPSVQGNHYERGPQMMACENKGYIYELPSIGATR 420
 KGEERAOEIPFNKYNKKVRFPSVQGNHYERGPQMMACENKGYIYELPSIGATR 420
 KGEERAOEIPFNKYNKKVRFPSVQGNHYERGPQMMACENKGYIYELPSIGATR 420
 JELDLVGRPMVLGAKAQVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
 JELDLVGRPMVLGAKAQVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
 JELDLVGRPMVLGAKAQVQNTVYLDALGLVITGTLPVFNITGOFENKTNLK 480
 LGVMGVDSLEDIKRLTRFTLCPNGYYPADIPNGVYLLHPLNLPKNPKSQEPVTL 540
 LGVMGVDSLEDIKRLTRFTLCPNGYYPADIPNGVYLLHPLNLPKNPKSQEPVTL 540
 LGVMGVDSLEDIKRLTRFTLCPNGYYPADIPNGVYLLHPLNLPKNPKSQEPVTL 540
 JAELENDIKVEIRNKMIDGESGKTRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
 JAELENDIKVEIRNKMIDGESGKTRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
 JAELENDIKVEIRNKMIDGESGKTRTLVKSODERYIDKGNRTYTWTPVNGTDYSL 600
 JPYSPYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFIAPRDYCNLDKI 660
 JPYSPYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFIAPRDYCNLDKI 660
 JPYSPYIKAKLEETITQARSKKGMKDSITLKPDPNFESGYTFIAPRDYCNLDKI 660
 VTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR 720
 VTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR 720
 VTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQNKIKGVKAR 720
 FDGGITRVYFKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYENKSGPGAYESGI 780
 FDGGITRVYFKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYENKSGPGAYESGI 780
 FDGGITRVYFKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYENKSGPGAYESGI 780
 KAVEIYIQGLKLPVAVVGIKIDVNSWIENTFKTSIRDPKAGPVCDCRNSDVMDCVI 840
 KAVEIYIQGLKLPVAVVGIKIDVNSWIENTFKTSIRDPKAGPVCDCRNSDVMDCVI 840
 KAVEIYIQGLKLPVAVVGIKIDVNSWIENTFKTSIRDPKAGPVCDCRNSDVMDCVI 840
 JGFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQVCPGPAAPKQ 900
 JGFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQVCPGPAAPKQ 900
 JGFLMANHDDYTNQIGRFGEIDPSLMRHLVNI SVYAFNKSVDYQVCPGPAAPKQ 900
 JRSAYVPSVADIIQIGHWATAAASIIQQFLLSITFPRLLEAVEMEDDDFTASLSKQ 960
 JRSAYVPSVADIIQIGHWATAAASIIQQFLLSITFPRLLEAVEMEDDDFTASLSKQ 960
 JRSAYVPSVADIIQIGHWATAAASIIQQFLLSITFPRLLEAVEMEDDDFTASLSKQ 960
 TEQTYQFFDNDKSKFSFGLDCGNSRIFHGEKLMNTNLII FIMVESKGTCPDTEL 1018
 TEQTYQFFDNDKSKFSFGLDCGNSRIFHGEKLMNTNLII FIMVESKGTCPDTEL 1018
 TEQTYQFFDNDKSKFSFGLDCGNSRIFHGEKLMNTNLII FIMVESKGTCPDTEL 1018

ndard; Protein; 1091 AA.

(updated)
(first entry)

XX Sequence of the alpha 2 human calcium channel subunit.
 DE Human calcium channel subunit; diagnosis; agonist; antagonist;
 XX Human calcium channel subunit; diagnosis; agonist; antagonist;
 KW Lambert Eaton syndrome.
 XX Homo sapiens.
 XX WO9304083-A1.
 XX 04-MAR-1993.
 XX 14-AUG-1992; 92WO-US06903.
 XX 15-AUG-1991; 91US-0745206.
 XX 10-APR-1992; 92US-0868354.
 XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 XX Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
 PI Williams ME;
 XX WPI: 1993-093936/11.
 XX N-PSDB; AAQ37821.
 XX DNA encoding specific human calcium channel sub-units - used for
 PT identifying calcium channel agonists and antagonists and
 PT diagnosing Lambert Eaton syndrome
 XX Disclosure; Page 134-138; 150pp; English.
 XX DNA encoding a human neuronal calcium channel alpha 2 subunit wa
 CC isolated from a human genomic DNA library probed under low and h
 CC stringency conditions with a fragment of DNA encoding the rabbit
 CC skeletal muscle calcium channel alpha 2 subunit. The fragment
 CC included nucleotides having a sequence corresponding to the
 CC nucleotide sequence between nucleotides 43 and 272 inclusive of
 CC rabbit back skeletal muscle calcium channel alpha 2 subunit cDNA
 CC PCR analysis identified splice variants of the human calcium alp
 CC 2 subunit transcript. In particularly preferred embodiments, the
 CC DNA encoding the alpha 2 subunit is produced by alternative
 CC processing of a primary transcript that includes DNA encoding th
 CC amino acids set forth in AAR3353 and the DNA of AAQ37823 insert
 CC between nucleotides 1624 and 1625 of AAQ37821.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 1091 AA;

Query Match 99.9%; Score 5340; DB 14; Length 1091;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1017; Conservative 0; Mismatches 1; Indels 0;

QY 1 MAAGCLLALTLTQLSLLIGPSSEPPPSAVTIKSWDKMQEDLVLTAKTASGVN
 DB 1 MAAGCLLALTLTQLSLLIGPSSEPPPSAVTIKSWDKMQEDLVLTAKTASGVN
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHOMRE
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKQVAAHOMRE
 QY 121 EVVYTNKADLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEG
 DB 121 EVVYTNKADLDPEKNDSEPGSRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEG
 QY 181 NELNWTLSALDEVFKKNDREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDL
 DB 181 NELNWTLSALDEVFKKNDREDEPDLQVFGSATGLARYYPASPWVDSNRPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVASFN
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVASFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFQOLLNINVSFRANC

FOHLVQANVRNKKVLDKDAVNNTAKGIDTYKKGSFAFEQLLNTVNSRANCKIIML 360
 GGEERAQEIENKYNKDKKVRPVSQGHNYERGPQWMAKCNKGYVEIPSGAIR 420
 GGEERAQEIENKYNKDKKVRPVSQGHNYERGPQWMAKCNKGYVEIPSGAIR 420
 QEYLDVLGRPMVLAGDKAKQVQWNTNVYLDALGLGLVITGTLPVFNITGQFENKTNLK 480
 QEYLDVLGRPMVLAGDKAKQVQWNTNVYLDALGLGLVITGTLPVFNITGQFENKTNLK 480
 ILGVMGVDSLEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKNPKSOEVPVL 540
 ILGVMGVDSLEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKNPKSOEVPVL 540
 DAELENDIKVEIRNKMIDGSEKGTFTLVKSQDERVIDKGNRYTWTVPVNGTDYSL 600
 DAELENDIKVEIRNKMIDGSEKGTFTLVKSQDERVIDKGNRYTWTVPVNGTDYSL 600
 LPTYSFYIKAKLEETITQARSKKGMKDSITLKPDPFESGYTFIAPRDYCNLDKI 660
 LPTYSFYIKAKLEETITQARSKKGMKDSITLKPDPFESGYTFIAPRDYCNLDKI 660
 NTEFLMFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSKQNIKGVKAR 720
 NTEFLMFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSKQNIKGVKAR 720
 TDGGITRVYPKEAGENQENPETYEDSFYKSLDNNDNVVFTAPYFNKSGPGAYESGI 780
 TDGGITRVYPKEAGENQENPETYEDSFYKSLDNNDNVVFTAPYFNKSGPGAYESGI 780
 KAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 GGFLLMANHDDYTQIGRFGEIDPSLMRHLVNTSVVAFNKSVDYQSVCEPGAAPKQ 900
 GGFLLMANHDDYTQIGRFGEIDPSLMRHLVNTSVVAFNKSVDYQSVCEPGAAPKQ 900
 HRSAYVPSVADILQIGMWATAAASILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGMWATAAASILQQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 TEQTQYFPDNDKSGFSGLDCGNCGRIFPHGKLANMTNLIFIMVBSKGTCPDTRL 1018
 TEQTQYFPDNDKSGFSGLDCGNCGRIFPHGKLANMTNLIFIMVBSKGTCPDTRL 1018

ndard; Protein; 1110 AA.

(updated)
 (first entry)

m channel alpha-2 subunit.

nit; human; calcium channel; assay; detection;
 tion; Lambert Eaton Syndrome; LES; diagnosis.

95US-0455543.

94US-0223305.

88US-0176899.

89WO-US01408.

20-FEB-1990; 90US-0482384.
 08-NOV-1990; 90US-0603751.
 30-NOV-1990; 90US-0620250.
 15-AUG-1991; 91US-0745206.
 XX (SIBI-) SIBIA NEUROSCIENCES INC.
 PA Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
 Williams ME;
 XX WPI; 1998-456192/39.
 DR N-PSDB; AAV42694.
 XX DNA encoding human calcium channel alpha 1B subunit protein -
 PT useful for recombinant production of the channel for screening c
 PT its modulators, and diagnosis of Lambert Eaton Syndrome
 XX Disclosure; Columns 131-138; 166pp; English.
 PS
 XX The present sequence represents the alpha-2 subunit of a human c
 CC channel. Calcium channels are membrane-spanning, multi-subunit p
 CC that allow controlled entry of calcium ions into cells. This lea
 CC to depolarisation events required for muscle contraction. The re
 CC subunit, when expressed with nucleic acids encoding the complete
 CC channel, can be used in assays for the detection and characteris
 CC compounds that modulate the channel. The DNA encoding the subuni
 CC be alternatively spliced when transcribed, giving more than one
 CC the protein from the same transcript, each having slightly diffe
 CC properties. In addition, the reactivity of the alpha 1 subunit w
 CC molecules from the serum of an individual with Lambert Eaton Syn
 CC (LES) can be used as a diagnostic for the disease.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX

Sequence 1110 AA;

Query Match 99.6%; Score 5326.5; DB 19; Length 1110;
 Best Local Similarity 98.2%; Pred. No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 19;

QY 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN
 DB 1 MAAGCLLALTTLTFLQSLLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQWRE
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQWRE
 QY 121 EVVYNAKDDLOPEKNDSEPGSORIKPVFTEDANFGROIYQHAHVHPTDIYEG
 DB 121 EVVYNAKDDLOPEKNDSEPGSORIKPVFTEDANFGROIYQHAHVHPTDIYEG
 QY 181 NELNWTSSALDEVEFKQNEEDPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDI
 DB 181 NELNWTSSALDEVEFKQNEEDPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDI
 QY 241 RPWYIQGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETSLDDDFVNVASFN
 DB 241 RPWYIQGAASPKDMLILVDVSGSVSGITLKLIRTSVSEMLETSLDDDFVNVASFN
 QY 301 VSCFQHLVQANVRNKKVLDKDAVNNTAKGIDTYKKGSFAFEQLLNTVNSRANCK
 DB 301 VSCFQHLVQANVRNKKVLDKDAVNNTAKGIDTYKKGSFAFEQLLNTVNSRANCK
 QY 361 FTDGGEERAQEIENKYNKDKKVRPVSQGHNYERGPQWMAKCNKGYVEIPSGAIR
 DB 361 FTDGGEERAQEIENKYNKDKKVRPVSQGHNYERGPQWMAKCNKGYVEIPSGAIR
 QY 421 INTQYLDVLGRPMVLAGDKAKQVQWNTNVYLDALGLGLVITGTLPVFNITGQFEN
 DB 421 INTQYLDVLGRPMVLAGDKAKQVQWNTNVYLDALGLGLVITGTLPVFNITGQFEN
 QY 481 NQILGVMGVDSLEDIKRLTPRTLCPNGYFFAIDPNGYVLLHPNLQPKNPKSOEVPVL

07:56:50 2004

us-10-090-827-13.rag

[illegible]

February 20, 2004, 16:55:12
1 BECS

GenCore version 5.1.6

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in search, using sw model

February 20, 2004, 16:47:50 ; Search time 37.5579 Seconds
(without alignments)
4378.325 Million cell updates/sec

i-10-090-827-14

43

AAAGLLALTLFQSLIG.....RLLIQAQTSQGNPCDMVK 1036

OSUM62

pop 10.0 , Gapext 0.5

.07863 seqs, 158726573 residues

its satisfying chosen parameters:

1107863

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

1 Genesec 19Jun03:*

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2: /SIDSI/gcgdata/genesec/genesecp-emb1/AA1981.DAT:*

3: /SIDSI/gcgdata/genesec/genesecp-emb1/AA1982.DAT:*

4: /SIDSI/gcgdata/genesec/genesecp-emb1/AA1983.DAT:*

5: /SIDSI/gcgdata/genesec/genesecp-emb1/AA1984.DAT:*

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24: /SIDSI/gcgdata/genesec/genesecp-emb1/AA2003.DAT:*

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
00.0	1036	22	AAU01033	Human secreted sol
00.0	1036	22	AAB62257	Porcine calcium ch
00.0	1063	22	AAU01034	Human secreted sol
00.0	1063	22	AAB62258	Porcine calcium ch
00.0	1091	16	AAU01035	Human neuronal cal
00.0	1091	19	AAW63145	Human calcium chan
00.0	1091	21	AAB10576	Human calcium chan
00.0	1091	22	AAU01035	Human secreted sol
00.0	1091	22	AAB62259	Porcine calcium ch

10	5443	100.0	1091	23	AAE24789	Human cal
11	5439	99.9	1091	19	AAW37879	Human cal
12	5437	99.9	1091	14	AAW33553	Sequence
13	5423.5	99.6	1110	19	AAW63148	Human cal
14	5403.5	99.3	1086	16	AAW71013	Human neu
15	5403.5	99.3	1086	19	AAW63153	Human cal
16	5403.5	99.3	1086	21	AAU010587	Human cal
17	5403.5	99.3	1086	23	AAE24799	Human cal
18	5386.5	99.0	1084	16	AAW71015	Human neu
19	5386.5	99.0	1084	19	AAW63155	Human cal
20	5386.5	99.0	1084	21	AAU010589	Human cal
21	5386.5	99.0	1084	23	AAE24801	Human cal
22	5380	98.8	1036	22	AAU01029	Pig secre
23	5380	98.8	1036	22	AAU01029	Pig secre
24	5380	98.8	1036	22	AAU01030	Pig secre
25	5380	98.8	1063	22	AAU01030	Pig secre
26	5380	98.8	1063	22	AAU01031	Pig secre
27	5380	98.8	1069	22	AAU01031	Pig secre
28	5380	98.8	1069	22	AAU01031	Pig secre
29	5380	98.8	1091	22	AAU01027	Pig secre
30	5367	98.6	1103	16	AAW71012	Human neu
31	5367	98.6	1103	19	AAW63151	Human cal
32	5367	98.6	1103	21	AAU010586	Human cal
33	5367	98.6	1103	23	AAE24798	Human cal
34	5347	98.2	1079	19	AAW63154	Human cal
35	5347	98.2	1079	21	AAU010588	Human cal
36	5347	98.2	1079	23	AAE24800	Human cal
37	5346	98.2	1018	22	AAU01032	Human sec
38	5346	98.2	1018	22	AAU01032	Human sec
39	5341	98.1	1079	16	AAW71014	Human neu
40	5288	97.2	1018	22	AAU01028	Pig secre
41	5288	97.2	1018	22	AAU01028	Pig secre
42	5229.5	96.1	1106	18	AAW37712	Rabbit sk
43	5229.5	96.1	1106	18	AAW18389	Rabbit sk
44	5229.5	96.1	1106	21	AAU01035	Rabbit sk
45	5208.5	95.7	1106	16	AAW73056	Rabbit sk

ALIGNMENTS

RESULT 1
AAU01033
ID AAU01033 standard; Protein; 1036 AA.
AC AAU01033,
XX
XX
DT 04-JUL-2001 (first entry)
XX
XX
DE Human secreted soluble alpha2delta calcium channel subunit #13 F
XX
XX
KW Human; secreted calcium channel alpha2delta subunit; alpha2delta
KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;
KW gabapentin; scintillation proximity assay; SPA; nickel flashplat
KW filter binding assay; wheat germ lectin flashplate assay.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200119870-A2.
XX
XX
PD 22-MAR-2001.
XX
XX
PF 18-SEP-2000; 2000WO-EP09137.
XX
XX
PR 16-SEP-1999; 99US-0397550.
XX
XX
PA (WARN) WARNER LAMBERT CO.
XX
XX
PI Brown JP, Bertelli F;
XX
XX
DR WPI; 2001-235262/24.
XX
XX
DR N-PSDB; AAS01424.
XX

nel alpha2delta subunits, useful in e.g. SPA assays, assays, Nickel Flashplate assays, Filter binding assays or ectin Flashplate assays -

ge 134-137; 160pp; English.

sequence represents human secreted calcium channel subunit #13 which is soluble and retains the functional ics of the full length or wild type alpha2delta subunit from which it is derived. The invention relates to truncated 2, alpha2delta-3 or alpha2delta-4 subunit soluble proteins, their affinity for radioactively labelled gabapentin. The subunit is 1 of the components of the heteromultimeric ndent calcium channel (VDCC) complexes present in neuronal onal tissues including heart and skeletal muscle. Numerous s of the human calcium channel alpha2delta subunits 01024 and AAU01032-AAU01038 and 5 soluble forms of the :um channel alpha2delta subunits (AAU01027-AAU01031) are he secreted soluble alpha2delta subunit may be used in assays lation proximity assay (SPA), flashplate, nickel flashplate, ng or wheat germ lectin flashplate assays to detect or binding or interaction of a ligand (e.g. gabapentin, L-Allo-Isoleucine, L-methionine, L-leucine, L-Isoleucine, ermine and/or L-Phenylalanine) of a calcium channel subunit.

.036 AA;

.arity 100.0%; Score 5443; DB 22; Length 1036;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AGCLLALTTLFOSLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
AGCLLALTTLFOSLLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGVGNQLVDI 60
CYQDLTYVEPNNAQQLVEIAARDIEKLSNRKALVSLALEAEKVQAAHQRDFASN 120
CYQDLTYVEPNNAQQLVEIAARDIEKLSNRKALVSLALEAEKVQAAHQRDFASN 120
YTNNAKDDLPKNDSEPGSQRIPVIEDANFRQISYQAAVHIPTDIYEGSTVL 180
YTNNAKDDLPKNDSEPGSQRIPVIEDANFRQISYQAAVHIPTDIYEGSTVL 180
LNTSALDEVKKNREDDPSLLMQVGSAGLARYYPASPDVNSRTPNKIDLYDVR 240
LNTSALDEVKKNREDDPSLLMQVGSAGLARYYPASPDVNSRTPNKIDLYDVR 240
YTIQGAASPKDMLILVDVSGSVSLTLKLRITSVSEMLETLDSDDDFVNVSFNSAQD 300
YTIQGAASPKDMLILVDVSGSVSLTLKLRITSVSEMLETLDSDDDFVNVSFNSAQD 300
YFOHLVQANVRNKKVLKDAVNNITAKGITYKKGFSFAPQLNLYNVSANCNKIIML 360
YFOHLVQANVRNKKVLKDAVNNITAKGITYKKGFSFAPQLNLYNVSANCNKIIML 360
OGGEERAQEIFNKNYKDKVVRPFSVQGNRYERGPIQWACENKGYIIPISGAIR 420
OGGEERAQEIFNKNYKDKVVRPFSVQGNRYERGPIQWACENKGYIIPISGAIR 420
TOEYLDVLRPMVLADKAKQVQWNTVYLDALGLVITGLPVFNITGQFENKTNLK 480
TOEYLDVLRPMVLADKAKQVQWNTVYLDALGLVITGLPVFNITGQFENKTNLK 480
LILGVMGVDSLEDIKLTFRPTLCNPGYFADIPNGVLLHPNLQPNKPSQBPVTL 540
LILGVMGVDSLEDIKLTFRPTLCNPGYFADIPNGVLLHPNLQPNKPSQBPVTL 540
LDALENDIKVEIENKMDGSGSKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
LDALENDIKVEIENKMDGSGSKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
VLPTYSFYIKAKLEETITQARSKKGMKQSETLKPONFEESGYTFFIAPRDYCNLDKI 660

601 ALVLPYTFYIKAKLEETITQARSKKGMKQSETLKPONFEESGYTFFIAPRDY
661 SDNNTFRLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVYWSKQKNI
661 SDNNTFRLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVYWSKQKNI
721 FVYTDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
721 FVYTDGGITRVYKPEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
781 MVSKAIVEIYQGLIKLPVAVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSD
781 MVSKAIVEIYQGLIKLPVAVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSD
841 LDDGGFLMANHDDYTNQIGRFGGEIDPISLMRHLVNIISVYAFNKSYYQSVCEK
841 LDDGGFLMANHDDYTNQIGRFGGEIDPISLMRHLVNIISVYAFNKSYYQSVCEK
901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSLTPRLLLEAVEMEDDDFT
901 GAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSLTPRLLLEAVEMEDDDFT
961 SCITEQTOYFEDNDKSPSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCP
961 SCITEQTOYFEDNDKSPSGVLDGCGNSRIFHGEKLMNTNLIIFIMVESKGTCP
1021 QAEQTSDDGPNPCDMVK 1036
1021 QAEQTSDDGPNPCDMVK 1036

RESULT 2

AA662257

ID AA662257 standard; Protein; 1036 AA.

AC AA662257;

DT 11-JUN-2001 (first entry)

DE Porcine calcium channel alpha2delta subunit.

KW Calcium channel alpha2delta subunit; alpha2delta-1; cerebral co
nervous system disorder; pain; epilepsy; anxiety; pig.

OS Sus scrofa.

FN WO200120336-A2.

PD 22-MAR-2001.

PF 18-SEP-2000; 2000WO-EP09136.

PR 16-SEP-1999; 99US-0397549.

PA (WARN) WARNER LAMBERT CO.

PI Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee N

XX WPI: 2001-257902/26.

XX N-PSDB; AAF57561.

XX Competitive binding assay for screening ligands which bind a ce
rtical voltage-dependent calcium channel alpha2delta-1 subun
where the ligands identified are useful for treating disorders
nervous system, including pain -

PS Claim 8; Page 132-135; 150pp; English.

XX The invention relates to a new method for screening ligands wh
cerebral cortical voltage-dependent calcium channel alpha2delta
preferably alpha2delta-1 subunit. The method comprises contacti
secreted soluble recombinant alpha2delta-1 subunit with a ligand

a labelled compound which binds the subunit, followed by level of binding of the labelled compound to alpha2delta-1 active products that modulate a nervous system function, cerebral cortical voltage-dependent calcium channel subunit. The ligands identified by the method are useful disorders of the nervous system, including pain, epilepsy. The present sequence represents a porcine calcium channel subunit.

36 AA;

100.0%; Score 5443; DB 22; Length 1036;
arity 100.0%; Pred. No. 0;
conservative 0; Mismatches 0; Indels 0; Gaps 0;

ICLLALTLFLQSLIGPSSEPPFSAVTKGWVDMQEDLVTLAKTASGVNQLVDI 60
ICLLALTLFLQSLIGPSSEPPFSAVTKGWVDMQEDLVTLAKTASGVNQLVDI 60
QDLYTVENNAQQLVEIARDEKLLSNRSKALVSLAEAKVQAHHQWRDFAFN 120
QDLYTVENNAQQLVEIARDEKLLSNRSKALVSLAEAKVQAHHQWRDFAFN 120
YNKADLLDPEKNDSPGSRQIKPVEIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
YNKADLLDPEKNDSPGSRQIKPVEIEDANFGROIYSQHAHVHIPTDIYEGSTIVL 180
WTSALDEVFKQNRDEPDLMLQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
WTSALDEVFKQNRDEPDLMLQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
TQGAASPKDMLLVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVAFSNNAQD 300
TQGAASPKDMLLVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVAFSNNAQD 300
QHLVQANVRNKKVLKADAVNNITAKGITYDKKGFSPAFQQLNNVSRANCKNIIML 360
QHLVQANVRNKKVLKADAVNNITAKGITYDKKGFSPAFQQLNNVSRANCKNIIML 360
KGEERAQEI FNKYNKDKKVRFRFVSQGNHYERGP IQWMAKCNKGYIYPSIGAIR 420
KGEERAQEI FNKYNKDKKVRFRFVSQGNHYERGP IQWMAKCNKGYIYPSIGAIR 420
JELVDLGRPMWLAGKAKQVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
JELVDLGRPMWLAGKAKQVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480
LGVMGVDSVLEDIKRLTPRFTLCPNGYTFPAIDPNGVYLLHPNLQPKNPKSQEPVTL 540
LGVMGVDSVLEDIKRLTPRFTLCPNGYTFPAIDPNGVYLLHPNLQPKNPKSQEPVTL 540
JAELENDIKVEIHNRKIMDESGSEKTRFTLVKSDQERYIDKGNRTYTPVNGTDSL 600
JAELENDIKVEIHNRKIMDESGSEKTRFTLVKSDQERYIDKGNRTYTPVNGTDSL 600
JPTYSFYIYKAKLEETITQARSKKGKKOSETLKPONFEESGYTFIAPRDYCNLDKI 660
JPTYSFYIYKAKLEETITQARSKKGKKOSETLKPONFEESGYTFIAPRDYCNLDKI 660
JTEFLNFNEFIDRTPNPNCSNADLINRVLLDAGFTNELVQVYNSKQNKIKGVKAR 720
JTEFLNFNEFIDRTPNPNCSNADLINRVLLDAGFTNELVQVYNSKQNKIKGVKAR 720
JDCGGITRVYKPEAGENQWENPETYEDSFYKRSIDNDNYVTPAFYFNKSGPGAYESGI 780
JDCGGITRVYKPEAGENQWENPETYEDSFYKRSIDNDNYVTPAFYFNKSGPGAYESGI 780
JXVEIYIQGLKLPVAVGIIKIDVNSWLENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
JXVEIYIQGLKLPVAVGIIKIDVNSWLENFTKTSIRDPKAGPVCDCKRNSDVMDCVI 840
JGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGAAPKQ 900

841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGI
901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTTA
901 GAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTTA
961 SCITETOTYFFDNDKSKSPSVGLDCGNCRSRIFHGEKLMNTNLI FIMVESKGTGCPCDY
961 SCITETOTYFFDNDKSKSPSVGLDCGNCRSRIFHGEKLMNTNLI FIMVESKGTGCPCDY
1021 QAEQTS DGNPCDMVK 1036
1021 QAEQTS DGNPCDMVK 1036

RESULT 3
AAU01034
ID AAU01034 standard; Protein; 1063 AA.

XX AC AAU01034;
XX DT 04-JUL-2001 (first entry)
XX DE Human secreted soluble alpha2delta calcium channel subunit #14 p;
XX KW Human; secreted calcium channel alpha2delta subunit; alpha2delta;
XX KW alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel;
XX KW gabapentin; scintillation proximity assay; SPA; nickel flashplate;
XX KW filter binding assay; wheat germ lectin flashplate assay.
XX OS Homo sapiens.
XX PK WO200119870-A2
XX PD 22-MAR-2001.
XX PF 18-SEP-2000; 2000WO-EP09137.
XX PR 16-SEP-1999; 99US-0397550.
XX PA (WARN) WARNER LAMBERT CO.
XX PI Brown JP, Bertelli F;
XX DR WPI; 2001-235262/24.
XX DR N-PSDB; AAS01425.
XX PT Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
XX PT Flashplate assays, Nickel Flashplate assays, Filter binding ass.
XX PT Wheat Germ Lectin Flashplate assays -
XX PS Claim 31; Page 137-140; 160pp; English.
XX CC The present sequence represents human secreted calcium channel
XX CC alpha2delta subunit #14 which is soluble and retains the function
XX CC characteristics of the full length or wild type alpha2delta subunit
XX CC (AAU01025) from which it is derived. The invention relates to tr
XX CC alpha2delta-2, alpha2delta-3 or alpha2delta-4 subunit soluble pr
XX CC which retain their affinity for radioactively labelled gabapenti
XX CC alpha2delta subunit is 1 of the components of the heteromultimer
XX CC voltage-dependent calcium channel (VDCC) complexes present in nei
XX CC and non-neuronal tissues including heart and skeletal muscle. Nu
XX CC soluble forms of the human calcium channel alpha2delta subunits
XX CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of
XX CC porcine calcium channel alpha2delta subunits (AAU01027-AAU01031)
XX CC described. The secreted soluble alpha2delta subunit may be used
XX CC e.g. scintillation proximity assay (SPA), flashplate, nickel fla
XX CC filter binding or wheat germ lectin flashplate assays to detect
XX CC measure the binding or interaction of a ligand (e.g. gabapentin,
XX CC L-Norleucine, L-Allo-isoleucine, L-methionine, L-leucine, L-isol
XX CC L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel
XX CC alpha2delta subunit.

063 AA;	100.0%; Score 5443; DB 22; Length 1063;
larity 100.0%; Pred. No. 0;	
Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
3CLIALTLTLFQSLILIGSSSEPPPSAVTIKSWYDKMQEDLVTLAKTASGVNQI	60
3CLIALTLTLFQSLILIGSSSEPPPSAVTIKSWYDKMQEDLVTLAKTASGVNQI	60
YQDLYTVEPNAROLVETAAARDIEKLLSNRSKALVSLALEAEKVOAAHQWREDFASN	120
YQDLYTVEPNAROLVETAAARDIEKLLSNRSKALVSLALEAEKVOAAHQWREDFASN	120
YYNAKDLDLPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHAVHIPDTDIYEGSTIVL	180
YYNAKDLDLPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHAVHIPDTDIYEGSTIVL	180
NWTSALDEVFKKNEEDPSLLIQQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR	240
NWTSALDEVFKKNEEDPSLLIQQVFGSATGLARYYPASPMVDNSRTPNKIDLYDVR	240
YIOGAASPQMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD	300
YIOGAASPQMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD	300
FQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEOLLNVNVRANCNKIIML	360
FQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEOLLNVNVRANCNKIIML	360
3GEERAQEIFNKYNKOKKVRFRFSVGQHNHYERGIQWMAACENKGYIYEIPSIGAIR	420
3GEERAQEIFNKYNKOKKVRFRFSVGQHNHYERGIQWMAACENKGYIYEIPSIGAIR	420
DEYLDVLGRPMVLADGAKAQVQNTVYLDALGLGVIITGTLPVENITGQFENKTNLK	480
DEYLDVLGRPMVLADGAKAQVQNTVYLDALGLGVIITGTLPVENITGQFENKTNLK	480
ILGVMGVDVSLIEDIKRITPRTLCPNGYYPALDPNGYVLLHPNLQPNPKSQBPVTL	540
ILGVMGVDVSLIEDIKRITPRTLCPNGYYPALDPNGYVLLHPNLQPNPKSQBPVTL	540
DAELENDIKVEIRNKMIDGESGEXTFTLTKSQDERYIDKGNRTYITWTPVNGTIDYSL	600
DAELENDIKVEIRNKMIDGESGEXTFTLTKSQDERYIDKGNRTYITWTPVNGTIDYSL	600
JPYTSFYIYKAKLBETITQARSKKGKMKDSETLKPDNFESGYTFIAPROYCNDLKI	660
JPYTSFYIYKAKLBETITQARSKKGKMKDSETLKPDNFESGYTFIAPROYCNDLKI	660
NYTEFLANFEPIDRKTPNPNPCSNADLNRVLDDAGFTNELVQNTWSKQKNIKGVKAR	720
NYTEFLANFEPIDRKTPNPNPCSNADLNRVLDDAGFTNELVQNTWSKQKNIKGVKAR	720
TDGGITRVYPKEAGENQENPETTYEDSFYKRSLNDNDNYVFTAPYFNKSGPGAYESGI	780
TDGGITRVYPKEAGENQENPETTYEDSFYKRSLNDNDNYVFTAPYFNKSGPGAYESGI	780
KAVEIYITQGLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI	840
KAVEIYITQGLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCKRNSDVMDCVI	840
3GFLLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAPKQ	900
3GFLLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAPKQ	900
IRSAVYPSVADILOIGWATAAASWILQQFLSLTFFRLLLEAVEMEDDDFTASLSKQ	960
IRSAVYPSVADILOIGWATAAASWILQQFLSLTFFRLLLEAVEMEDDDFTASLSKQ	960
TEQTYQFFDNDSDKSFSGVLDCGNCRSIRPHGEKLMNTNLIIFIMVESKGTCPDCTELLI	1020

Db	961	SCITBQTQYFFDNDSKSFSGVLDCGNCRSRIPHGEKLMNTNLIFIMVESKGTGTCPC	
Qy	1021	QAEQTS DSGN PCDMYK 1036	
Db	1021	QAEQTS DSGN PCDMYK 1036	
RESULT 4			
AAB62258	ID	AAB62258 standard; Protein; 1063 AA.	
AC	AC	AAB62258;	
XX	XX	11-JUN-2001 (first entry)	
XX	XX	Porcine calcium channel alpha2delta subunit.	
DE	DE	Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cor	
XX	KW	nervous system disorder; pain; epilepsy; anxiety; p.g.	
KW	XX	Sus scrofa.	
XX	OS	WQ200120336-A2.	
XX	PN	22-MAR-2001.	
XX	XX	18-SEP-2000; 2000WO-EP09136.	
XX	PF	16-SEP-1999; 99US-0397549.	
PR	XX	(WARN) WARNER LAMBERT CO.	
XX	PA	Bertelli F, Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS	
PI	PI	WPI; 2001-257902/26.	
DR	DR	N-PSDB; AAF57562.	
XX	XX	Competitive binding assay for screening ligands which bind a cer	
PT	PT	tical voltage-dependent calcium channel alpha2delta-1 subuni	
PT	PT	where the ligands identified are useful for treating disorders o	
PT	PT	nervous system, including pain -	
XX	XX	Claim 8; Page 135-139; 150pp; English.	
XX	PS	The invention relates to a new method for screening ligands whi	
CC	CC	cerebral cortical voltage-dependent calcium channel alpha2delta	
CC	CC	preferably alpha2delta-1 subunit. The method comprises contacti	
CC	CC	secreted soluble recombinant alpha2delta-1 subunit with a ligand	
CC	CC	interest and a labelled compound which binds the subunit, follow	
CC	CC	measuring the level of binding of the labelled compound to alpha	
CC	CC	subunit. The method is useful for screening ligands, preferably	
CC	CC	biologically active products that modulate a nervous system func	
CC	CC	which bind a cerebral cortical voltage-dependent calcium channel	
CC	CC	alpha2delta-1 subunit. The ligands identified by the method are i	
CC	CC	for treating disorders of the nervous system, including pain, ep	
CC	CC	and anxiety. The present sequence represents a porcine calcium c	
CC	CC	alpha2delta subunit.	
XX	XX	Sequence 1063 AA;	
SQ	SQ	Query Match 100.0%; Score 5443; DB 22; Length 1063;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 1036; Conservative 0; Mismatches 0; Indels 0;	
Qy	1	MAAGCLIALTLTFLQSLIGPSSSEPPPSAVTTIKSWDMQMEDLVTLAKTASGVN	
Db	1	MAAGCLIALTLTFLQSLIGPSSSEPPPSAVTTIKSWDMQMEDLVTLAKTASGVN	
Qy	61	YKYYQDLYTVFPNNARQLVTAARDTEKLSNRSKALVSLALEAEKVQAAHOMREI	
Db	61	YKYYQDLYTVFPNNARQLVTAARDTEKLSNRSKALVSLALEAEKVQAAHOMREI	
Qy	121	EVVYTNAKDDLDPKNDSEPGSORIKPFVTFEDANFGQISYQHAAVHIPTDIYEG	

EYLDVLRPMVLADGKAKQVQWNTVYLLDALELGLVITGTLFVFNITGQFENKTNLK 480
 BYLDVLRPMVLADGKAKQVQWNTVYLLDALELGLVITGTLFVFNITGQFENKTNLK 480
 LGVWGVSLEDDIKELTLPRTLCFNGYYFAIDPNGYVLLHNLQPNKPSQEPVTL 540
 LGVWGVSLEDDIKELTLPRTLCFNGYYFAIDPNGYVLLHNLQPNKPSQEPVTL 540
 ALENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 ALENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGTDSL 600
 PTYSFYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCNLDKI 660
 PTYSFYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCNLDKI 660
 TEFLLNFNEFIDRKTTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720
 TEFLLNFNEFIDRKTTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720
 DGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSPGAYESGI 780
 DGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNVYFTAPYFNKSPGAYESGI 780
 AVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCCKRNSDVMDCVI 840
 AVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCCKRNSDVMDCVI 840
 GFLLMANHDDVTNOIGRFFGSDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900
 GFLLMANHDDVTNOIGRFFGSDPSLMRHLNIVSYAFNKSVDYQSVCEPGAAPKQ 900
 RSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 RSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
 EQTYFPDNDKSPSGVLDGNCNCSRIIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
 EQTYFPDNDKSPSGVLDGNCNCSRIIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
 TSDGNPCDMVK 1036
 TSDGNPCDMVK 1036

Standard; Protein; 1091 AA.

(first entry)

channel alpha-2 subunit protein.

channel; calcium channel subunit; diagnosis;
Syndrome; calcium channel subunit alpha-2.

95US-0450562.

88US-0176899.
 90US-0482384.
 90US-0603751.
 90US-0620250.
 91US-0745206.
 92US-0868354.
 92US-0914231.

PR 11-AUG-1993; 93US-0105536.
 PR 05-NOV-1993; 93US-0149097.
 PR 07-FEB-1994; 94US-0193078.
 PR 04-APR-1994; 94US-0223305.
 PR 11-AUG-1994; 94US-0290012.
 PR 23-SEP-1994; 94US-0311363.
 PR 28-SEP-1994; 94US-0314083.
 PR 07-NOV-1994; 94US-0336257.
 PR 13-MAR-1995; 95US-0404950.
 XX
 PA (STBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Ellis SB, Williams ME, McCue AF, Harpold MM;
 XX
 DR WPI; 2000-548230/50.
 DR N-PSDB; AAA71707.
 XX
 PT Human calcium channel beta subunit polynucleotides, useful for
 PT producing recombinant eukaryotic cells and for diagnosing Lambert
 PT Syndrome -
 XX
 PS Example IV; Column 135-144; 153pp; English.
 CC This invention describes a novel isolated DNA molecule (I) compri
 CC sequence encoding a beta3-1 subunit of a human calcium channel.
 CC Nucleic acid probes comprising 14-30 contiguous nucleotides of
 CC beta 3 subunit encoding DNA are useful for isolation and cloning
 CC calcium channel subunit-encoding DNA. Recombinant eukaryotic cell
 CC express heterologous calcium channel are useful for identifying
 CC that modulate calcium channel activity and in assays for identify
 CC agonists and antagonists of calcium channel activity in humans. I
 CC calcium channel subunit or eukaryotic cells expressing the channe
 CC useful for diagnosing Lambert Eaton Syndrome (LES) in a human. Th
 CC sequence represents the human calcium channel alpha-2 subunit whi
 CC described in the method of the invention.
 XX
 SQ Sequence 1091 AA;
 Query Match 100.0%; Score 5443; DB 21; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; G
 QY 1 MAACCLALATLTLFQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNC
 DB 1 MAACCLALATLTLFQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVNC
 QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 DB 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQHAHAVHIPTDIYEGS
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGQISYQHAHAVHIPTDIYEGS
 QY 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWWNSRTNKIDLY
 DB 181 NELNWTSSALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWWNSRTNKIDLY
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVASFNS
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVASFNS
 QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQELLNINVRANCNK
 DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQELLNINVRANCNK
 QY 361 FTDGGERAQEIFKNYKMDKKVRFRFSPVSGQHNRYERGPICWMACENKGYTYEIPSI
 DB 361 FTDGGERAQEIFKNYKMDKKVRFRFSPVSGQHNRYERGPICWMACENKGYTYEIPSI
 QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLLDALELGLVITGTLFVFNITGQFENK
 DB 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLLDALELGLVITGTLFVFNITGQFENK

ILGVMGVDSLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPLNLPKNPKSQBPVTL 540
 ILGVMGVDSLEDIKRLTPRTFLCPNGYFAIDPNGYVLLHPLNLPKNPKSQBPVTL 540
 DAELNDIKVEIRKMDIGESGKTFRLVKSQDERYLDKGNRTYTTWTPVNGTDSL 600
 DAELNDIKVEIRKMDIGESGKTFRLVKSQDERYLDKGNRTYTTWTPVNGTDSL 600
 LPTYSFYIKAKLBETITQARSKKGMKDSKTLKPDNFEESGYTFIAPRDYCNLDKI 660
 LPTYSFYIKAKLBETITQARSKKGMKDSKTLKPDNFEESGYTFIAPRDYCNLDKI 660
 NTEFLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSQKNKIGVKAR 720
 NTEFLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNTWSQKNKIGVKAR 720
 TDGGITRVYPKEAGENWQENPETVEDSPYKESLNDNDNVFTAPYFNKSGPGAYESGI 780
 TDGGITRVYPKEAGENWQENPETVEDSPYKESLNDNDNVFTAPYFNKSGPGAYESGI 780
 KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVMDCVI 840
 GGFLLMANHDYTNQIGRFFGEIDPSLMRHLVNI SVTAFNKSQYQSVCEPGAAPKQ 900
 GGFLLMANHDYTNQIGRFFGEIDPSLMRHLVNI SVTAFNKSQYQSVCEPGAAPKQ 900
 HRSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGWATAAASILQOFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
 TEOTQYFDDNDSKFSGLDCGNCRI PHGKLMNTNLIFIMVESKGTCPCDTRLLI 1020
 TEOTQYFDDNDSKFSGLDCGNCRI PHGKLMNTNLIFIMVESKGTCPCDTRLLI 1020
 QTSQGNPCDMVK 1036
 QTSQGNPCDMVK 1036

ndard; Protein; 1091 AA.

(first entry)

ed soluble alphasdelta calcium channel subunit #15 protein.

ted calcium channel alphasdelta subunit; alphasdelta-2;
 3; alphasdelta-4; voltage-dependent calcium channel; VDCC;
 scintillation proximity assay; SPA; nickel flashplate assay;
 ng assay; wheat germ lectin flashplate assay.

A2.

2000WO-EP09137.

99US-0397550.

ER LAMBERT CO.

ertelli F;

5262/24.
 1426.

XX Calcium channel alphasdelta subunits, useful in e.g. SPA assays,
 PT Flashplate assays, Nickel Flashplate assays, Filter binding as-
 PT Wheat Germ Lectin Flashplate assays -
 XX
 PS Claim 30; Page 141-144; 160pp; English.

XX The present sequence represents human secreted calcium channel
 CC alphasdelta subunit #15 which is soluble and retains the func-
 CC characteristics of the full length or wild type alphasdelta sub-
 CC (AAU01025) from which it is derived. The invention relates to
 CC alphasdelta-2, alphasdelta-3 or alphasdelta-4 subunit soluble pr-
 CC which retain their affinity for radioactively labelled gabapenti-
 CC alphasdelta subunit is 1 of the components of the heteromultimer
 CC voltage-dependent calcium channel (VDCC) complexes present in ne-
 CC and non-neuronal tissues including heart and skeletal muscle. N
 CC soluble forms of the human calcium channel alphasdelta subunits
 CC (AAU01014-AAU01024 and AAU01032-AAU01038) and 5 soluble forms of
 CC porcine calcium channel alphasdelta subunits (AAU01027-AAU01031)
 CC described. The secreted soluble alphasdelta subunit may be used
 CC e.g. scintillation proximity assay (SPA), flashplate, nickel fla-
 CC filter binding or wheat germ lectin flashplate assays to detect
 CC measure the binding or interaction of a ligand (e.g. gabapentin,
 CC L-Norleucine, L-Allo-isoleucine, L-methionine, L-leucine, L-Iso-
 CC L-valine, Spermine and/or L-Phenylalanine) of a calcium channel
 CC alphasdelta subunit.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 22; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTLTLFQSLLIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGV
 DB 1 MAAGCLLALTLTLFQSLLIGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGV
 QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQWRF
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQWRF
 QY 121 EVVYNAKDDLDPEKNDSEPGSRIKPVRTIEDANFGROI SYQHAHVHIPTDIYEG
 DB 121 EVVYNAKDDLDPEKNDSEPGSRIKPVRTIEDANFGROI SYQHAHVHIPTDIYEG
 QY 181 NELNWTSSALDEVPKKNREEDPSLLWQVFGSATGLARYYPASPWVDSRSTENKIDI
 DB 181 NELNWTSSALDEVPKKNREEDPSLLWQVFGSATGLARYYPASPWVDSRSTENKIDI
 QY 241 RPWYIQGAASPDKMLILVDVSGSVSGITLKLINTSVSEMLETSDDDFVNVSFN
 DB 241 RPWYIQGAASPDKMLILVDVSGSVSGITLKLINTSVSEMLETSDDDFVNVSFN
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKGFSFAFEQLLNYSRANCN
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITYDKGFSFAFEQLLNYSRANCN
 QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSQGHNYERGPQIMACENKGYEYIIPS
 DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFVSQGHNYERGPQIMACENKGYEYIIPS
 QY 421 INTQEYLDVLGRPMWLAGDKAKQVQNTNVLDALELGLVITGTLPVFNITGQFEN
 DB 421 INTQEYLDVLGRPMWLAGDKAKQVQNTNVLDALELGLVITGTLPVFNITGQFEN
 QY 481 NQLILGVMGVDVSLIEDIKLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKNPKSQ
 DB 481 NQLILGVMGVDVSLIEDIKLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKNPKSQ
 QY 541 DFLDAELENIDIKVEIRKMDIGESGKTFRLVKSQDERYLDKGNRTYTTWTPVNG
 DB 541 DFLDAELENIDIKVEIRKMDIGESGKTFRLVKSQDERYLDKGNRTYTTWTPVNG

PTSYIYKAKLEETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCNLKI 660
PTSYIYKAKLEETITQARSKGKMDSETLKPDNFESGYTFIAPRDYCNLKI 660
TEFLINFEFIDRKTNNPSCNADLINRVLLDAGFTNHLVQYWSKQNIKVAK 720
TEFLINFEFIDRKTNNPSCNADLINRVLLDAGFTNHLVQYWSKQNIKVAK 720
TGGITRVYPKAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAYESGI 780
TGGITRVYPKAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAYESGI 780
TAVEYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDMDCVI 840
TAVEYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDMDCVI 840
GFLMANHDDYTNQIGRFFGEIDPSLMRLVNI SVYAFNKSYDYQSVCEPGAAPKQ 900
GFLMANHDDYTNQIGRFFGEIDPSLMRLVNI SVYAFNKSYDYQSVCEPGAAPKQ 900
RSAYVPSVADILQIGWATAAAMSILQOFLSLTPPRLLEAVEMEDDDFTASLSKQ 960
RSAYVPSVADILQIGWATAAAMSILQOFLSLTPPRLLEAVEMEDDDFTASLSKQ 960
TQTYFFDNDKSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRLII 1020
TQTYFFDNDKSGVLDGNCNCSRI FHGEKLMNTNLI FIMVESKGTCPDTRLII 1020
TSDGPNPCDMVK 1036
TSDGPNPCDMVK 1036

dard; Protein; 1091 AA.

(first entry)

um channel alpha2delta subunit.

el alpha2delta subunit; alpha2delta-1; cerebral cortex;
m disorder; pain; epilepsy; anxiety; pig.

2.

2000WO-EP09136.

98US-0397549.

R LAMBERT CO.

Brown JP, Dissanayake V, Suman-Chauhan N, Gee NS;

902/26.
563.

inding assay for screening ligands which bind a cerebral
age-dependent calcium channel alpha2-delta-1 subunit,
ands identified are useful for treating disorders of the
m, including pain -

139-142; 158pp; English.

relates to a new method for screening ligands which bind a
ical voltage-dependent calcium channel alpha2delta subunit,
pha2delta-1 subunit. The method comprises contacting a

CC secreted soluble recombinant alpha2delta-1 subunit with a ligand
CC interest and a labelled compound which binds the subunit, follow
CC measuring the level of binding of the labelled compound to alpha
CC subunit. The method is useful for screening ligands, preferably
CC biologically active products that modulate a nervous system func
CC which bind a cerebral cortical voltage-dependent calcium channel
CC alpha2delta-1 subunit. The ligands identified by the method are
CC for treating disorders of the nervous system, including pain, ep
CC and anxiety. The present sequence represents a porcine calcium C
CC alpha2delta subunit.

XX Sequence 1091 AA;

Query Match 100.0%; Score 5443; DB 22; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTTLTFLQSLIIGPSSSEPPFSAVTIKSVVDKMQEDLVTLAKTAGVNI
Db 1 MAAGCLLALTTLTFLQSLIIGPSSSEPPFSAVTIKSVVDKMQEDLVTLAKTAGVNI
QY 61 YEKYQDLTYVEPNARQVETAAARDIEKLSNRSKALVSLAEAEKQVAAHOREI
Db 61 YEKYQDLTYVEPNARQVETAAARDIEKLSNRSKALVSLAEAEKQVAAHOREI
QY 121 EVVYNAKDDLDPKNDSEPGSORIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
Db 121 EVVYNAKDDLDPKNDSEPGSORIKPVFIEDANFGROI SYOHAHVHIPTDIYEG
QY 181 NELNWTISALDEVFKKQREDEPSLLWQVFGSATGLARYYPASVWVNSRTPNKIDL
Db 181 NELNWTISALDEVFKKQREDEPSLLWQVFGSATGLARYYPASVWVNSRTPNKIDL
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSLDDDFNVNASFNI
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLRISVSEMLETSLDDDFNVNASFNI
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAGITDYKKGFSFAFEQLLNNVSRANCI
Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAGITDYKKGFSFAFEQLLNNVSRANCI
QY 361 FTDGGEERAQEI FNKYNKKVRVFRFSGVGHYERGPIONMACENKGYIYEIPSI
Db 361 FTDGGEERAQEI FNKYNKKVRVFRFSGVGHYERGPIONMACENKGYIYEIPSI
QY 421 INTQYLDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITQGFENI
Db 421 INTQYLDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITQGFENI
QY 481 NQLILGYMGVDVSLIEDIKRLTPRFTLCPNGYYPFADIPNGYVLLHPNLPKPKSQE
Db 481 NQLILGYMGVDVSLIEDIKRLTPRFTLCPNGYYPFADIPNGYVLLHPNLPKPKSQE
QY 541 DFLDAELENDIKVEIRNKMIDGESSEKTFRTLKVSQDERYIDKGNRTYVTPVNGT
Db 541 DFLDAELENDIKVEIRNKMIDGESSEKTFRTLKVSQDERYIDKGNRTYVTPVNGT
QY 601 ALVLPYTSFYIYKAKLETTITQARSKGKMDSETLKPDNFESGYTFIAPRDYCN
Db 601 ALVLPYTSFYIYKAKLETTITQARSKGKMDSETLKPDNFESGYTFIAPRDYCN
QY 661 SDNNTTEFLANFEFIDRKTNNPSCNADLINRVLLDAGFTNHLVQYWSKQNIKV
Db 661 SDNNTTEFLANFEFIDRKTNNPSCNADLINRVLLDAGFTNHLVQYWSKQNIKV
QY 721 FVVTGIGITRVYPKAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAY
Db 721 FVVTGIGITRVYPKAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGAY
QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDVM
Db 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDVM

3GFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSYDQSVCEPGAAPKQ 900
3GFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNSVYAFNKSYDQSVCEPGAAPKQ 900

ERSAVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
 |||||
 ERSAVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLAEVEMEDDDFTASLSKQ 960
 |||||

TEQTQYFFDNDKSFSGVLDCGNCSPIFHGEKLMNTNLI FIMVSKGTCPCDTRLLI 1020
|||||
TEQTQYFFDNDKSFSGVLDCGNCSPIFHGEKLMNTNLI FIMVSKGTCPCDTRII 1020
|||||

CTSDGPNPCDMVK 1036
|||||
CTSDGPNPCDMVK 1036

Standard: Protein: 1091 AA.

(first entry)

n channel alpha 2b subunit protein.

um channel protein; therapeutic; autoimmune disease;
ambert Eaton Syndrome: alpha 2b subunit.

95US-0450272.

89WO-US01408.
90US-0603751.
92US-0914231.
90US-0482384.
90US-0620250.
91US-0745206.
92WO-US06903.
93US-0105536.
93US-0149097.
94US-0193078.
94US-0311363.
94US-0336257.
95US-0404354.

K & CO. INC.

Ellis SB, Williams ME, McCue AF;

0318/50.
0959.

cells expressing a functional heterologous human calcium encoding nucleic acid isolated from human cerebellum for and to diagnose Lambert Eaton Syndrome -

Column 137-144: 154pp: English.

invention relates to novel human calcium channel proteins or peptides encoding such proteins. The invention also relates to cells expressing a functional heterologous human calcium channel $\alpha 1$, $\alpha 2$, β and γ subunits. The eukaryotic cells or screening for potential calcium channel antagonists or select compounds that have potential as disease or tissue-repurgic agents. The subunits may be used in diagnostic or autoimmune disease Lambert Eaton Syndrome. The present

CC	sequence is human calcium channel alpha 2b subunit protein.														
XX															
SQ	Sequence	1091 AA;													
	Query Match	100.0%;	Score	5443;	DB	23;	Length	1091;							
	Best Local Similarity	100.0%;	Pred. No.	0;											
	Matches 1036;	Conservative	0;	Mismatches	0;	Indels	0;								
QY	1	MAAGCLLALTLTFLQSLILIGPSSSEPPSPASVTIKSWVDKMQEDLVTLAKTAGSVN													
Db	1	MAAGCLLALTLTFLQSLILIGPSSSEPPSPASVTIKSWVDKMQEDLVTLAKTAGSVN													
QY	61	YEKYQDLVTVPNNAQLVEIARIDIEKLISNRKALVLSLAEKVKQAQAHQWRE													
Db	61	YEKYQDLVTVFPNARQLVEIARIDIEKLISNRKALVLSLAEKVKQAQAHQWRE													
QY	121	EVVYNAKDDLDPEKNSEPGSQRIKEPVFIEDANFGRQISYQHAAVHIPTDIYEG													
Db	121	EVVYNAKDDLDPEKNSEPGSQRIKEPVFIEDANFGRQISYQHAAVHIPTDIYEG													
QY	181	NELNWTSSALDEVFKKNREEDPSLLQVFGSATGLARYYPASPWDNSRTPNKIDL													
Db	181	NELNWTSSALDEVFKKNREEDPSLLQVFGSATGLARYYPASPWDNSRTPNKIDL													
QY	241	RPWYIQTGAASPKDMLILVDYSGVSGVLTGLIKRTSVSEMLETLISDDDFVNVASFN													
Db	241	RPWYIQTGAASPKDMLILVDYSGVSGVLTGLIKRTSVSEMLETLISDDDFVNVASFN													
QY	301	VSCFOHLVQAVNRNKKVLKQAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCN													
Db	301	VSCFOHLVQAVNRNKKVLKQAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCN													
QY	361	FTDGGEERAQEIFNKYNKKVVRFRFSVUGHYVERGPIQWMAKENKGYIYEIIPS													
Db	361	FTDGGEERAQEIFNKYNKKVVRFRFSVUGHYVERGPIQWMAKENKGYIYEIIPS													
QY	421	INTQBYLDVLGRPMVLADGKAKQVQWNTNVYLDLLEGLVITGTLVPFNITGQFEN													
Db	421	INTQBYLDVLGRPMVLADGKAKQVQWNTNVYLDLLEGLVITGTLVPFNITGQFEN													
QY	481	NQLILGVNGVDVSLIEDIKRLTPRTLCPNGYYFAIDPBGVYVLHPLNLPKNPKSQ													
Db	481	NQLILGVNGVDVSLIEDIKRLTPRTLCPNGYYFAIDPBGVYVLHPLNLPKNPKSQ													
QY	541	DFDLDAELENDIKVIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYIWTVPWG													
Db	541	DFDLDAELENDIKVIRNKMIDGESGKFTRTLKVSQDERYIDKGNRTYIWTVPWG													
QY	601	ALVLPETISFYIYKAKLBETITQARKKGKMDSETLKPDNFBESGYTFTAPRDYC													
Db	601	ALVLPETISFYIYKAKLBETITQARKKGKMDSETLKPDNFBESGYTFTAPRDYC													
QY	661	SDNNTEFLNNEFIIDRKTNNPNSCNADLNRLVDAGFTNELVQNYMSKQNKIK													
Db	661	SDNNTEFLNNEFIIDRKTNNPNSCNADLNRLVDAGFTNELVQNYMSKQNKIK													
QY	721	FVVTDDGTRIVYPKEAGENQENPETYDSFYKRSLDNDNYVFTAPYFNKSGPGA													
Db	721	FVVTDDGTRIVYPKEAGENQENPETYDSFYKRSLDNDNYVFTAPYFNKSGPGA													
QY	781	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCCDKRNSDV													
Db	781	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCCDKRNSDV													
QY	841	LDDGGFLLMANHDDYTQIGRFFGEIDPSLMRLHLNIVSYAFNKSVDYQSVCEPGI													

|||||
 EQTYFFDNDKSFSGVLDCGNCRIHFGKLMNTLFIWVESKGTCPCTRLLI 1020

TS DGNPCDMVK 1036
 |||||
 TS DGNPCDMVK 1036

Idard; Protein; 1091 AA.

(first entry)

channel a2d subunit.

el; human; central nervous system disorder;
 syndrome; diagnosis; therapy.

97WO-US16146.

96US-0713118.

CAN HOME PROD CORP.

anco R, Shuey DJ;

325/18.

1060.

human neuronal calcium channel subunit(a) - useful for
 and treatment of central nervous system disorders, e.g.
 syndrome

Fig 2; 89pp; English.

ide comprises the a2d subunit of the human neuronal
 el. cDNA clones (see AAV29059-61) encoding the a1B
 AAW37878), the a2d subunit and a b3 subunit (see AAW37880)
 lated. These have been inserted into expression
 are stably expressed in transformed cell lines. The
 cells show omega-conotoxin GVIA binding activity. The
 ototoxin GVIA toxin sensitive potassium-stimulated
 ke, indicating that the proteins expressed by the
 iple of forming a functioning calcium channel.
 encoding the 3 subunits, as well as vectors, host
 hods of isolating nucleic acids encoding related
 els are disclosed. Fusion proteins incorporating the
 ins, antibodies, and assays for identifying agents
 calcium channel activity are also provided. Such
 used to treat certain central nervous system
 altering calcium channel activity. Methods of
 eases associated with particular calcium channels,
 art-Eaton syndrome, are disclosed.

991 AA;

99.9%; Score 5439; DB 19; Length 1091;

larity 99.9%; Pred. No. 0;

conservative 0; Mismatches 1; Indels 0; Gaps 0;

LCALLATLTLFQSLIGPSEEPFPPSAVTKSMWDKMQEDLVTLAKTAGVNLVDI 60

LCALLATLTLFQSLIGPSEEPFPPSAVTKSMWDKMQEDLVTLAKTAGVNLVDI 60

QY 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQRRE
 DB 61 YEKYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAAHQRRE
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHPTDIYEG
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYOHAHVHPTDIYEG
 QY 181 NELNWTSAALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 DB 181 NELNWTSAALDEVFKKNREDEPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETLSDDDFVNVSFN
 DB 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRISVSEMLETLSDDDFVNVSFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFQQLNLYNVRANCN
 DB 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFQQLNLYNVRANCN
 QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVGOHNYERGPIQWMACENKGYIYIIPS
 DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVGOHNYERGPIQWMACENKGYIYIIPS
 QY 421 INTQEYLDVLGRPMVLADGKAKQVQMTNLYLDALBLGLVITGLTFVFNITQGFEN
 DB 421 INTQEYLDVLGRPMVLADGKAKQVQMTNLYLDALBLGLVITGLTFVFNITQGFEN
 QY 481 NQLILGVNGVDVSLIEDIIRLTPRFLCPNGYFPAIDPNGYVLLHNPLOPKNPKSQ
 DB 481 NQLILGVNGVDVSLIEDIIRLTPRFLCPNGYFPAIDPNGYVLLHNPLOPKNPKSQ
 QY 541 DFLDAELNDIKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 DB 541 DFLDAELNDIKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPYSFYIYIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRDYCI
 DB 601 ALVLPYSFYIYIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRDYCI
 QY 661 SDNTEFLINFEPIIDRKTNNPNSCNADLINRVLLDAGFTNBLVONTYWSKQNNIK
 DB 661 SDNTEFLINFEPIIDRKTNNPNSCNADLINRVLLDAGFTNBLVONTYWSKQNNIK
 QY 721 FVVTGGITRVYVPEKAGNMQENPETYDSFYKRSIDNDNYVFTAPYFNKSGPGA
 DB 721 FVVTGGITRVYVPEKAGNMQENPETYDSFYKRSIDNDNYVFTAPYFNKSGPGA
 QY 781 MVSKAVEIYIQGLLKPAVVGKIDVNSWNIENFTKTSIRDPCAGPVCDCRNSDVI
 DB 781 MVSKAVEIYIQGLLKPAVVGKIDVNSWNIENFTKTSIRDPCAGPVCDCRNSDVI
 QY 841 LDGCGFLLMANHDDYTNOIGRPFGEIDSLMRHLNYSVYAFNKSYDYQSVCEPG
 DB 841 LDGCGFLLMANHDDYTNOIGRPFGEIDSLMRHLNYSVYAFNKSYDYQSVCEPG
 QY 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAVEMEDDDFTA
 DB 901 GAGHSAYVPSVADILQIGWATAAWSILOQFLLSLTFPRLEAVEMEDDDFTA
 QY 961 SCITEQTYFFDNDKSFSGVLDCGNCRSRI FHGEKLMNTLFIWVESKGTCPD
 DB 961 SCITEQTYFFDNDKSFSGVLDCGNCRSRI FHGEKLMNTLFIWVESKGTCPD
 QY 1021 QABQTS DGNPCDMVK 1036
 DB 1021 QABQTS DGNPCDMVK 1036

RESULT 12

AAR33553

ID AAR33553 standard; Protein; 1091 AA.

XX

95US-0455543.
94US-0223305.
88US-0176899.
89WO-US01408.
90US-0482384.
90US-0603751.
90US-0620250.
91US-0745206.
NEUROSCIENCES INC.
llie SB, Feidman DH, Harpold MM, McCue AF;
192/39.
594.
human calcium channel alpha 1B subunit protein -
combinant production of the channel for screening of
3, and diagnosis of Lambert Eaton Syndrome
columns 131-138; 166pp; English.
sequence represents the alpha-2 subunit of a human calcium
ium channels are membrane-spanning, multi-subunit proteins
attrolled entry of calcium ions into cells. This leads
ion events required for muscle contraction. The recombinant
expressed with nucleic acids encoding the complete calcium
be used in assays for the detection and characterization of
e modulate the channel. The DNA encoding the subunits can
ely spliced when transcribed, giving more than one form of
rom the same transcript, each having slightly different
a addition, the reactivity of the alpha 1 subunit with IgG
n the serum of an individual with Lambert Eaton Syndrome
used as a diagnostic for the disease.
5-MAR-2003 to correct PR field.)
10 AA;
99.6%; Score 5423.5; DB 19; Length 1110;
arity 98.2%; Pred. No. 0;
nservative 0; Mismatches 0; Indels 19; Gaps 1;
CLALTLTLFQSLILIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
|||||
CLALTLTLFQSLILIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
QDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAKVQAQAHQWREDFASN 120
QDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAKVQAQAHQWREDFASN 120
YNAKDDLDPKNDSEPSQRIKPVIFEDANFGROIYQHAHVHTPTDIYEGSTIVL 180
YNAKDDLDPKNDSEPSQRIKPVIFEDANFGROIYQHAHVHTPTDIYEGSTIVL 180
WTSALDVEFKKREEDPSLLWQVFGSATGLARYYPASFWVDSRTPNKIDLYDVR 240
WTSALDVEFKKREEDPSLLWQVFGSATGLARYYPASFWVDSRTPNKIDLYDVR 240
IQGAASPKDMLILVDVSGVSGSLTLKILRTSVSEMLTSLDDDFNVASFNNAQD 300
IQGAASPKDMLILVDVSGVSGSLTLKILRTSVSEMLTSLDDDFNVASFNNAQD 300
QHLVQANVRNKKVLKQAVNNITAKGIDTYKKGFSFAFEQLLNYNVSRANCKIIML 360
QHLVQANVRNKKVLKQAVNNITAKGIDTYKKGFSFAFEQLLNYNVSRANCKIIML 360
GEERAQEIFNKNYKDKKVRVFSVQGHNYERGPIQWMACENKGYVEIPSI 420
|||||

Db 361 FTDGGERRAQEIEFNKNKDKKVRVFRFSPVQGHNYERGPIQWMACENKGYVEIPSI
Qy 421 INTQEYLDVLGRPMVLADGAKAQVQWNTNVYLDALGLVITGLPVFNITQGFENK
Db 421 INTQEYLDVLGRPMVLADGAKAQVQWNTNVYLDALGLVITGLPVFNITQGFENK
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYYFAIDPBGVVLHPNLQPK-----
Db 481 NQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYYFAIDPBGVVLHPNLQPKPIGVGI
Qy 531 -----NPKSQEPVTLDFDAELENDIKVEIRNKMIDGESSEKTFRTLKVSQD
Db 541 LRKERPNIQPKSQEPVTLDFDAELENDIKVEIRNKMIDGESSEKTFRTLKVSQD
Qy 582 DKGNTYTTWTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARSKKGMKQDSETLK
Db 601 DKGNTYTTWTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARSKKGMKQDSETLK
Qy 642 EESGYTFIAPRDYCNLDKISDNNTEFLNFEFIDRKTNNPSCNADLINRVLLDA
Db 661 EESGYTFIAPRDYCNLDKISDNNTEFLNFEFIDRKTNNPSCNADLINRVLLDA
Qy 702 ELQNVYWSKQNIKGKVKARFVTDGGITRVYPKEAGENWOENPETYEDSFYKRLD
Db 721 ELQNVYWSKQNIKGKVKARFVTDGGITRVYPKEAGENWOENPETYEDSFYKRLD
Qy 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTS
Db 781 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTS
Qy 822 CAGPVCCKNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI
Db 841 CAGPVCCKNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI
Qy 882 FNKSYDYQSCECAAPKQAGHRSAYVPSVADILQIGMWATAAASWILQOFLLSL
Db 901 FNKSYDYQSCECAAPKQAGHRSAYVPSVADILQIGMWATAAASWILQOFLLSL
Qy 942 LLRAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKSPSGVLDCNCRSRIFHGEKLM
Db 961 LLRAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKSPSGVLDCNCRSRIFHGEKLM
Qy 1002 IFIMVESKGTCPDTRLIIQAEQTSDGNPCDMVK 1036
Db 1021 IFIMVESKGTCPDTRLIIQAEQTSDGNPCDMVK 1055
RESULT 14
AAR71013
ID AAR71013 standard; Protein; 1086 AA.
XX
AC AAR71013;
XX
AC
DT 25-MAR-2003 (updated)
DT 01-DEC-1995 (first entry)
XX Human neuronal calcium channel subunit alpha 2c.
DE
XX
KW Calcium channel subunit; antagonist; agonist; diagnosis;
KW Lambert Eaton Syndrome.
XX Homo sapiens.
XX
XX WO9504822-A1.
XX
PD 16-FEB-1995.
XX
PF 11-AUG-1994; 94WO-US09230.
XX
PR 11-AUG-1993; 93US-0105536.
PR 05-NOV-1993; 93US-0149097.
XX
PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

J. Lespie A, Harpold MM, McCue AF, Williams ME;

900/12.

1667.

human calcium channel sub-unit (a) - used for
ods. for studying calcium channels, e.g. for
mists and antagonists

Page 237-242; 285pp; English.

il alpha 2 coding sequence (AA084664) transcript is
y processed in skeletal muscle, aorta, and CNS in
resp. to nt 1595-1942 of AA084664 in each of the
a alternatively spliced variant transcripts that differ
ice or absence or one to three different portions of
There are three sequences involved (see AA084664. FT
FI), sequence 1, sequence 2 and sequence 3. The five
ing transcripts from the different tissues include
binations of the three sequences, except for one of
transcripts expressed in aorta which lacks all three
e five alpha 2 forms identified are (1) a form that
e 3 called alpha 2a, expressed in skeletal muscle
lacks sequence 1 called alpha 2b, expressed in CNS
lacks sequences 1 and 2 called alpha 2c, expressed in
a that lacks sequences 1, 2 and 3 called alpha 2d,
aorta and (5) one that lacks sequences 1 and 3
2e. The DNA and AA sequences of alpha 2a - alpha 2e
1 in AA084666-Q84669 and AAR71012-R71015 respectively.
15-MAR-2003 to correct PN field.)

86 AA;

arity 99.3%; Score 5403.5; DB 16; Length 1086;

larity 99.5%; Pred. No. 0;

conservative 0; Mismatches 0; Indels 5; Gaps 1;

XCLLAULTLTFQSLIGPSSEPPPSAVTIKSWDKMQEDLVLTAKTAGVNLVDI 60
XCLLAULTLTFQSLIGPSSEPPPSAVTIKSWDKMQEDLVLTAKTAGVNLVDI 60
QDLTYTEPNNAQLVEIAARDIEKLSNRKALVSLALEAEKVQAAHQWREDFASN 120
QDLTYTEPNNAQLVEIAARDIEKLSNRKALVSLALEAEKVQAAHQWREDFASN 120
YNKADDLPEKNDSPGSRQIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
YNKADDLPEKNDSPGSRQIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
WTSALDEVPKNREEDPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240
WTSALDEVPKNREEDPSLLMQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240
ZIQGAASPKDMLTLVDVSGSVGLTKLIRTSVSEMLETSLDDDFNVNASFNSNAOD 300
ZIQGAASPKDMLTLVDVSGSVGLTKLIRTSVSEMLETSLDDDFNVNASFNSNAOD 300
FOHLVQANVNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNNVSRANCKNIIML 360
FOHLVQANVNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNNVSRANCKNIIML 360
ZGERAQEI FNKNKDKKVRFRFSPVQGHNYERGPQIOMMACENKGYIYEIPSGAIR 420
ZGERAQEI FNKNKDKKVRFRFSPVQGHNYERGPQIOMMACENKGYIYEIPSGAIR 420
ZEVLDVLRPMVLGADKAKOVNTNYLDLLEGLVITGTPLPNTTQGFENKTNLK 480
ZEVLDVLRPMVLGADKAKOVNTNYLDLLEGLVITGTPLPNTTQGFENKTNLK 480
ILGVMGVDSLEDKRLTPRTFLCPNGYGYFAIDPNGVYLLHPNLQPNKPSQBPVTL 540
ILGVMGVDSLEDKRLTPRTFLCPNGYGYFAIDPNGVYLLHPNLQPK-----EPVTL 535

QY 541 DFLDAELNDIKVEIRNKIMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
DB 536 DFLDAELNDIKVEIRNKIMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
QY 601 ALVLTYSFYIKAKLEETITQARSKKGKMDSETLKPDNFESGYTFTIAPRDYC
DB 596 ALVLTYSFYIKAKLEETITQARSKKGKMDSETLKPDNFESGYTFTIAPRDYC
QY 661 SDNTEFLNFEFIDRKTNNPNCNADLINRVLLDAGFTNELVQNYMSKQKNIK
DB 656 SDNTEFLNFEFIDRKTNNPNCNADLINRVLLDAGFTNELVQNYMSKQKNIK
QY 721 FVVTGGITRVYVPKEAGENQWNPETYEDSFYKRSIDNDNYVFTAPYFNKSGPGA
DB 716 FVVTGGITRVYVPKEAGENQWNPETYEDSFYKRSIDNDNYVFTAPYFNKSGPGA
QY 781 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCRNSDVI
DB 776 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWNIENFTKTSIRDPKAGPVCDCRNSDVI
QY 841 LDGGFLMANHDDYTNOIGREFGIDPFLMHLVNI SVYAFNKSYDYQSVCEPG.
DB 836 LDGGFLMANHDDYTNOIGREFGIDPFLMHLVNI SVYAFNKSYDYQSVCEPG.
QY 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTA
DB 896 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTA
QY 961 SCITQOTQYFFNDNSKSPGVLDGNCGRIPHEKLMNTLIFIMVESKGTCPCD
DB 956 SCITQOTQYFFNDNSKSPGVLDGNCGRIPHEKLMNTLIFIMVESKGTCPCD
QY 1021 QAEQTSDEGNPCDMVK 1036
DB 1016 QAEQTSDEGNPCDMVK 1031
RESULT 15
AAW63153
ID AAW63153 standard; Protein; 1086 AA.
XX
AC AAW63153;
XX
DT 25-MAR-2003 (updated)
DT 12-OCT-1998 (first entry)
XX
DE Human calcium channel alpha-2c subunit.
XX
KW Alpha-2 subunit; human; calcium channel; assay; detection;
KW Characterisation; Lambert Eaton Syndrome; LES; diagnosis.
XX
OS Homo sapiens.
XX
PN US5792846-A.
XX
PD 11-AUG-1998.
XX
PF 31-MAY-1995; 95US-0455543.
XX
PR 04-APR-1994; 94US-0223305.
PR 04-APR-1988; 88US-0176899.
PR 04-APR-1989; 89WO-US01408.
PR 20-FEB-1990; 90US-0482384.
PR 08-NOV-1990; 90US-0603751.
PR 30-NOV-1990; 90US-0620250.
PR 15-AUG-1991; 91US-0745206.
XX
PA (SIBI-) SIBIA NEUROSCIENCES INC.
XX
PI Brenner R, Ellis SB, Feldman DH, Harpold MM, McCue AF;
PI Williams ME;
XX

661	QY	SDNNTEFLLFNFEFIDRKTENNPNPCNADLINRVLLDAGFTNELVQNYNSKQXNIIK
656	Db	SDNNTEFLLFNFEFIDRKTENNPNPCNADLINRVLLDAGFTNELVQNYNSKQXNIIK
721	QY	FVVTDDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGA
716	Db	FVVTDDGGITRVYPKEAGENQENPETEYDSFYKRSLDNDNYVFTAPYFNKSGPGA
781	QY	MVSKAVEIYIQGKLLKPAVVGIIKDYNWIENTFTKTSIRDPCAGPVCDCRNSDVI
776	Db	MVSKAVEIYIQGKLLKPAVVGIIKDYNWIENTFTKTSIRDPCAGPVCDCRNSDVI
841	QY	LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGI
836	Db	LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGI
901	QY	GAGHSAYVPSVADILQIGHWATAAAMSIIQQFLLSLTFPRLLLEAVEMEDDDFTA
896	Db	GAGHSAYVPSVADILQIGHWATAAAMSIIQQFLLSLTFPRLLLEAVEMEDDDFTA
961	QY	SCITEQTQYFPDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIIFIMVYESKGTCPCDY
956	Db	SCITEQTQYFPDNDKSFSGVLDCGNCRSRIFHGEKLMNTNLIIFIMVYESKGTCPCDY
1021	QY	QAEQTSQGNPCDMVK 1036
1016	Db	QAEQTSQGNPCDMVK 1031

Search completed: February 20, 2004, 16:55:15
Job time : 40.5579 secs

GenCore version 5.1.6
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in search, using sw model

bruary 20, 2004, 16:53:09 ; Search time 18.0748 Seconds
(without alignments)
2488.357 Million cell updates/sec

10-090-827-15

MAAGCLLALTLFOSLLIG.....PDVCFDNNVLDYDTCGVVS 1063

OSUM62

pop 10.0 , Gapext 0.5

8717 seqs, 42310858 residues

ts satisfying chosen parameters: 328717

gth: 0

gth: 2000000000

imum Match 0%

isting first 45 summaries

ssued Patents AA:*

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/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pap:*

/cgn2_6/ptodata/1/1aa/backfiles1.pap:*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ery	tch	Length	DB	ID	Description
0.0	0.0	1091	1	US-07-745-543A-25	Sequence 25, Appl
0.0	1091	1	US-08-455-543A-52	Sequence 52, Appl	
0.0	0.0	1091	2	US-08-223-305C-52	Sequence 52, Appl
0.0	0.0	1091	2	US-08-311-363-25	Sequence 25, Appl
9.9	1091	3	US-08-713-118-4	Sequence 4, Appl	
9.9	1091	3	US-09-452-007-4	Sequence 4, Appl	
9.3	1086	1	US-08-455-543A-54	Sequence 54, Appl	
9.3	1086	2	US-08-223-305C-54	Sequence 54, Appl	
9.0	1084	1	US-08-455-543A-56	Sequence 56, Appl	
9.0	1084	2	US-08-223-305C-56	Sequence 56, Appl	
8.6	1103	1	US-08-455-543A-53	Sequence 53, Appl	
8.6	1103	2	US-08-223-305C-53	Sequence 53, Appl	
8.3	1079	1	US-08-455-543A-55	Sequence 55, Appl	
8.3	1079	2	US-08-223-305C-55	Sequence 55, Appl	
16.2	1106	1	US-08-435-675B-5	Sequence 5, Appl	
15.9	1106	1	US-08-435-675B-8	Sequence 8, Appl	
11.7	1086	6	5386025-8	Patent No. 5386025	
13.7	1145	4	US-09-470-443-2	Sequence 2, Appl	
13.7	1145	4	US-09-470-443-4	Sequence 4, Appl	
13.3	1076	4	US-09-470-443-6	Sequence 6, Appl	
16.1	508	1	US-08-435-675B-6	Sequence 6, Appl	
3.3	885	3	US-09-074-579-5	Sequence 5, Appl	
3.3	885	3	US-09-388-774-5	Sequence 5, Appl	
3.3	846	3	US-09-388-774-3	Sequence 3, Appl	
2.8	946	3	US-09-074-579-3	Sequence 3, Appl	
2.8	946	3	US-09-388-774-3	Sequence 3, Appl	
2.8	894	4	US-09-071-035-248	Sequence 248, App	
2.8	962	4	US-09-071-035-246	Sequence 246, App	

28	158.5	2.8	962	4	US-09-071-035-250	Sequence
29	158.5	2.8	962	4	US-09-071-035-254	Sequence
30	158.5	2.8	962	4	US-09-071-035-470	Sequence
31	158.5	2.8	962	4	US-09-071-035-474	Sequence
32	158.5	2.8	962	4	US-09-071-035-478	Sequence
33	154.5	2.8	946	4	US-09-546-153-1	Sequence
34	154	2.8	903	1	US-08-021-601-12	Sequence
35	154	2.8	903	1	US-08-082-849B-12	Sequence
36	154	2.8	903	5	PCT-US94-01624-12	Sequence
37	152.5	2.7	789	1	US-08-471-033-32	Sequence
38	152.5	2.7	789	2	US-08-471-044-32	Sequence
39	152.5	2.7	789	2	US-08-463-483A-32	Sequence
40	152.5	2.7	789	2	US-08-471-046A-32	Sequence
41	152.5	2.7	789	2	US-08-470-566B-32	Sequence
42	152.5	2.7	789	2	US-08-838-219B-4	Sequence
43	152.5	2.7	789	2	US-08-469-334-32	Sequence
44	152.5	2.7	789	3	US-09-300-529-32	Sequence
45	152.5	2.7	789	3	US-09-233-336A-4	Sequence

ALIGNMENTS

RESULT 1
US-07-745-206A-25
; Sequence 25, Application US/07745206A
; Patent No. 5429921

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745.206A
FILING DATE: 19910815
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELEPHONE: 312-372-7842

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1091 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-745-206A-25

Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTLFOSLLIGPSSREPPFSAVTIKSWDKMOEDLVTLAKTAGVNM
DB 1 MAAGCLLALTLFOSLLIGPSSREPPFSAVTIKSWDKMOEDLVTLAKTAGVNM

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QY QYAKDLDLPEKNDSEPGSRIKPVFTEDANFRQISYQAAHVHPDIDYEGSTIVL 180
DE QYAKDLDLPEKNDSEPGSRIKPVFTEDANFRQISYQAAHVHPDIDYEGSTIVL 180
QY NWTSLALDEVFKONREBPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDLDVRR 240
DE NWTSLALDEVFKONREBPSLLWQVFGSATGLARYYPASPWVDSRTPNKIDLDVRR 240
QY YIQGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFNVASFNSNAQD 300
DE YIQGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETISDDDFNVASFNSNAQD 300
QY FOHLVQANVRNKKVLKDAVNNITAKGIDTKGFSFAFQGLLNNVSRANCKLIML 360
DE FOHLVQANVRNKKVLKDAVNNITAKGIDTKGFSFAFQGLLNNVSRANCKLIML 360
QY GGEERAQIEIFKNYKDKKVRFRPSVQHNVERGPIQMMACENKGYIYEIPSIGAIR 420
DE GGEERAQIEIFKNYKDKKVRFRPSVQHNVERGPIQMMACENKGYIYEIPSIGAIR 420
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DE QEYLDVLRGPMVLADGKAKQVQWTVNYLDLLEGLVITGTLPVFNITQGFENKTNLK 480
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DE ILGVMGVDSVLEDKRLTPRTLCPCNGYFAIDPENGVLHPNLQPKNPKSQBPVTL 540
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DE DAELENDIKVEIRNMKIDGSEKTRTLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
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DE NTEFLNFNEFIDRKTNNPNSCNADLNRVLDDAGFTNELVQNTWSKQKIKGVKAR 720
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DE GGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGAAPKQ 900
QY HRSAYTPSVADILQIGMWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
DE HRSAYTPSVADILQIGMWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
QY TEQTOYFPDNDKSFSGVLDGNCNRSRI FHGKLMNTNLI FTMVSKGTCPCDTRLLI 1020
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QY QTSQGNPCDMVKQPRYKRGPDVCFDNNVLEDDYTDGCGVS 1063
DE QTSQGNPCDMVKQPRYKRGPDVCFDNNVLEDDYTDGCGVS 1063

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lication US/08455543A

846

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GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Weldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-455-543A-52
Query Match 100.0%; Score 5599; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0;

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DB 1 MAAGCLLALTLTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVK

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YTSNGNPNCDMWKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063

Patent No. 5951824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA: US 08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
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REFERENCE/DOCKET NUMBER: 52516 (P519739)
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TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-52

Query Match 100.0%; Score 5599; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0;
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DB 1 MAAGCLLALTLTFLQSLIGPSSBEPFSAVTIKSWDKMQEDLVTLAKTAGVNN
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3QTSQDGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063
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Application US/08311363

5958

ATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25

Query Match 100.0%; Score 5599; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MAACGLALALTTLFQSLIIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGV
Db 1 MAACGLALALTTLFQSLIIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGV
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Db 121 EVVYNNAKDLDPEKNDSEPGSQRIKPVFFEDANFGHQISYQHAHVHIPTDIYK
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ication US/08713118
36
TION:
ranco, Rodrigo
Jun Chen, Ai Ru
ney, David J.
NTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
NTION: CALCIUM CHANNEL SUBUNITS
JENCES: 6
E ADDRESS:
Hamilton, Brook, Smith & Reynolds, P.C.
o Militia Drive
ngton
ISA
-4799
ABLE FORM:
3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.30
CATION DATA:
3 NUMBER: US/08/713,118
3: 16-SEP-1996
TION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Nata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-713-118-4
Query Match 99.9%; Score 5595; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1062; Conservative 0; Mismatches 1; Indels 0;
QY 1 MAAGCLLALTLTFLQSLIGPSSEPPSPSAVTIKSWDKMQEDLVTLAKTASGVN
Db |||
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QY 181 NELNWTSDALDFVKQKREEDPSLWQVFGSATGLARYYPASPDVNSRTPNKIDL
Db |||
QY 241 RPWYIOGASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFN
Db |||
QY 241 RPWYIOGASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETLSDDDFVNVASFN
Db |||
QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNNVSRANCN
Db |||
QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNNVSRANCN
Db |||
QY 361 FTDGGEERAQIFNKYNKDKKVRVFRFVSGQHNVERGPIQWMAKNGKYIYEIPS
Db |||
QY 361 FTDGGEERAQIFNKYNKDKKVRVFRFVSGQHNVERGPIQWMAKNGKYIYEIPS
Db |||
QY 421 INTQBYLDVLRPMVLADGKAKQVQNTNVLDALEGLVITGTLFVNITGOFEN
Db |||
QY 421 INTQBYLDVLRPMVLADGKAKQVQNTNVLDALEGLVITGTLFVNITGOFEN
Db |||
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPQKPKSQ
Db |||
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPQKPKSQ
Db |||
QY 541 DPLDALENDIKVEIRNMIDGESSEKFTLTKSDERYIDKGNRTYTPVNG
Db |||
QY 541 DPLDALENDIKVEIRNMIDGESSEKFTLTKSDERYIDKGNRTYTPVNG
Db |||
QY 601 ALVLPYSPFYIYKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCI
Db |||
QY 601 ALVLPYSPFYIYKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCI
Db |||
QY 661 SDNTEFLNFNEFDRTKTPNNPNCNADLINRVLLDAGFTNVLQVYWSKQNIKI
Db |||
QY 661 SDNTEFLNFNEFDRTKTPNNPNCNADLINRVLLDAGFTNVLQVYWSKQNIKI
Db |||
QY 721 FVVTGGITRVYPKEAGENWQENPTYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
Db |||
QY 721 FVVTGGITRVYPKEAGENWQENPTYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
Db |||
QY 781 MYSKAVEIYIOGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPGAGVPCDCKRNSDVI
Db |||

KAVEIYIQGLKLLPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDVMDCVI 840
 GGFLLMANHDDYTNOIGRFFGEIDPDLMRHLVNI SVAFNKS YDYQSVCEPGAAPKQ 900
 GGFLLMANHDDYTNOIGRFFGEIDPDLMRHLVNI SVAFNKS YDYQSVCEPGAAPKQ 900
 HRSAYVPSVADILQIGWMATAAASIIQQFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
 HRSAYVPSVADILQIGWMATAAASIIQQFLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
 TEQTYQYFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCPDTRLLI 1020
 TEQTYQYFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCPDTRLLI 1020
 QTSQGPNCMDVQKOPRYRKGPDVCFDNNVLEDYDCCGVS 1063
 QTSQGPNCMDVQKOPRYRKGPDVCFDNNVLEDYDCCGVS 1063

lication US/09452007

485

ATION:

Franco, Rodrigo

Sun Chen, Ai Ru

Suey, David J.

ENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

ENTION: CALCIUM CHANNEL SUBUNITS

QUENCES: 6

ICE ADDRESS:

Hamilton, Brook, Smith & Reynolds, P.C.

wo Militia Drive

ington

USA

3-4799

DABLE FORM:

E: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

ICATION DATA:

IN NUMBER: US/09/452,007

E:

ATION:

ATION DATA:

IN NUMBER: US/08/713,118

E: 16-SEP-1996

NT INFORMATION:

a, Elizabeth W.

ON NUMBER: 38,236

DOCKET NUMBER: ACC96-01

ATION INFORMATION:

: 617-861-6240

617-861-9540

OR SEQ ID NO: 4:

ARACTERISTICS:

1091 amino acids

ino acid

linear

?E: protein

99.9%; Score 5595; DB 3; Length 1091;

ilarity 99.9%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

AGCLLALTLFQSLIGPSSPPFPSPAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

AGCLLALTLFQSLIGPSSPPFPSPAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

KYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWREDFASN 120

Db 61 YEYQDLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAEKVQAAHQWRE
 QY 121 EVYYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRIQISYQAAVHIPTDIYEG
 Db 121 EVYYNAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRIQISYQAAVHIPTDIYEG
 QY 181 NELNWTLSALDEVEFKKREEDPSLLMQVFGSATGLIARYYPASPWVDSRPNKIDLI
 Db 181 NELNWTLSALDEVEFKKREEDPSLLMQVFGSATGLIARYYPASPWVDSRPNKIDLI
 QY 241 RPWYIQGAASPDKMLIILVDVSGSVGLTLKLI RTSVSEMLETSLDSDDDFVNVSFN
 Db 241 RPWYIQGAASPDKMLIILVDVSGSVGLTLKLI RTSVSEMLETSLDSDDDFVNVSFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYSRANCK
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYSRANCK
 QY 361 FTDGGERAQEI FNKNYKOKKVRVFRPSVQGHYERGP IOMMACENKGYIYEIPE
 Db 361 FTDGGERAQEI FNKNYKOKKVRVFRPSVQGHYERGP IOMMACENKGYIYEIPE
 QY 421 INTOEYLDVLGRPMVLADGKAKOVQNTVYLDALGLVITGTLPVFNITQGFEN
 Db 421 INTOEYLDVLGRPMVLADGKAKOVQNTVYLDALGLVITGTLPVFNITQGFEN
 QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPNLQPNKPKSC
 Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPNLQPNKPKSC
 QY 541 DFDAELENDIKVEIRNKMDIGESGKTFRTLVKSQDERVIDKGNRTYTWTVMC
 Db 541 DFDAELENDIKVEIRNKMDIGESGKTFRTLVKSQDERVIDKGNRTYTWTVMC
 QY 601 ALVLPYTSFYIYKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYK
 Db 601 ALVLPYTSFYIYKAKLEETITQARSKGKMKDSETLKPDNFESGYTFIAPRDYK
 QY 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
 Db 661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNII
 QY 721 FVVTGGGITRVPYKBAENQENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGI
 Db 721 FVVTGGGITRVPYKBAENQENPETYEDSFYKRSLDNDNVFTAPYFNKSGPGI
 QY 781 MVSKAVEIYIQGLKLLPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDY
 Db 781 MVSKAVEIYIQGLKLLPAVVGKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDY
 QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPDLMRHLVNI SVAFNKS YDYQSVCEPK
 Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPDLMRHLVNI SVAFNKS YDYQSVCEPK
 QY 901 GAGHSAYVPSVADILQIGWMATAAASIIQQFLSLTFFPRLLEAVEMEDDDFTI
 Db 901 GAGHSAYVPSVADILQIGWMATAAASIIQQFLSLTFFPRLLEAVEMEDDDFTI
 QY 961 SCITEQTYQYFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCPCI
 Db 961 SCITEQTYQYFPDNDKSFSGVLDGCGNSRIFPHGKLMNTNLIFIMVESKGTCPCI
 QY 1021 QAEQTSQGPNCMDVQKOPRYRKGPDVCFDNNVLEDYDCCGVS 1063
 Db 1021 QAEQTSQGPNCMDVQKOPRYRKGPDVCFDNNVLEDYDCCGVS 1063

RESULT 7

US-08-455-543A-54

; Sequence 54, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

arpold, Michael
 lls, Steven
 illiams, Mark
 eldman, Daniel
 Cue, Ann
 renner, Robert
 NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NCES: 57
 ADDRESS:
 Brown, Martin, Haller & McClain
 60 Union Street
 Diego
 ifornia
 SA

-2926
 ABLE FORM:
 : Diskette
 IBM Compatible
 YSTEM: DOS
 FastSEQ Version 1.5
 CATION DATA:
 : May 31, 1995
 : NUMBER: US/08/455.543A
 : TION DATA:
 : April 4, 1994
 : TION DATA:
 : NUMBER: 07/868.354
 : April 10, 1992
 : TION DATA:
 : NUMBER: US 07/745.206
 : 15-AUG-1991
 : TION DATA:
 : NUMBER: US 07/620.250
 : 30-NOV-1990
 : TION DATA:
 : NUMBER: US 07/482.384
 : 20-FEB-1990
 : TION DATA:
 : NUMBER: US 07/603.751
 : 04-APR-1989
 : TION DATA:
 : NUMBER: WO PCT/US89/01408
 : 04-APR-1989
 : TION DATA:
 : NUMBER: US 07/176.899
 : 04-APR-1988
 : TION DATA:
 : INFORMATION:
 : man, Stephanie L.
 : NUMBER: 33,779
 : XCKET NUMBER: 6362-52517
 : TION INFORMATION:
 : (619)238-0999
 : (619)238-0062
 : r SEQ ID NO: 54:
 : RACTERISTICS:
 : 86 amino acids
 : to acid
 : SS: single
 : linear
 : 3: protein
 : 3: internal

99.3%; Score 5559.5; DB 1; Length 1086;
 larity 99.5%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 5; Gaps 1;

3CLLALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 |||||
 3CLLALTLTLFQSLIGPSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

QY 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLSNRSKALVSLALEAKVQAAHQWREI
 DB 61 YEKYQDLTYVEPNNAQQLVEIAARDIEKLSNRSKALVSLALEAKVQAAHQWREI
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGS
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHPTDIYEGS
 QY 181 NELNWTISALDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLY
 DB 181 NELNWTISALDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLY
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETSLDDDDFVNVSFNE
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETSLDDDDFVNVSFNE
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNVNVSANCN
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNVNVSANCN
 QY 361 FTGGEERAQEI FNKYNDKKVRFRFSVGOHNYERGEPIOMACENKGYIYEIPI
 DB 361 FTGGEERAQEI FNKYNDKKVRFRFSVGOHNYERGEPIOMACENKGYIYEIPI
 QY 421 INTOEYLDVLRPMVLADGKAKQVQWNTNVYLDALGLVITGTLVPVFNITQGFENI
 DB 421 INTOEYLDVLRPMVLADGKAKQVQWNTNVYLDALGLVITGTLVPVFNITQGFENI
 QY 481 NQLILGVNGVDVSLIEDIKLTPRFTLCPNGYVFAIDPNGYVLLHNPLOPKPKSQI
 DB 481 NQLILGVNGVDVSLIEDIKLTPRFTLCPNGYVFAIDPNGYVLLHNPLOPKPKSQI
 QY 541 DFLDAELENKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYVTPVNG
 DB 536 DFLDAELENKVEIRNMIDGESSEKTRTLVKSQDERYIDKGNRTYVTPVNG
 QY 601 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESYTRTAPRDYCI
 DB 596 ALVLPYTFYIYKAKLEETITQARSKKGMKDSITLKPONFEESYTRTAPRDYCI
 QY 661 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRVLDDAGFTNVLQVYNSKQKNIKI
 DB 656 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRVLDDAGFTNVLQVYNSKQKNIKI
 QY 721 FVVTGGITRVYPKEAGENWQENPTYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 DB 716 FVVTGGITRVYPKEAGENWQENPTYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 QY 781 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVPCCKRNSDI
 DB 776 MVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVPCCKRNSDI
 QY 841 LDDGGFLMANHDDVTNOIGRPFGEIDPSLMHLVNI SVYAFNKSVDYQSVCEPGI
 DB 836 LDDGGFLMANHDDVTNOIGRPFGEIDPSLMHLVNI SVYAFNKSVDYQSVCEPGI
 QY 901 GAGHSAYVPSVADILQIGMWATAAASILQQFLSLTFPRLLEAVEMEDDDFTAI
 DB 896 GAGHSAYVPSVADILQIGMWATAAASILQQFLSLTFPRLLEAVEMEDDDFTAI
 QY 961 SCITEQTQYFFDNDKSPSGVLDGNCNSRI FHGEKLMNTNLI FIMVESKGTCPCD
 DB 956 SCITEQTQYFFDNDKSPSGVLDGNCNSRI FHGEKLMNTNLI FIMVESKGTCPCD
 QY 1021 QAEQTSDEGNPCDMVKQPRYKGPVPCFNNVLEDTDCGGVS 1063
 DB 1016 QAEQTSDEGNPCDMVKQPRYKGPVPCFNNVLEDTDCGGVS 1058

RESULT 8
 US-08-223-305C-54
 ; Sequence 54, Application US/08223305C
 ; Patent No. 5851824

ATION:
 Harpold, Michael
 Ellis, Steven
 Williams, Mark
 Feldman, Daniel
 McCue, Ann
 Brenner, Robert
 ACTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ACTION: METHODS
 REFERENCES: 57
 Brown, Martin, Haller & McClain
 560 Union Street
 Diego
 lifornia
 JSA
 1-2926
 TABLE FORM:
 E: Diskette
 IBM Compatible
 SYSTEM: DOS
 FASTSEQ Version 1.5
 ICATION DATA:
 N NUMBER: US/08/223,305C
 E: April 4, 1994
 ACTION DATA:
 N NUMBER: 07/868,354
 E: April 10, 1992
 ACTION DATA:
 N NUMBER: US 07/745,206
 E: 15-AUG-1991
 ACTION DATA:
 N NUMBER: US 07/620,250
 E: 30-NOV-1990
 ACTION DATA:
 N NUMBER: US 07/482,384
 E: 20-FEB-1990
 ACTION DATA:
 N NUMBER: US 07/603,751
 E: 04-APR-1989
 ACTION DATA:
 N NUMBER: WO PCT/US89/01408
 E: 04-APR-1989
 ACTION DATA:
 N NUMBER: US 07/176,899
 E: 04-APR-1988
 ACTION DATA:
 N NUMBER: 33,779
 DOCKET NUMBER: 52516 (P519739)
 ACTION INFORMATION:
 (619)238-0999
 (619)238-0062
 R SEQ ID NO: 54:
 CHARACTERISTICS:
 086 amino acids
 no acid
 SS: single
 linear
 E: protein
 E: internal

ilarity 99.3%; Score 5559.5; DB 2; Length 1086;
 Conservative 0; Mismatches 0; Indels 5; Gaps 1;

AGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
 |||||
 AGCLLALTTLFOSLLIGPSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60
 |||||
 CYQDLTYVPNNARQLVEIARDEIKLNSRKALVSLALEAEKVQAAHQRREI 120
 |||||

Db 61 YEKYQDLYTVBPNNAQQLVEIARDEIKLNSRKALVSLALEAEKVQAAHQRREI
 QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEG;
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEG;
 QY 181 NELNWTSSALDEVFKQREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDL;
 Db 181 NELNWTSSALDEVFKQREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDL;
 QY 241 RPYIQQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDDFNVASFNI;
 Db 241 RPYIQQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDDFNVASFNI;
 QY 301 VSCFQHLVOANVRNKKVLKDAVNNTAKGITYKKGFSPAFQOLLNINVSRAVNC;
 Db 301 VSCFQHLVOANVRNKKVLKDAVNNTAKGITYKKGFSPAFQOLLNINVSRAVNC;
 QY 361 FTDGGEERAQEIENKYNKDKKVRFRFSGQHYERGPQIOWMACENKGYIYIIPS
 Db 361 FTDGGEERAQEIENKYNKDKKVRFRFSGQHYERGPQIOWMACENKGYIYIIPS
 QY 421 INTOEYLDVLRPMVLGDKAKQVQWNTVYLDALRLGLVITGLPVFNITGQFEN
 Db 421 INTOEYLDVLRPMVLGDKAKQVQWNTVYLDALRLGLVITGLPVFNITGQFEN
 QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPNLQPNPKSQ
 Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPADIPNGYVLLHPNLQPNPKSQ
 QY 541 DFLDAELENDIKVEIRNKMDIGESGEKTRTLVKSODERYIDKGNRTYITWTPVNG
 Db 536 DFLDAELENDIKVEIRNKMDIGESGEKTRTLVKSODERYIDKGNRTYITWTPVNG
 QY 601 ALVLPYTSFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGVTFTIAPRDYC
 Db 596 ALVLPYTSFYIKAKLEETITQARSKKGMKDSITLKPDPNFESGVTFTIAPRDYC
 QY 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIK
 Db 656 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQKNIK
 QY 721 FVVTGGITRVYPKEAGENWQENPEYEDSFYKRSKSDNDNDNVFTAPYFNKSGPGP
 Db 716 FVVTGGITRVYPKEAGENWQENPEYEDSFYKRSKSDNDNDNVFTAPYFNKSGPGP
 QY 781 MVS KAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDI
 Db 776 MVS KAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDI
 QY 841 LDDGGFLLMANHDDYTNQIRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
 Db 836 LDDGGFLLMANHDDYTNQIRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
 QY 901 GAGHRSAYVPSVADILQIGWATAAASIIQQFLLSLTFFPRLLAEVEMEDDDFTI
 Db 896 GAGHRSAYVPSVADILQIGWATAAASIIQQFLLSLTFFPRLLAEVEMEDDDFTI
 QY 961 SCITEQTQYFFDNDKSFSGVLDGNCNCSIRIFHGEKLMNTNLIFIMVESKGTCPCI
 Db 956 SCITEQTQYFFDNDKSFSGVLDGNCNCSIRIFHGEKLMNTNLIFIMVESKGTCPCI
 QY 1021 QAEQTSQGNPNCMDVKQPRYKGPVDFCDNNVLEDYTDGCGVS 1063
 Db 1016 QAEQTSQGNPNCMDVKQPRYKGPVDFCDNNVLEDYTDGCGVS 1058

RESULT 9
 US-08-455-543A-56
 ; Sequence 56, Application US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael

LINE	DESCRIPTION	DATE	TIME	STATUS	REMARKS
1	llis, Steven				
2	Williams, Mark				
3	eldman, Daniel				
4	cCue, Ann				
5	reuner, Robert				
6	NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND				
7	NTION: METHODS				
8	ENCES: 57				
9	E ADDRESS:				
10	Brown, Martin, Haller & McClain				
11	60 Union Street				
12	Diego				
13	ifornia				
14	SA				
15	-2926				
16	ABLE FORM:				
17	: Diskette				
18	IBM Compatible				
19	YSTEM: DOS				
20	FastSeq Version 1.5				
21	CATION DATA:				
22	NUMBER: US/08/455,543A				
23	: May 31, 1995				
24	TION DATA:				
25	NUMBER: 08/223,305				
26	: April 4, 1994				
27	TION DATA:				
28	NUMBER: 07/868,354				
29	: April 10, 1992				
30	TION DATA:				
31	NUMBER: US 07/745,206				
32	: 15-AUG-1991				
33	TION DATA:				
34	NUMBER: US 07/620,250				
35	: 30-NOV-1990				
36	TION DATA:				
37	NUMBER: US 07/482,384				
38	: 20-FEB-1990				
39	TION DATA:				
40	NUMBER: US 07/603,751				
41	: 04-APR-1989				
42	TION DATA:				
43	NUMBER: WO PCT/US89/01408				
44	: 04-APR-1989				
45	TION DATA:				
46	NUMBER: US 07/176,899				
47	: 04-APR-1988				
48	TION DATA:				
49	NUMBER: 33,779				
50	CTION NUMBER: 6362-52517				
51	CTION INFORMATION:				
52	(619)238-0999				
53	(619)238-0062				
54	SEQ ID NO: 56:				
55	ACTERISTICS:				
56	84' amino acids				
57	io acid				
58	IS: single				
59	linear				
60	: protein				
61	: internal				

QY 1021 QAEQTS DGFNCFDMVKQPRYKGP DVCF DNNVLEDYTD CGVS 1063
 |||||
 Db 1014 QAEQTS DGFNCFDMVKQPRYKGP DVCF DNNVLEDYTD CGVS 1056
 |||||

RESULT 10
 US-08-223-305C-56
 ; Sequence 56, Application US/08223305C
 ; Patent No. 5851824
 ; GENERAL INFORMATION:

arpold, Michael
 illis, Steven
 illiams, Mark
 eldman, Daniel
 McCue, Ann
 renner, Robert
 NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NTION: METHODS
 UENCES: 57
 E ADDRESS:
 Brown, Martin, Haller & McClain
 60 Union Street
 Diego
 .ifornia
 ISA
 l-2926
 ABLE FORM:
 3: Diskette
 IBM Compatible
 SYSTEM: DOS
 FastSEQ Version 1.5
 [CATION DATA:
 Y NUMBER: US/08/223,305C
 3: April 4, 1994
 ATION DATA:
 Y NUMBER: 07/868,354
 3: April 10, 1992
 ATION DATA:
 Y NUMBER: US 07/745,206
 3: 15-AUG-1991
 ATION DATA:
 Y NUMBER: US 07/620,250
 3: 30-NOV-1990
 ATION DATA:
 Y NUMBER: US 07/482,384
 E: 20-FEB-1990
 ATION DATA:
 N NUMBER: US 07/603,751
 E: 04-APR-1989
 ATION DATA:
 N NUMBER: WO PCT/US89/01408
 E: 04-APR-1989
 ATION DATA:
 N NUMBER: US 07/176,899
 E: 04-APR-1988
 NT INFORMATION:
 dman, Stephanie L.
 ON NUMBER: 33,779
 DOCKET NUMBER: 52516 (P519739)
 ATION INFORMATION:
 (619)238-0999
 R SEQ ID NO: 56:
 RACTERISTICS:
 084 amino acids
 no acid
 SS: single
 linear
 E: protein
 E: internal

99.0%; Score 5542.5; DB 2; Length 1084;
 larity 99.2%; Pred. No. 0;
 Conservative 0; Mismatches 1; Indels 7; Gaps 1;
 GCLLALTLTQSLIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60
 GCLLALTLTQSLIGPSSEPPPSAVTIKSWDKMOEDLVTLAKTAGSVNQLVDI 60
 TQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAHHOWREDFASN 120
 TQDLTYVEPNARQLVEIAARDIEKLLSNRSKALVSLAEAKVQAHHOWREDFASN 120

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIPVFIEDANFGROI SYOHA AVHLPTDIYEG
 DB 121 EVVYNAKDDLDPEKNDSEPGSQRIPVFIEDANFGROI SYOHA AVHLPTDIYEG
 QY 181 NELNWTSSALDEVFKQKREDEPSLLWQVFGSATGLARYYPASVPWVDSNRTPNKIDL
 DB 181 NELNWTSSALDEVFKQKREDEPSLLWQVFGSATGLARYYPASVPWVDSNRTPNKIDL
 QY 241 RPWYIQAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETLSDDDDFNVASFNI
 DB 241 RPWYIQAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETLSDDDDFNVASFNI
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAGITDYKKGFSFAPFQQLNLYNVRANCNI
 DB 301 VSCFOHLVQANVRNKKVLKDAVNNTAGITDYKKGFSFAPFQQLNLYNVRANCNI
 QY 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHNYERGPIONMACENKGYYYIPIS
 DB 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVQGHNYERGPIONMACENKGYYYIPIS
 QY 421 INTQBYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGOFEN
 DB 421 INTQBYLDVLGRPMVLADGKAKQVQWNTVYLDALGLVITGTLPVFNITGOFEN
 QY 481 NQLILGWGVDVSLEDIKELTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPNPKSQ
 DB 481 NQLILGWGVDVSLEDIKELTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPNPKSQ
 QY 541 DFDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 DB 541 DFDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 QY 601 ALVLPITYSYIYKAKLEETITQARSKKGKMDSETLKPDNFESGVTFTAPRDYC
 DB 601 ALVLPITYSYIYKAKLEETITQARSKKGKMDSETLKPDNFESGVTFTAPRDYC
 QY 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 DB 654 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 QY 721 FVVTGCGITRVYPKEAGENWQNPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 DB 714 FVVTGCGITRVYPKEAGENWQNPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGA
 QY 781 MVS KAVEIYIQGLKLPAAVVGKIDVNSWLENFTKTSIRDPCAGPVCDCCKNSDV
 DB 774 MVS KAVEIYIQGLKLPAAVVGKIDVNSWLENFTKTSIRDPCAGPVCDCCKNSDV
 QY 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 DB 834 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 QY 901 GAGHSAYVPSVADILQIGWATAAAWSILQQFLLSLTPRLLLEAVEMEDDDFTA
 DB 894 GAGHSAYVPSVADILQIGWATAAAWSILQQFLLSLTPRLLLEAVEMEDDDFTA
 QY 961 SCITEQTYFFDNDSDKSPGVLDGNCRSIFHGEKLMNTNLIIFIMVESKGTCPCL
 DB 954 SCITEQTYFFDNDSDKSPGVLDGNCRSIFHGEKLMNTNLIIFIMVESKGTCPCL
 QY 1021 QABQTSQGNPCDMVKQPRYKGPVDFCNVNLVLEDDYDCGGVS 1063
 DB 1014 QABQTSQGNPCDMVKQPRYKGPVDFCNVNLVLEDDYDCGGVS 1056

RESULT 11
 US-08-455-543A-53
 ; Sequence 53, Application US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven

Williams, Mark
eldman, Daniel
cCue, Ann
renner, Robert
NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
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CATION DATA:
: NUMBER: US/08/455,543A
: May 31, 1995
TION DATA:
: NUMBER: 08/223,305
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TION DATA:
: NUMBER: 33,779
: 04-APR-1988
TION DATA:
: NUMBER: 6362-52517
: (619)238-0999
: (619)238-0062
: SEQ ID NO: 53:
: CHARACTERISTICS:
: 03 amino acids
: 10 acid
: 18: single
: linear
: 3: protein
: 3: internal

98.6%; Score 5523; DB 1; Length 1103;
larity 97.5%; Pred. No. 0;
Conservative 0; Mismatches 1; Indels 26; Gaps 2;
3C L L A L T L T L F Q S L I G S S E E P P S A V T I K S W D K M Q E D L V T L A K T A S G V N Q L V D I 60
|||||
3C L L A L T L T L F Q S L I G S S E E P P S A V T I K S W D K M Q E D L V T L A K T A S G V N Q L V D I 60
|||||
Y O O L Y T V E P N N A R Q L V E I A A R D I E K L L S N R S K A L V S L A L E A K V Q A A H Q W R E I 120
|||||

Db 61 Y E K Y O D L Y T V E P N N A R Q L V E I A A R D I E K L L S N R S K A L V S L A L E A K V Q A A H Q W R E I
Qy 121 E V Y Y N A K D L D P E K N D S E P G S Q R I K P V F I E D A N F G R Q I S Y Q H A A V H I P T D I Y E G S
Db 121 E V Y Y N A K D L D P E K N D S E P G S Q R I K P V F I E D A N F G R Q I S Y Q H A A V H I P T D I Y E G S
Qy 181 N E L N W T S A L D S E V F K K N R E E D P S L L W Q V F G S A T G L A R Y P A S P W D N S R T P N K I D L I
Db 181 N E L N W T S A L D S E V F K K N R E E D P S L L W Q V F G S A T G L A R Y P A S P W D N S R T P N K I D L I
Qy 241 R P W Y I Q G A A S P K M L I L V D V S G S V G L T L K I R T S V S E M L E T L S D D D F V N V A S F N K
Db 241 R P W Y I Q G A A S P K M L I L V D V S G S V G L T L K I R T S V S E M L E T L S D D D F V N V A S F N K
Qy 301 V S C F O H L V Q A N V R N K K V L K D A V N N I T A K G I T D Y K K G F S F A F E Q L L N Y N V S R A N C M I
Db 301 V S C F O H L V Q A N V R N K K V L K D A V N N I T A K G I T D Y K K G F S F A F E Q L L N Y N V S R A N C M I
Qy 361 F T D G G E R A Q B I F N K Y N K D K K V R F R F S V G Q H N Y E R G P I Q M A C E N K G Y Y E I P S I
Db 361 F T D G G E R A Q B I F N K Y N K D K K V R F R F S V G Q H N Y E R G P I Q M A C E N K G Y Y E I P S I
Qy 421 I N T Q E Y L D V L G R P M V L A G D K A K Q V M T N V Y L D A L E G L V I T G T L P V F N I T G O F E N I
Db 421 I N T Q E Y L D V L G R P M V L A G D K A K Q V M T N V Y L D A L E G L V I T G T L P V F N I T G O F E N I
Qy 481 N O L I L G V M G V D V S L E D I K R L T P R F T L C P N G Y Y F A I D P N G Y V L L H P N L O P K - - - - -
Db 481 N O L I L G V M G V D V S L E D I K R L T P R F T L C P N G Y Y F A I D P N G Y V L L H P N L O P K P I G V G .
Qy 531 - - - - - N P K S Q E P V T L D F L D A E L N D I K V E I R N K M I D G S G E K T F R T L V K S Q I
Db 541 L R K R P N I Q N P K S Q E P V T L D F L D A E L N D I K V E I R N K M I D G S G E K T F R T L V K S Q I
Qy 582 D K G N E T Y T W T P V N G T D Y S I A L V L P T Y S F Y I K A K L E E T I T O A R S K K G M K D S E T L I
Db 601 D K G N E T Y T W T P V N G T D Y S I A L V L P T Y S F Y I K A K L E E T I T O A R S K K G M K D S E T L I
Qy 642 E S G Y T F I A P R D Y C N D L K I S D N N T F L L N F N E F I D R K T P N N P S C N A D L I N R V L L D .
Db 654 E S G Y T F I A P R D Y C N D L K I S D N N T F L L N F N E F I D R K T P N N P S C N A D L I N R V L L D .
Qy 702 E L V Q N Y M S K Q N I K G V K A R F V V T D G G I T R V Y P K B A G E N W Q E N P E T Y E D S F Y K R S L .
Db 714 E L V Q N Y M S K Q N I K G V K A R F V V T D G G I T R V Y P K B A G E N W Q E N P E T Y E D S F Y K R S L .
Qy 762 V F T A P Y F N K S G P G A Y E S G I M V S K A V E I Y I Q G K L A P V V G I K I D V N S W I E N T F K T .
Db 774 V F T A P Y F N K S G P G A Y E S G I M V S K A V E I Y I Q G K L A P V V G I K I D V N S W I E N T F K T .
Qy 822 C A G P V C D C K R N S D V M D C V I L D D G G F L L M A N H D D Y T N Q I G R F F G E I D P S L M R H L V N
Db 834 C A G P V C D C K R N S D V M D C V I L D D G G F L L M A N H D D Y T N Q I G R F F G E I D P S L M R H L V N
Qy 882 F N K S Y D Y Q S V C E P G A A P Q G A G H R S A Y V P S V A D I L Q I G W A T A A A W S I L Q Q F L L S
Db 894 F N K S Y D Y Q S V C E P G A A P Q G A G H R S A Y V P S V A D I L Q I G W A T A A A W S I L Q Q F L L S
Qy 942 L L E A V E M E D D D F T A S I S K Q S C I T E T O Y F F D N D S K S F S G V L D C G N C S R I F H G E K L I
Db 954 L L E A V E M E D D D F T A S L S K Q S C I T E T O Y F F D N D S K S F S G V L D C G N C S R I F H G E K L I
Qy 1002 I F I M V E S K G T C P C D T R L L I Q A E Q T S D G P N P C D M V K Q P R Y R K G P D V C F D N N V L E D Y
Db 1014 I F I M V E S K G T C P C D T R L L I Q A E Q T S D G P N P C D M V K Q P R Y R K G P D V C F D N N V L E D Y
Qy 1062 V S 1063
Db 1074 V S 1075

plication US/08223305C
824

ATION:

Harbold, Michael

Ellis, Steven

Williams, Mark

Feldman, Daniel

McCue, Ann

Brenner, Robert

ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ENTION: METHODS

QUENCES: 57

CE ADDRESS:

Brown, Martin, Haller & McClain

660 Union Street

Diego

lifornia

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1-2926

DABLE FORM:

E: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

N NUMBER: US/08/223,305C

E: April 4, 1994

ATION DATA:

N NUMBER: 07/868,354

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ATION DATA:

N NUMBER: WO PCT/US89/01408

E: 04-APR-1989

ATION DATA:

N NUMBER: US 07/176,899

E: 04-APR-1988

NT INFORMATION:

dman, Stephanie L.

ON NUMBER: 33,779

DOCKET NUMBER: 52516 (P519739)

ATION INFORMATION:

(619)238-0999

(619)238-0062

R SEQ ID NO: 53:

ACTERISTICS:

103 amino acids

no acid

.SS: single

linear

E: protein

E: internal

!

98.6%; Score 5523; DB 2; Length 1103;

larity 97.5%; Pred.No. 0;

Conservative 0; Mismatches 1; Indels 26; Gaps 2;

AGCLLALTTLFQSLIGSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

|||||

AGCLLALTTLFQSLIGSSSEPPFPSSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

|||||

61	QY	YEKYQDLTYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALAEKVKQAAHQWRE
61	Db	YEKYQDLTYTVEPNNAQQLVEIAARDIEKLLSNRSKALVSLALAEKVKQAAHQWRE
121	QY	EVVYNAKODLDPEKNDSEPGSQRIRKPVFIEDANFGROI SYQHAAVHIPTDIYEG
121	Db	EVVYNAKODLDPEKNDSEPGSQRIRKPVFIEDANFGROI SYQHAAVHIPTDIYEG
181	QY	NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDL
181	Db	NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDL
241	QY	RPWYIQGAASPDKMLILVDVSGSVSLITLKLIRTSVSEMLETLSDDDFVNVSFN
241	Db	RPWYIQGAASPDKMLILVDVSGSVSLITLKLIRTSVSEMLETLSDDDFVNVSFN
301	QY	VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNVSFRANCN
301	Db	VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNVSFRANCN
361	QY	FTDGGERAQEI FNKYNKDKKVRVFRFSVGOHNYERGP IQWMA CENKGYIYIPE
361	Db	FTDGGERAQEI FNKYNKDKKVRVFRFSVGOHNYERGP IQWMA CENKGYIYIPE
421	QY	INTQEYLDVLGRPMVLADKAKOVNTNVYLDALGLGLVITGTLVPVNIITGQFEN
421	Db	INTQEYLDVLGRPMVLADKAKOVNTNVYLDALGLGLVITGTLVPVNIITGQFEN
481	QY	NQLILGVMGVDVSLIEDIKRLTPRTICPNGYIFAIIDPNGVYLLHPNLQPK----
481	Db	NQLILGVMGVDVSLIEDIKRLTPRTICPNGYIFAIIDPNGVYLLHPNLQPKIGVGC
531	QY	-----NPKSQEPVTLDFDLAELENDIKVEIRNMKIDGESGEKTFRTLKSC
541	Db	LRKRRPNMIQNPKSQEPVTLDFDLAELENDIKVEIRNMKIDGESGEKTFRTLKSC
582	QY	DKGNRTYTWTPVNGTDYSIALVLPVSPYIKAKLRETIITQASKKGKMDSETI
601	Db	DKGNRTYTWTPVNGTDYSIALVLPVSPYIKAKLRETIITQARY-----SETI
642	QY	EESGYTFIAPRDYCNLDKISDNNTEFLNFEPIIDRKTNNPSCNADLINRVLLI
654	Db	EESGYTFIAPRDYCNLDKISDNNTEFLNFEPIIDRKTNNPSCNADLINRVLLI
702	QY	ELYQNYWSKQNIKGVKARFVVDGGITRVYPKEAGENWQENPETYEDSFYKRSI
714	Db	ELYQNYWSKQNIKGVKARFVVDGGITRVYPKEAGENWQENPETYEDSFYKRSI
762	QY	VFTAPYFNKSGPGAYBSGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKI
774	Db	VFTAPYFNKSGPGAYBSGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKI
822	QY	CAGPVCDCCKENSVDVDCVILDDGGFLIMANHDDYTQIGRFFGEIDPFLMRHLVA
834	Db	CAGPVCDCCKENSVDVDCVILDDGGFLIMANHDDYTQIGRFFGEIDPFLMRHLVA
882	QY	FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQOFLLE
894	Db	FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQOFLLE
942	QY	LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSPSGVLDGNCNCSRIIFHGEKI
954	Db	LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSPSGVLDGNCNCSRIIFHGEKI
1002	QY	IFIMVESKGTCPDCTRLLIQAEQTSQGNPCDMVKQPRYKGPDPVCFDNNVLEDY
1014	Db	IFIMVESKGTCPDCTRLLIQAEQTSQGNPCDMVKQPRYKGPDPVCFDNNVLEDY
1062	QY	VS 1063
1074	Db	VS 1075

RE
US

plication US/08455543A
346

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Harold, Michael
Ellis, Steven
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Feldman, Daniel
McCue, Ann

renner, Robert

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SOURCES: 57

CE ADDRESS:

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NUMBER: US 07/176,899

3: 04-APR-1988

IT INFORMATION:

man, Stephanie L.

AN NUMBER: 33,779

OCKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQ ID NO: 55:

ACTERISTICS:

179 amino acids

10 acid

IS: single

linear

protein

internal

conservative

0; Mismatches

1; Indels

12; Gaps

2;

98.3%; Score 5503; DB 1; Length 1079;

arity 98.8%; Pred.No. 0;

conservative 0; Mismatches

1; Indels

12; Gaps

2;

1	MAAGCLLALTLTLFQSLILGPSSEPPSAVTIKSWVDKMOEDLVTLAKTASGVK	QY
1	MAAGCLLALTLTLFQSLILGPSSEPPSAVTIKSWVDKMOEDLVTLAKTASGVK	Db
61	YEKYQDLTYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALAEAKVQAAHORE	QY
61	YEKYQDLTYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALAEAKVQAAHORE	Db
121	EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEG	QY
121	EVVYNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROISYQHAHVHIPTDIYEG	Db
181	NELNWTLSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDL	QY
181	NELNWTLSALDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDNSRTPNKIDL	Db
241	RPWYIQGAASPDKMLILVDVSGVSGLTILKLRITSVSEMLETSLDDDFNVASFN	QY
241	RPWYIQGAASPDKMLILVDVSGVSGLTILKLRITSVSEMLETSLDDDFNVASFN	Db
301	VSCFOHLVQANVRNKKVLDAVNNITAKGITDYKKGFSFAFQQLNLYNVRANCN	QY
301	VSCFOHLVQANVRNKKVLDAVNNITAKGITDYKKGFSFAFQQLNLYNVRANCN	Db
361	FTDGGEEAQAEIFNKYNKDKKVRFRFVSQGHYERGPQWACENKGYYYEIPS	QY
361	FTDGGEEAQAEIFNKYNKDKKVRFRFVSQGHYERGPQWACENKGYYYEIPS	Db
421	INTQEYLDVLRPMVLGADKAKQVQNTVYLDALGLVITGTLPVFNITGQFEN	QY
421	INTQEYLDVLRPMVLGADKAKQVQNTVYLDALGLVITGTLPVFNITGQFEN	Db
481	NQLILGVMGVDSLEDIKELTFRPTLCPNGYYFAIDPNCYVLLHPLNLPKPKSQ	QY
481	NQLILGVMGVDSLEDIKELTFRPTLCPNGYYFAIDPNCYVLLHPLNLPKPKSQ	Db
541	DFDLAELENDIKVEIRNNKMDGSEKTRTLVKSQDERYIDKGNRTYTWTPVNG	QY
536	DFDLAELENDIKVEIRNNKMDGSEKTRTLVKSQDERYIDKGNRTYTWTPVNG	Db
601	ALVLPYSPYYIKAKLEETITQARSKKGMKQSETLKPDPNFEESGYTFIAPRDYC	QY
596	ALVLPYSPYYIKAKLEETITQARY-----SETLKPDPNFEESGYTFIAPRDYC	Db
661	SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQNNIK	QY
649	SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYNSKQNNIK	Db
721	FVVTDDGIGITRVYPKEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA	QY
709	FVVTDDGIGITRVYPKEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA	Db
781	MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDP CAGPVCDCRNSDVI	QY
769	MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDP CAGPVCDCRNSDVI	Db
841	LDDGGFLMANHDDVTNQGIRPFGEIDPSLMRHLVNI SVYAFNKSDYQSVCEPGI	QY
829	LDDGGFLMANHDDVTNQGIRPFGEIDPSLMRHLVNI SVYAFNKSDYQSVCEPGI	Db
901	GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTFPRLLEAVEMEDDDFTAI	QY
889	GAGHSAYVPSVADILQIGWATAAAMSILQOFLSLTFPRLLEAVEMEDDDFTAI	Db
961	SCITTEQTOYFFDNDNSKSPSGVLDCNCRSRI FHGEKLMNTNLI FIMVSKGTCPCD	QY
949	SCITTEQTOYFFDNDNSKSPSGVLDCNCRSRI FHGEKLMNTNLI FIMVSKGTCPCD	Db
1021	QAEQTSQDGNPCDMVYQPRYKGPVCFDNNVLEDTYDCGGVS 1063	QY
1009	QAEQTSQDGNPCDMVYQPRYKGPVCFDNNVLEDTYDCGGVS 1051	Db

07:56:54 2004

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plication US/08223305C

824

ATTION:

Harpold, Michael

Ellis, Steven

Williams, Mark

Feldman, Daniel

McCue, Ann

Brenner, Robert

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R SEQ ID NO: 55:

ACTERISTICS:

079 amino acids

no acid

SS: single

linear

E: protein

E: internal

98.3%; Score 5503; DB 2; Length 1079;

larity 98.8%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 12; Gaps 2;

GCLLALTTLFQSLIGPSSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60

1	MAAGCLLALTTLFQSLIGPSSSEPPSAVTIKSWVDKMQEDLVTLAKTASGVN	Db
61	YEKYQDLYTVENPNARQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRE	Qy
61	YEKYQDLYTVENPNARQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRE	Db
121	EVVYNAKDDLDPEKNDSPEGSQRIKPVFIEDANFGQRI SYQHAAVHIPTDIYEG	Qy
121	EVVYNAKDDLDPEKNDSPEGSQRIKPVFIEDANFGQRI SYQHAAVHIPTDIYEG	Db
181	NELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDSNRSPNKIDL	Qy
181	NELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASPMVDSNRSPNKIDL	Db
241	RPWYIQGAASPDKMLILVDVSGVSLTLKLI RTSVSEMLETLSDDDFVNVSFN	Qy
241	RPWYIQGAASPDKMLILVDVSGVSLTLKLI RTSVSEMLETLSDDDFVNVSFN	Db
301	VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVRANCN	Qy
301	VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNYNVRANCN	Db
361	FTDGEERAQEI FNKYNKDKKVRVFRFSVGOHNYERGP IOMMACENKGYIYEIPS	Qy
361	FTDGEERAQEI FNKYNKDKKVRVFRFSVGOHNYERGP IOMMACENKGYIYEIPS	Db
421	INTQEVLDVLGRPMVLGADKAKQVQNTVYLDALGLVITGLTPVFNITGQFEN	Qy
421	INTQEVLDVLGRPMVLGADKAKQVQNTVYLDALGLVITGLTPVFNITGQFEN	Db
481	NQILGVMGVDVLSLEDIKRLTPRFTLCPNGYYPAIDPNGVYLLHPLNLPKPKSC	Qy
481	NQILGVMGVDVLSLEDIKRLTPRFTLCPNGYYPAIDPNGVYLLHPLNLPKPKSC	Db
541	DFLDAELENDIKVIRNKMDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNG	Qy
536	DFLDAELENDIKVIRNKMDGESGKTFRTLVKSODERYIDKGNRTYTWTPVNG	Db
601	ALVLPYTSFYI KAKLEETITQARSKKGMKMDSETLKPDPNFESGYTFTIAPRDYC	Qy
596	ALVLPYTSFYI KAKLEETITQARY-----SETLKPDPNFESGYTFTIAPRDYC	Db
661	SDNNTFLLNFNFIDRKTNPNSCNADLINRVLLDAGFTNVLQVYFWSKQKNIR	Qy
649	SDNNTFLLNFNFIDRKTNPNSCNADLINRVLLDAGFTNVLQVYFWSKQKNIR	Db
721	FVYTDGGITRVYPKEAGENQENPETVEDSFYKRSLDNDNYVFTAPYFNKSGFGP	Qy
709	FVYTDGGITRVYPKEAGENQENPETVEDSFYKRSLDNDNYVFTAPYFNKSGFGP	Db
781	MVSKAVEIYIQGKLLKPAVVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDV	Qy
769	MVSKAVEIYIQGKLLKPAVVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSDV	Db
841	LDDGGFLLMANHDDYTNQIGRFPEGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG	Qy
829	LDDGGFLLMANHDDYTNQIGRFPEGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG	Db
901	GAGHSAYVPSVADIILQIGHWATAAAWSILQQFLSLTFFPRLLLEAVEMEDDDFTF	Qy
889	GAGHSAYVPSVADIILQIGHWATAAAWSILQQFLSLTFFPRLLLEAVEMEDDDFTF	Db
961	SCITEQTYFFDNDKSKPSGVLDGCGNCSRI FHGKLMNTNLIIFIMVESKGTCPCL	Qy
949	SCITEQTYFFDNDKSKPSGVLDGCGNCSRI FHGKLMNTNLIIFIMVESKGTCPCL	Db
1021	QASQTSQGNPCDMVQPRYKGPVCFDNNVLEDYTDGCVS 1063	Qy
1009	QASQTSQGNPCDMVQPRYKGPVCFDNNVLEDYTDGCVS 1051	Db

RESULT 15

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location US/08435675B
50
TION:
illis, Steven Bradley
illiams, Mark E.
arpold, Michael Miller
chwartz, Arnold
renner, Robert
TION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
UENCES: 6
E ADDRESS:
Brown, Martin, Haller & McClain
60 Union Street
Diego

ISA
.-2926
ABLE FORM:
: Diskette
IBM Compatible
YSTEM: DOS
FastSEQ Version 1.5
ICATION DATA:
: NUMBER: US/08/435,675B
: : 05-MAY-1995
TION: 435
ATION DATA:
: NUMBER: US 08/314,083
: : 28-SEP-1994
: NUMBER: US 07/914,231
: : 13-JUL-1992
: NUMBER: US 07/603,751
: : 08-NOV-1990
IT INFORMATION:
man, Stephanie L
N NUMBER: 33,779
OCKET NUMBER: 6362-53193
TION INFORMATION:
619-238-0999
519-238-0062

{ SEQ ID NO: 5:
ACTERISTICS:
106 amino acids
to acid
S: single
linear
3: protein
3: internal

96.2%; Score 5385.5; DB 1; Length 1106;
larity 94.9%; Pred. No. 0;
Conservative 14; Mismatches 12; Indels 29; Gaps 4;

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ELNWTSSALDDVFKKREEDPSLLWQVFGSATGLARYYPASPVVDNSRTPNKIDLYD 240
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Search completed: February 20, 2004, 17:00:31
Job time : 22.0748 secs

us-10-090-827-14.rai

Category	ID	Length	DB	Description
Category A	1	1091	1	Sequence 25, Appl
	2	1091	1	Sequence 52, Appl
	3	1091	1	Sequence 52, Appl
	4	1091	1	Sequence 52, Appl
	5	1091	1	Sequence 25, Appl
	6	1091	1	Sequence 4, Appl
	7	1091	1	Sequence 4, Appl
	8	1091	1	Sequence 54, Appl
	9	1091	1	Sequence 54, Appl
	10	1091	1	Sequence 56, Appl
	11	1091	1	Sequence 56, Appl
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	14	1091	1	Sequence 55, Appl
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	25	1091	1	Sequence 8, Appl
	26	1091	1	Sequence 8, Appl
	27	1091	1	Sequence 8, Appl
	28	1091	1	Sequence 8, Appl

GENERAL INFORMATION:

APPLICANT: Harpold, Michael

APPLICANT: Ellis, Steven

APPLICANT: Williams, Mark

APPLICANT: Feldman, Daniel

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,543A

FILING DATE: May 31, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/223,305

FILING DATE: April 4, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/868,354

FILING DATE: April 10, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/745,206

FILING DATE: 15-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,250

FILING DATE: 30-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/482,384

FILING DATE: 20-FEB-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/603,751

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US89/01408

FILING DATE: 04-APR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/176,899

FILING DATE: 04-APR-1988

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-52517

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 1091 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-455-543A-52

Query Match 100.0%; Score 5443; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0;

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JTSNGENPCDMVK 1036

lication US/08223305C

Patent No. 5851824
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-52
Query Match 100.0%; Score 5443; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0;
QY 1 MAAGCLLALTLTLFQSLILGPSSEPPSPASVTIKSWDKMQEDLVTLAKTAGVNC
Db 1 MAAGCLLALTLTLFQSLILGPSSEPPSPASVTIKSWDKMQEDLVTLAKTAGVNC
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QTSDGPNPCDMVK 1036

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plication US/08311363

958

ATION:

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APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
METHODS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,363
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-311-363-25

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Query Match 100.0%; Score 5443; DB 2; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0;

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DB 1 MAAGCLLALTLTQSLILGPPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVK
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DB 61 YEKYQDLTYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHWR
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DB 121 EVVYNAKDDLDPKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEG
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DB 181 NELNWTLSALDEVFKQNRDEPSSLWQVFGSATGLARYYPASPVVDNSRTNPKIDL
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DB 241 RPYIYQGAASPKDMLILVDVSGSVGLTLKLIRTSVSEMLETLSDDDFVNVASFN
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DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQQLNYSRANCN
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DB 361 FTDDGGERAQBEIFNKNKOKKVRFRFSVQGHYERGPQIMACENKGYIYEIP

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07:56:52 2004

us-10-090-827-14.ra1

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QY LGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLPNKSPQEPVTL 540
DB LGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLPNKSPQEPVTL 540
QY LAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
DB LAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNGTDYSL 600
QY PTYSFYIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFTIAPRDYCNLDKI 660
DB PTYSFYIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFTIAPRDYCNLDKI 660
QY TEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNBLVQYNSKQNIKGVKAR 720
DB TEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNBLVQYNSKQNIKGVKAR 720
QY DGGITRVYPKAGENQWNPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
DB DGGITRVYPKAGENQWNPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
QY JAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVPCDCRNSDVMDCVI 840
DB JAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVPCDCRNSDVMDCVI 840
QY KFLMANHDDVTNOIGRFGEDPSLMHNLNISVYAFNKSVDYOSVCEPGAAPKQ 900
DB KFLMANHDDVTNOIGRFGEDPSLMHNLNISVYAFNKSVDYOSVCEPGAAPKQ 900
QY RSAYVPSVADILQIGWATAAASLQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
DB RSAYVPSVADILQIGWATAAASLQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
QY ETOYQFFNDKSKFSGLVDCGNSRIFHGEKLMNTNLIFIMVESKGTCPCDTRLII 1020
DB ETOYQFFNDKSKFSGLVDCGNSRIFHGEKLMNTNLIFIMVESKGTCPCDTRLII 1020
QY TSDGNPNCDMWK 1036
DB TSDGNPNCDMWK 1036

ication US/08713118
36
TION:
ranco, Rodrigo
un Chen, Ai Ru
uey, David J.
TION: NUCLEIC ACID ENCODING HUMAN NEURONAL
TION: CALCIUM CHANNEL SUBUNITS
JENCES: 6
E ADDRESS:
Hamilton, Brook, Smith & Reynolds, P.C.
o Militia Drive
ngton
ISA
-4799
ABLE FORM:
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.30
ICATION DATA:
I NUMBER: US/08/713,118
I: 16-SEP-1996
TION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mata, Elizabeth W.
REGISTRATION NUMBER: 38,236
REFERENCE/DOCKET NUMBER: ACC96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-713-118-4
Query Match 99.9%; Score 5439; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches 1; Indels 0;
QY 1 MAAGCLLALTTLTFLQSLLIGPSSEPPFPSPASVTKISWVDKMQEDLVTLAKTASGVNI
DB 1 MAAGCLLALTTLTFLQSLLIGPSSEPPFPSPASVTKISWVDKMQEDLVTLAKTASGVNI
QY 61 YEKYODLVTPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOMREI
DB 61 YEKYODLVTPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOMREI
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIPKFVIEDANFGROI SYOHAHVHPTDIYEG
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIPKFVIEDANFGROI SYOHAHVHPTDIYEG
QY 181 NELNWTSAALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
DB 181 NELNWTSAALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKIDL
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRITSVSEMLETLSDDDFVNVSFNI
DB 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLRITSVSEMLETLSDDDFVNVSFNI
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPELLNLYNVSRAVNCNI
DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPELLNLYNVSRAVNCNI
QY 361 FTDGGEERAQELFNKYNDKKVRVFRFVSQGNHYERGPLOMACENKGYIYIIPS.
DB 361 FTDGGEERAQELFNKYNDKKVRVFRFVSQGNHYERGPLOMACENKGYIYIIPS.
QY 421 INTQBYLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGLPVFNITGQFENI
DB 421 INTQBYLDVLRPMVLADGKAKQVQWTVNYLDALGLVITGLPVFNITGQFENI
QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLPNKSPQ
DB 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHNPQLPNKSPQ
QY 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNG
DB 541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKSQDERYIDKGNRTYTWTVPNG
QY 601 ALVLPYTFYTIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFTIAPRDYCI
DB 601 ALVLPYTFYTIKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFTIAPRDYCI
QY 661 SDNNTPELINFNEFIDRKTNNPNSCNADLINRVLLDAGFTNBLVQYNSKQNIK
DB 661 SDNNTPELINFNEFIDRKTNNPNSCNADLINRVLLDAGFTNBLVQYNSKQNIK
QY 721 FVVTDDGGITRVYPKAGENQWNPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAI
DB 721 FVVTDDGGITRVYPKAGENQWNPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAI
QY 781 MVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPGAGVPCDCRNSDVI

KAVEIYIQGLKLPAAVGIKIDVNSWIENFTKTSIRDFCAGPVCCKNSDVMDCVI 840
XGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEGAPKQ 900
XGFLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEGAPKQ 900
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TEQTYFFDNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCDTRLII 1020
TEQTYFFDNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCDTRLII 1020
XTSDGPNPCDMVK 1036
XTSDGPNPCDMVK 1036
lication US/09452007
485
ATION:
Franco, Rodrigo
Sun Chen, Ai Ru
Suey, David J.
ENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL
ENTION: CALCIUM CHANNEL SUBUNITS
SEQUENCES: 6
CE ADDRESS:
Hamilton, Brook, Smith & Reynolds, P.C.
wo Militia Drive
ington
USA
3-4799
DABLE FORM:
E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
ICATION DATA:
N NUMBER: US/09/452.007
E:
TION:
ATION DATA:
N NUMBER: US/08/713.118
E: 16-SEP-1996
NT INFORMATION:
a, Elizabeth W.
ON NUMBER: 38.236
DOCKET NUMBER: ACC96-01
ATION INFORMATION:
617-861-6240
617-861-9540
R SEQ ID NO: 4:
RACTERISTICS:
091 amino acids
no acid
linear
E: protein
99.9%; Score 5439; DB 3; Length 1091;
larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
GCLLALTLTFLQSLIGSPSEPPFPSPATIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
GCLLALTLTFLQSLIGSPSEPPFPSPATIKSWDKMQEDLVTLAKTAGSVNQLVDI 60
YQDLYTVEPNNAQLVEIARDIEKLLSNRSKALVSLALEAEKVAQAHHQWRDFASN 120

Db 61 YEYQDLYTVEPNNAQLVEIARDIEKLLSNRSKALVSLALEAEKVAQAHHQWR
Qy 121 EVVYNAKDDLPBKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHIPTDIYE
Db 121 EVVYNAKDDLPBKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHIPTDIYE
Qy 181 NELNWTSALEDEVFKCNREEDPSLLQVFGSATGLARYYPASWPVDNRTNPKIDI
Db 181 NELNWTSALEDEVFKCNREEDPSLLQVFGSATGLARYYPASWPVDNRTNPKIDI
Qy 241 RPWYIOGAASPDKMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVSFPI
Db 241 RPWYIOGAASPDKMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVSFPI
Qy 301 VSCFOHLVQANVRNKKVLDKAVANNITAKGITDYKKGFSFAFEQLLNTNVSBRNCI
Db 301 VSCFOHLVQANVRNKKVLDKAVANNITAKGITDYKKGFSFAFEQLLNTNVSBRNCI
Qy 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVGOHNYERGPIONMACENKGYIYEIPI
Db 361 FTDGGEERAQEIFNKYNKDKKVRVFRFSVGOHNYERGPIONMACENKGYIYEIPI
Qy 421 INTOEYLDVLGRPMVLGADKAKOVQWTVNYLDALDELGLVITGTLPVFNITGQFEI
Db 421 INTOEYLDVLGRPMVLGADKAKOVQWTVNYLDALDELGLVITGTLPVFNITGQFEI
Qy 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYVFAIDPENGVLLHPNLQPNPKS
Db 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYVFAIDPENGVLLHPNLQPNPKS
Qy 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERIVTDGNRTYTPTPVNK
Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTRTLVKSQDERIVTDGNRTYTPTPVNK
Qy 601 ALVLPYTSFYIYIKAKLEETITQARSKKGMKDSSETLKPDPNFBESGYTFIAPRDY
Db 601 ALVLPYTSFYIYIKAKLEETITQARSKKGMKDSSETLKPDPNFBESGYTFIAPRDY
Qy 661 SDNTEFLNPNFIDRKTNNPNSCNADLNNRVLDDAGFTNELLVQNYWSKOKNI
Db 661 SDNTEFLNPNFIDRKTNNPNSCNADLNNRVLDDAGFTNELLVQNYWSKOKNI
Qy 721 FVVTGDIITRVYKPEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPG
Db 721 FVVTGDIITRVYKPEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPG
Qy 781 MVSKAVEIYIQGLKLPAAVVGIIKIDVNSWIENFTKTSIRDPGAGPVCDCCKRNSDV
Db 781 MVSKAVEIYIQGLKLPAAVVGIIKIDVNSWIENFTKTSIRDPGAGPVCDCCKRNSDV
Qy 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
Qy 901 GAGERSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTFA
Db 901 GAGERSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLLEAVEMEDDDFTFA
Qy 961 SCITEQTYFFDNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCL
Db 961 SCITEQTYFFDNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCPCL
Qy 1021 QAEQTSIDGPNPCDMVK 1036
Db 1021 QAEQTSIDGPNPCDMVK 1036

RESULT 7
US-08-455-543A-54
; Sequence 54, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:

Harold, Michael
 Ellis, Steven
 Williams, Mark
 Feldman, Daniel
 McCue, Ann
 Brenner, Robert
 INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 INVENTION: METHODS
 REFERENCES: 57
 ADDRESS:
 Brown, Martin, Haller & McClain
 560 Union Street
 Diego
 California
 USA
 1-2926
 TABLE FORM:
 3: Diskette
 IBM Compatible
 SYSTEM: DOS
 FASTSEQ Version 1.5
 ICATION DATA:
 NUMBER: US/08/455,543A
 3: May 31, 1995
 ACTION DATA:
 NUMBER: 08/223,305
 3: April 4, 1994
 ACTION DATA:
 NUMBER: 07/868,354
 3: April 10, 1992
 ACTION DATA:
 NUMBER: US 07/745,206
 3: 15-AUG-1991
 ACTION DATA:
 NUMBER: US 07/620,250
 3: 30-NOV-1990
 ACTION DATA:
 NUMBER: US 07/482,384
 3: 20-FEB-1990
 ACTION DATA:
 NUMBER: US 07/603,751
 3: 04-APR-1989
 ACTION DATA:
 NUMBER: WO PCT/US89/01408
 3: 04-APR-1989
 ACTION DATA:
 NUMBER: US 07/176,899
 3: 04-APR-1988
 ACTION DATA:
 NUMBER: 33,779
 SOCKET NUMBER: 6362-52517
 ACTION INFORMATION:
 (619)238-0999
 (619)238-0062
 SEQ ID NO: 54:
 CHARACTERISTICS:
 86 amino acids
 no acid
 IS: single
 linear
 3: protein
 3: internal

99.3%; Score 5403.5; DB 1; Length 1086;
 Parity 99.5%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 5; Gaps 1;

ICLLALTLTLFQSLIGPSSEPPGSAVTIKSWVDKMQEDLVTLAKTASGVNLVDI 60
 ICLLALTLTLFQSLIGPSSEPPGSAVTIKSWVDKMQEDLVTLAKTASGVNLVDI 60

QY 61 YEKYQDLYTVFPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHORE
 DB 61 YEKYQDLYTVFPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHORE
 QY 121 EYVYNAKDDLDPEKNDSEPGSRQIKPVFIEDANFGROI SYQHAHVHITDIYEG
 DB 121 EYVYNAKDDLDPEKNDSEPGSRQIKPVFIEDANFGROI SYQHAHVHITDIYEG
 QY 181 NELNWTSSALDEVKKNREEDPSLLMWQVFGSATGLARYYPASPWVNSRTPNKIDL
 DB 181 NELNWTSSALDEVKKNREEDPSLLMWQVFGSATGLARYYPASPWVNSRTPNKIDL
 QY 241 RPYIYQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVSFN
 DB 241 RPYIYQGAASPKDMLILVDVSGSVGLTLKLRITSVSEMLETLSDDDFVNVSFN
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQQLNLYNVSRAVCN
 DB 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQQLNLYNVSRAVCN
 QY 361 FTDGGEERAQEI FNKYNKDKVVRVFRFSGQHNBERGPIQWACENKGYYYEIPS
 DB 361 FTDGGEERAQEI FNKYNKDKVVRVFRFSGQHNBERGPIQWACENKGYYYEIPS
 QY 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDLLELGLVITGTLPVFNITGQFEN
 DB 421 INTQEYLDVLRPMVLADGKAKQVQWNTVYLDLLELGLVITGTLPVFNITGQFEN
 QY 481 NQLILGWVGVDVSLIEDIKELTPRFLCPNGYYPADPNQGYVLLHNLQENKPSQ
 DB 481 NQLILGWVGVDVSLIEDIKELTPRFLCPNGYYPADPNQGYVLLHNLQENKPSQ
 QY 541 DFLDAELNDIKVEIRNKMIDGESGEKTRTLVKQODERYIDKGNRTYTWTPVNG
 DB 536 DFLDAELNDIKVEIRNKMIDGESGEKTRTLVKQODERYIDKGNRTYTWTPVNG
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 DB 596 ALVLPYSPYIYKAKLEETITQARSKKGMKQSETLKPDNFEESGYTFTAPRDYC
 QY 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLADAGFTNELVQVNSKQKNIK
 DB 656 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLADAGFTNELVQVNSKQKNIK
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 DB 716 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
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 DB 776 MYSKAVEIYIQKLLKPAVVGKIDVNSWIENFTKTSIRDP CAGPVCDCKRNSDV
 QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMHVLNIVYAFNKSYDVQSVCEPG
 DB 836 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMHVLNIVYAFNKSYDVQSVCEPG
 QY 901 GAGHSAYVPSVADILQIGWATAAASWLSLQOFLLSLTPRLEAVEMEDDDFTAL
 DB 896 GAGHSAYVPSVADILQIGWATAAASWLSLQOFLLSLTPRLEAVEMEDDDFTAL
 QY 961 SCITEQTQYFFDNDKSFSGVLDGNCNCSRIIFHGEKLMNTNLIFIMVESKGTCPD
 DB 956 SCITEQTQYFFDNDKSFSGVLDGNCNCSRIIFHGEKLMNTNLIFIMVESKGTCPD
 QY 1021 QABQTSQDGNPCDMVK 1036
 DB 1016 QABQTSQDGNPCDMVK 1031

RESULT 8
 US-08-223-305C-54
 ; Sequence 54, Application US/08223305C
 ; Patent No. 5851824

ATION:
 Harpold, Michael
 Ellis, Steven
 Williams, Mark
 Feldman, Daniel
 McCue, Ann
 Brenner, Robert
 ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ENTION: METHODS
 QUENCES: 57

ICE ADDRESS:
 Brown, Martin, Haller & McClain
 660 Union Street
 , Diego
 , California
 USA

1-2926
 LABLE FORM:
 'E: Diskette
 IBM Compatible
 SYSTEM: DOS
 FastSeq Version 1.5

ICATION DATA:
 N NUMBER: US 08/223,305C
 'E: April 4, 1994
 ACTION DATA:
 N NUMBER: 07/868,354
 'E: April 10, 1992

'E: 15-AUG-1991
 ACTION DATA:
 N NUMBER: US 07/620,250
 'E: 30-NOV-1990
 ACTION DATA:
 N NUMBER: US 07/482,384
 'E: 20-FEB-1990

'E: 04-APR-1989
 ACTION DATA:
 N NUMBER: US 07/176,899
 'E: 04-APR-1988
 ACTION DATA:
 N NUMBER: WO PCT/US89/01408
 'E: 04-APR-1989

'E: 04-APR-1988
 ACTION DATA:
 N NUMBER: 33,779
 DOCKET NUMBER: 52516 (P519739)
 ACTION INFORMATION:
 (619)238-0999

R SEQ ID NO: 54:
 CHARACTERISTICS:
 086 amino acids
 no acid
 .SS: single
 linear
 'E: protein
 'E: internal

99.3%; Score 5403.5; DB 2; Length 1086;
 larity 99.5%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 5; Gaps 1;

GLIALTLTLFQSLIGSSSEPPPSAVTIKSWDMQEDLVTLAKTASGYNQLVDI 60
 GLIALTLTLFQSLIGSSSEPPPSAVTIKSWDMQEDLVTLAKTASGYNQLVDI 60
 YQDLYTVPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWR 120

Db 61 YEKYQDLYTVPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWR
 QY 121 EVVYNAKDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEK
 Db 121 EVVYNAKDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEK
 QY 181 NELNWTSADEVFQKNREEDPSLLWQVFGSATGLARYYPASPMVDNSRTNPKIDI
 Db 181 NELNWTSADEVFQKNREEDPSLLWQVFGSATGLARYYPASPMVDNSRTNPKIDI
 QY 241 RPYIQGAASPKDMLILVDVSGSVSLGLTKLIRTSVSEMLETSLDDDDPNNVASF
 Db 241 RPYIQGAASPKDMLILVDVSGSVSLGLTKLIRTSVSEMLETSLDDDDPNNVASF
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNTNVSRA
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNTNVSRA
 QY 361 FTGGEERAQEIIFNKYNKDKKRVFRFSVQHNHYERGPIONMACENKGYTTEIP
 Db 361 FTGGEERAQEIIFNKYNKDKKRVFRFSVQHNHYERGPIONMACENKGYTTEIP
 QY 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVLDALELGLVITGLPVFNITGQPE
 Db 421 INTOEYLDVLGRPMVLADGKAKOVQNTNVLDALELGLVITGLPVFNITGQPE
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 Db 481 NQLILGVMGVDVSLIEDIKRLTPRTCLCPNGYYPFAIDPENGYYLLHPNLQPKNPKS
 QY 541 DFLDAELENDIKVEIRNKMIDGSGSEKTFRTLVKSQDERVIDKGRNRYTWTTPVK
 Db 536 DFLDAELENDIKVEIRNKMIDGSGSEKTFRTLVKSQDERVIDKGRNRYTWTTPVK
 QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFIAPRDY
 Db 596 ALVLPYTSFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFEEGYTFIAPRDY
 QY 661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKQKNII
 Db 656 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKQKNII
 QY 721 FVVTGGITRVPYKAGEWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGI
 Db 716 FVVTGGITRVPYKAGEWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGI
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 Db 776 MVSKAVEIYIQGLKLPVAVVGIKIDVNSWIENFTKTSIRDPGAGPVCDCRNSDI
 QY 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
 Db 836 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
 QY 901 GAGHRSAYVESVADILQIGMWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDPTF
 Db 896 GAGHRSAYVESVADILQIGMWATAAASIIQQFLLSLTFPRLLLEAVEMEDDDPTF
 QY 961 SCITEQTQYFFDNDKSKFSVGLDCGNCRIFFHGEKLMNTNLIPTMVESKGTCPCI
 Db 956 SCITEQTQYFFDNDKSKFSVGLDCGNCRIFFHGEKLMNTNLIPTMVESKGTCPCI
 QY 1021 QABQTSQDPNCPDMVK 1036
 Db 1016 QABQTSQDPNCPDMVK 1031

RESULT 9
 US-08-455-543A-56
 ; Sequence 56, Application US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael

Illis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTION: METHODS
SEQUENCES: 57
DE ADDRESS:
Brown, Martin, Haller & McClain
560 Union Street
Diego
California
USA
1-2926
TABLE FORM:
3: Diskette
IBM Compatible
SYSTEM: DOS
FastSEQ Version 1.5
LOCATION DATA:
1 NUMBER: US/08/455,543A
3: May 31, 1995
LOCATION DATA:
1 NUMBER: 08/223,305
3: April 4, 1994
LOCATION DATA:
1 NUMBER: 07/868,354
3: April 10, 1992
LOCATION DATA:
1 NUMBER: US 07/745,206
3: 15-AUG-1991
LOCATION DATA:
1 NUMBER: US 07/620,250
3: 30-NOV-1990
LOCATION DATA:
1 NUMBER: US 07/482,384
3: 20-FEB-1990
LOCATION DATA:
1 NUMBER: US 07/603,751
3: 04-APR-1989
LOCATION DATA:
1 NUMBER: WO PCT/US89/01408
3: 04-APR-1989
LOCATION DATA:
1 NUMBER: US 07/176,899
3: 04-APR-1988
man, Stephanie L.
N NUMBER: 33,779
XCKET NUMBER: 6362-52517
LOCATION INFORMATION:
(619)238-0999
(619)238-0062
1 SEQ ID NO: 56:
ACTERISTICS:
184 amino acids
10 acid
1S: single
linear
1: protein
1: internal

99.0%; Score 5386.5; DB 1; Length 1084;

arity 99.2%; Pred. No. 0;

conservative 0; Mismatches 1; Indels 7; Gaps 1;

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4
5
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7
8
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61 YEKYQDLYTVEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOWRE
121 EYVYTNAXDDLDPEKNDSEPGSQRIPKVFIEDANFGROI SYQHAAVHIPTDIYEG
121 EYVYTNAXDDLDPEKNDSEPGSQRIPKVFIEDANFGROI SYQHAAVHIPTDIYEG
181 NELNMTSALDVPYKKNREEDPSLLMQVFGSATGLARYYPASPVWDSRTPNKIDL
181 NELNMTSALDVPYKKNREEDPSLLMQVFGSATGLARYYPASPVWDSRTPNKIDL
241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLTSTVSEMLETLSDDDFVNVSFN
241 RPWYIQGAASPKOMLILVDVSGSVGLTLKLTSTVSEMLETLSDDDFVNVSFN
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQOLLNYSRANCN
301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFQOLLNYSRANCN
361 FTDGGEERAQEI FNKYNKDKKVRFRFSVQGNHYERGP IQMACENKGYIYIIPS
361 FTDGGEERAQEI FNKYNKDKKVRFRFSVQGNHYERGP IQMACENKGYIYIIPS
421 INTQSYLDVILGRPMVLADKAKQVQWNTNYLDLALGLVITGTLPVFNITGQFEN
421 INTQSYLDVILGRPMVLADKAKQVQWNTNYLDLALGLVITGTLPVFNITGQFEN
481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKNPKSQ
481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPLNLPKNPKSQ
541 DFLDAELENDIKVEIRNKMIDGESGEKTPRTLKVSQDERYIDKGNRTYTWTPVNG
541 DFLDAELENDIKVEIRNKMIDGESGEKTPRTLKVSQDERYIDKGNRTYTWTPVNG
601 ALVLPITYSPYIIKAKLEETITQARSKKKKKKSEITLKPDPNPEESGYTTPAPRDYC
601 ALVLPITYSPYIIKAKLEETITQARSKKKKKKSEITLKPDPNPEESGYTTPAPRDYC
661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVONYNSKQKNIK
661 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVONYNSKQKNIK
654 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVONYNSKQKNIK
654 SDNNTFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVONYNSKQKNIK
721 FVVTGGITRVYVPEAGENQWENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGA
721 FVVTGGITRVYVPEAGENQWENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGA
714 FVVTGGITRVYVPEAGENQWENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGA
714 FVVTGGITRVYVPEAGENQWENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPGA
781 MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDV
781 MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDV
774 MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDV
774 MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDV
841 LDDGGFLLMANHDDVTNQIGREFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
841 LDDGGFLLMANHDDVTNQIGREFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
834 LDDGGFLLMANHDDVTNQIGREFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
834 LDDGGFLLMANHDDVTNQIGREFGIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTFA
901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTFA
894 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTFA
894 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTFA
961 SCITETQYFFPNDSDSKSPGVLDCCGCSRI FHGEKLMNTNLI FIMVESKGTCPD
961 SCITETQYFFPNDSDSKSPGVLDCCGCSRI FHGEKLMNTNLI FIMVESKGTCPD
954 SCITETQYFFPNDSDSKSPGVLDCCGCSRI FHGEKLMNTNLI FIMVESKGTCPD
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1021 QAEQTSQGNPCDMVK 1036
1021 QAEQTSQGNPCDMVK 1036
1014 QAEQTSQGNPCDMVK 1029
1014 QAEQTSQGNPCDMVK 1029

RESULT 10
US-08-223-305C-56
; Sequence 56, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:

07:56:52 2004

us-10-090-827-14.ra1

Harpold, Michael
Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
/ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
/ENTION: METHODS
SEQUENCES: 57
ICE ADDRESS:
Brown, Martin, Haller & McClain
160 Union Street
i Diego
ilifornia
USA
01-2926
ADABLE FORM:
PE: Diskette
IBM Compatible
SYSTEM: DOS
FastSEQ Version 1.5
ICATION DATA:
N NUMBER: US/08/223,305C
E: April 4, 1994
ATION DATA:
N NUMBER: 07/868,354
E: April 10, 1992
ATION DATA:
N NUMBER: US 07/745,206
E: 15-AUG-1991
ATION DATA:
N NUMBER: US 07/620,250
E: 30-NOV-1990
ATION DATA:
N NUMBER: US 07/482,384
E: 20-FEB-1990
ATION DATA:
N NUMBER: US 07/603,751
E: 04-APR-1989
ATION DATA:
N NUMBER: WO PCT/US89/01408
E: 04-APR-1989
ATION DATA:
N NUMBER: US 07/176,899
E: 04-APR-1988
ENT INFORMATION:
dman, Stephanie L.
ON NUMBER: 33,779
DOCKET NUMBER: 52516 (P519739)
ATION INFORMATION:
(619)238-0999
R SEQ ID NO: 56:
ARACTERISTICS:
.084 amino acids
.no acid
SS: single
linear
PE: protein
B: internal

99.0%; Score 5386.5; DB 2; Length 1084;
ilarity 99.2%; Pred. No. 0;
Conservative 1; Mismatches 1; Indels 7; Gaps 1;

AGCLLALTLFQSLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLYDI 60
|||||
AGCLLALTLFQSLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLYDI 60
|||||
CYQDLTYVNNARQLVEITAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
|||||
CYQDLTYVNNARQLVEITAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
|||||

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIPKFVIEDANFGRQISYQHAHVHIPTDIYK
|||
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIPKFVIEDANFGRQISYQHAHVHIPTDIYK
|||
QY 181 NELNWTSALEDEVFKKREEDPSLLWQVFGSATGLARYYPASPPWVDNSTRPNKID
|||
DB 181 NELNWTSALEDEVFKKREEDPSLLWQVFGSATGLARYYPASPPWVDNSTRPNKID
|||
QY 241 RPWTIOGAASPDKMLILVDVSGSVSLGLTLKIRTSVSEMLETLSDDDFVNVASF
|||
DB 241 RPWTIOGAASPDKMLILVDVSGSVSLGLTLKIRTSVSEMLETLSDDDFVNVASF
|||
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSAFAEQLLNTNVSRA
|||
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSAFAEQLLNTNVSRA
|||
QY 361 FTDCGERAQEIFNKYNKDKKVRVFRFSVQGHYERGPIONMACENKGYEYIPI
|||
DB 361 FTDCGERAQEIFNKYNKDKKVRVFRFSVQGHYERGPIONMACENKGYEYIPI
|||
QY 421 INTOEYLDVLRPMVLADGKAKOVQWNTNVLDALELGLVITGLTPVFNITGOPEI
|||
DB 421 INTOEYLDVLRPMVLADGKAKOVQWNTNVLDALELGLVITGLTPVFNITGOPEI
|||
QY 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPNLOPKNPKS
|||
DB 481 NQLILGVMGVDVSLIEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPNLOPKNPKS
|||
QY 541 DFLDAELNDIKVEIRNKMIDGESGEXTFRLVKSODERYIDKGNRTYTWTVPVK
|||
DB 541 DFLDAELNDIKVEIRNKMIDGESGEXTFRLVKSODERYIDKGNRTYTWTVPVK
|||
QY 601 ALVLPTYSFYIYKAKLBETITQARSKKGMKDSSTLKPDPNPEESGYTFLAPRDY
|||
DB 601 ALVLPTYSFYIYKAKLBETITQARSKKGMKDSSTLKPDPNPEESGYTFLAPRDY
|||
QY 661 SDNNTFLLNPNFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTYWSKQKNI
|||
DB 661 SDNNTFLLNPNFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTYWSKQKNI
|||
QY 721 FVWTDGGITRVYPKEAGENQENPETYEDSFYKESLONDNDNYFTAPYFNKSGPG
|||
DB 721 FVWTDGGITRVYPKEAGENQENPETYEDSFYKESLONDNDNYFTAPYFNKSGPG
|||
QY 781 MVSXAVEIYIQGKLLKPAVVVGKIDVNSWIENFTKTSIRDPACGVPDCCKENS
|||
DB 781 MVSXAVEIYIQGKLLKPAVVVGKIDVNSWIENFTKTSIRDPACGVPDCCKENS
|||
QY 841 LDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSXYDYQSVCEPK
|||
DB 841 LDDGGFLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSXYDYQSVCEPK
|||
QY 901 GAGHRSAYVPSVADILQIGMWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFT
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DB 901 GAGHRSAYVPSVADILQIGMWATAAAWSILQQFLLSLTFPRLLEAVEMEDDDFT
|||
QY 961 SCITEQTQYFFDNDKSKSFGVLDGCGNCSRIFPHGEKLANNTNLIIFIMVESKGTCP
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DB 961 SCITEQTQYFFDNDKSKSFGVLDGCGNCSRIFPHGEKLANNTNLIIFIMVESKGTCP
|||
QY 1021 QAEQTSQGPNCPCMVK 1036
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DB 1014 QAEQTSQGPNCPCMVK 1029
|||

RESULT 11
US-08-455-543A-53
; Sequence 53, Application US/08455543A
; Patent No. 5792846
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven

Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTION: METHODS

SOURCES: 57

CE ADDRESS:

Brown, Martin, Haller & McClain

560 Union Street

Diego

California

USA

1-2926

ABLE FORM:

3: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

NUMBER: US/08/455,543A

3: May 31, 1995

ATION DATA:

NUMBER: 08/223,305

3: April 4, 1994

ATION DATA:

NUMBER: 07/869,354

3: April 10, 1992

ATION DATA:

NUMBER: US 07/745,206

3: 15-AUG-1991

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NUMBER: US 07/620,250

3: 30-NOV-1990

ATION DATA:

NUMBER: US 07/482,384

3: 20-FEB-1990

ATION DATA:

NUMBER: US 07/603,751

3: 04-APR-1989

ATION DATA:

NUMBER: WO PCT/US89/01408

3: 04-APR-1989

ATION DATA:

NUMBER: US 07/176,899

3: 04-APR-1988

nt INFORMATION:

man, Stephanie L.

IN NUMBER: 33,779

OCKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQ ID NO: 53:

ACTERISTICS:

103 amino acids

to acid

IS: single

linear

3: protein

3: internal

98.6%; Score 5367; DB 1; Length 1103;

larity 97.4%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 26; Gaps 2;

XCLLATLTFLQSLIGPSSEEPFSAVTIKSWVDKMWQEDLVTLAKTAGVNLVDI 60

XCLLATLTFLQSLIGPSSEEPFSAVTIKSWVDKMWQEDLVTLAKTAGVNLVDI 60

(QDLYTEPNARQLVEIARDEIKLSNRKALVSLALEAEKVQAAHQRRE 120

61 YEKYQDLYTEPNARQLVEIARDEIKLSNRKALVSLALEAEKVQAAHQRRE
121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGROIYQHAHVHIPTDIYEG
121 EVVYNAKDDLDPEKNDSEPGSORIKPVFTEDANFGROIYQHAHVHIPTDIYEG
181 NELNMTSALDEVFKKREEDPSLLWQVFGSATGLARYYPASPVVDNSRTPNKIDI
181 NELNMTSALDEVFKKREEDPSLLWQVFGSATGLARYYPASPVVDNSRTPNKIDI
241 RPWYIQGAASPDKMLILVDVSGVSGLTJLKLINTSVSEMLETSDDDFVNVAFFN
241 RPWYIQGAASPDKMLILVDVSGVSGLTJLKLINTSVSEMLETSDDDFVNVAFFN
301 VSCFQHLVQANVRNKKVLDAVNNITAKGTDYKKGPSFAFEOLLNINVRANCN
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361 FTDGGERAQEI FNKYNKDKVVRVFRFSGQHNYERGP IQMACENKGYIYEIPS
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421 INTQEVLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITQGFEN
421 INTQEVLDVLRPMVLGADKAKQVQNTNYLDALGLVITGTLPVFNITQGFEN
481 NOLILGVMGVDVLSLEDIKLTLPFTLCPNGYYFAIDPNGVYLLHPLNLPK-
481 NOLILGVMGVDVLSLEDIKLTLPFTLCPNGYYFAIDPNGVYLLHPLNLPK-
531 -----NPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQ
541 LRKRENIQNPKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLKVSQ
582 DKGNRTYTWTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARKKGGKMDSETL
601 DKGNRTYTWTPVNGTDYSLALVLPYTSFYIYKAKLEETITQARKKGGKMDSETL
642 EESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKT PNNPSCNADLINRVLLD
654 EESGYTFIAPRDYCNLDKISDNNTFELNFEFIDRKT PNNPSCNADLINRVLLD
702 ELVQNTWSKQKNI KGVARFVVTGDIITRVYKPEAGENWQENPETYEDSFYKRS
714 ELVQNTWSKQKNI KGVARFVVTGDIITRVYKPEAGENWQENPETYEDSFYKRS
762 VFTAPYFNKSGGAYESGIMVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKT
774 VFTAPYFNKSGGAYESGIMVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKT
822 CAGPVCDCRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLVN
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894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGHWATAAAWSILQQFLLS
942 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRIFFHGEKLI
954 LLEAVEMEDDDFTASLSKQSCITEQTYFFDNDKSFSGVLDCGNCRIFFHGEKLI
1002 IFIMVESKGTCPDTRLLIQAEQTSDDGNPCDMVK 1036
1014 IFIMVESKGTCPDTRLLIQAEQTSDDGNPCDMVK 1048

RESULT 12

US-08-223-305C-53

; Sequence 53, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTON: METHODS
SEQUENCES: 57

ICE ADDRESS:
Brown, Martin, Haller & McClain
660 Union Street
San Diego
California
USA

1-2926

DABLE FORM:

E: Diskette

IBM Compatible

SYSTEM: DOS

FastSEQ Version 1.5

ICATION DATA:

IC NUMBER: US/08/223,305C

E: April 4, 1994

ATION DATA:

IN NUMBER: 07/868,354

E: April 10, 1992

ATION DATA:

IN NUMBER: US 07/745,206

E: 15-AUG-1991

ATION DATA:

IN NUMBER: US 07/620,250

E: 30-NOV-1990

ATION DATA:

IN NUMBER: US 07/482,384

E: 20-FEB-1990

ATION DATA:

IN NUMBER: US 07/603,751

E: 04-APR-1989

ATION DATA:

IN NUMBER: WO PCT/US89/01408

E: 04-APR-1989

ATION DATA:

IN NUMBER: US 07/176,899

E: 04-APR-1988

NT INFORMATION:

man, Stephanie L.

ON NUMBER: 33,779

DOCKET NUMBER: 52516 (P519739)

ATION INFORMATION:

(619)238-0999

NR SEQ ID NO: 53:

ACTERISTICS:

103 amino acids

no acid

SS: single

linear

E: protein

E: internal

98.6%; Score 5367; DB 2; Length 1103;

ilarity 97.4%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 26; Gaps 2;

AGCLALTTLTQSLIGSSSEPPPSATYIKSWDKMQEDLVTLAKTASGVNQLVDI 60

AGCLALTTLTQSLIGSSSEPPPSATYIKSWDKMQEDLVTLAKTASGVNQLVDI 60

QDLYTVEPNARQLVEIAARDIEKLLNSRKALVSLALEAKVQAHHQWREDFASN 120

QDLYTVEPNARQLVEIAARDIEKLLNSRKALVSLALEAKVQAHHQWREDFASN 120

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121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYK
181 NELNWTSSALDEVFKQREEDPSLLWQVFGSATGLARYYPASPPWVDSNRTNPKIDI
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241 RPWYIQGAASPDKMLILVDVSGSVGLTLKLRITSVSEMLETSLDDDFVNVASF
301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQLLNTNVRANC
301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQLLNTNVRANC
361 PTDGGERAQEIENKYNKKKVVFRFVSQHNVERGPIOMMACENKGYVEIPE
361 PTDGGERAQEIENKYNKKKVVFRFVSQHNVERGPIOMMACENKGYVEIPE
421 INTQEYLDVLGRPMVLADGKAKQVQNTNVLDALEGLVITGTLPVFNITQGFEN
421 INTQEYLDVLGRPMVLADGKAKQVQNTNVLDALEGLVITGTLPVFNITQGFEN
481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPFADDPNGYVLLHPLNLPKPGV
481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPFADDPNGYVLLHPLNLPKPGV
531 -----NPKSQEPVTLPLDAELENLKVIRNKKIIDGESSEKTRTLVKS
541 LRKRPNIQPKSQEPVTLPLDAELENLKVIRNKKIIDGESSEKTRTLVKS
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601 DKGNTYTWTPVNGTDYSLALVLTPTSYFYIKAKLEETITQARSKKGMKMDSETI
642 EESGYTFIAPRDYCNLDKI SDNNTFELNNEFIDRKTNNPSCNADLINRVLLI
654 EESGYTFIAPRDYCNLDKI SDNNTFELNNEFIDRKTNNPSCNADLINRVLLI
702 ELVQYNSKOKNIGVKARFVWTDGGITRVYPKEAGENWQENPETYEDSFYKRSI
714 ELVQYNSKOKNIGVKARFVWTDGGITRVYPKEAGENWQENPETYEDSFYKRSI
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774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKI
822 CAGPVCCKRNSDVMOCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLV
834 CAGPVCCKRNSDVMOCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLV
882 FNKSIDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASILQOFLLE
894 FNKSIDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASILQOFLLE
942 LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSFSGVLDGNCNRSIFHGEKI
954 LLEAVEMEDDDFTASLSKQSCITEQTYQFPDNDKSFSGVLDGNCNRSIFHGEKI
1002 IFIMVESKGTCPDTRILLIOAEOQTSQGNPCDMVK 1036
1014 IFIMVESKGTCPDTRILLIOAEOQTSQGNPCDMVK 1048

RESULT 13

US-08-455-543A-55

; Sequence 55, Application US/08455543A

; Patent No. 5792846

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

feldman, Daniel
 leCue, Ann
 renner, Robert
 NTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 NTION: METHODS

REFERENCES: 57

ADDRESS:
 Brown, Martin, Haller & McClain
 60 Union Street
 Diego
 ifornia
 USA

--2926

ABLE FORM:

;; Diskette

IBM Compatible

SYSTEM: DOS

FastSEQ Version 1.5

CATION DATA:

NUMBER: US/08/455,543A

;; May 31, 1995

ATION DATA:

NUMBER: 08/223,305

;; April 4, 1994

ATION DATA:

NUMBER: 07/868,354

;; April 10, 1992

ATION DATA:

NUMBER: US 07/745,206

;; 15-AUG-1991

ATION DATA:

NUMBER: US 07/620,250

;; 30-NOV-1990

ATION DATA:

NUMBER: US 07/482,384

;; 20-FEB-1990

ATION DATA:

NUMBER: US 07/603,751

;; 04-APR-1989

ATION DATA:

NUMBER: WO PCT/US89/01408

;; 04-APR-1989

ATION DATA:

NUMBER: US 07/176,899

;; 04-APR-1988

IT INFORMATION:

man, Stephanie L.

AN NUMBER: 33,779

CKET NUMBER: 6362-52517

ATION INFORMATION:

(619)238-0999

(619)238-0062

SEQ ID NO: 55;

ACTERISTICS:

79 amino acids

to acid

;;S: single

linear

;; protein

;; internal

98.2%; Score 5347; DB 1; Length 1079;
 larity 98.7%; Pred. No. 0;
 conservative 0; Mismatches 1; Indels 12; Gaps 2;

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3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

3CLLALTLTLFQSLILGPSSEEPFPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60

QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHPTDIYEG
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQHAHVHPTDIYEG
 QY 181 NELNWTSALEDEVFKKREDEPSLLMQVFGSATGLIARYYPASPWVDSNRTPNKIDL
 Db 181 NELNWTSALEDEVFKKREDEPSLLMQVFGSATGLIARYYPASPWVDSNRTPNKIDL
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETSLDDDFVNVASFN
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTILKIRTSVSEMLETSLDDDFVNVASFN
 QY 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITYKKGFSFAFQQLLYNVSRANCN
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITYKKGFSFAFQQLLYNVSRANCN
 QY 361 FTDGGERAQAEIFNKYNKDKKRVFRFVSQGHYERGPIONMACENKGYIYIPIS
 Db 361 FTDGGERAQAEIFNKYNKDKKRVFRFVSQGHYERGPIONMACENKGYIYIPIS
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 Db 421 INTOEYLDVLGRPMVLADGKAKQVQWNTVNYLDALGLGLVITGLPVFNITGQFEN
 QY 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLQPNPKSQ
 Db 481 NQLILGVMGVDSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHHPNLQPNPKSQ
 QY 541 DELDAELENDAKVEIRNMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
 Db 541 DELDAELENDAKVEIRNMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNG
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 Db 596 ALVLTYSFYIYKAKLEETITQARY-----SETLKPDNFESGYTFIAPRDYC
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 Db 661 SDNTEFLNFEPIRDKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQKNIK
 QY 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 Db 721 FVVTGGITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 QY 769 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWNIENFTKTSIRDPCAGPVCDCRNSDV
 Db 769 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWNIENFTKTSIRDPCAGPVCDCRNSDV
 QY 841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCBPG
 Db 841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCBPG
 QY 901 GAGHSAYVPSVADILQIGMWATAAWSILQOFLSLSTFPRLLEAEMEDDDFTA
 Db 901 GAGHSAYVPSVADILQIGMWATAAWSILQOFLSLSTFPRLLEAEMEDDDFTA
 QY 961 SCITEQTQYFFDNDKSPSGVLDCGNCRIFFHGEKLMNTLIFIMVESKGTCPD
 Db 961 SCITEQTQYFFDNDKSPSGVLDCGNCRIFFHGEKLMNTLIFIMVESKGTCPD
 QY 1021 QAEQTSQDGNPCDMVK 1036
 Db 1009 QAEQTSQDGNPCDMVK 1024

RESULT 14

US-08-223-305C-55

; Sequence 55, Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

Williams, Mark
Feldman, Daniel
McCue, Ann
Brenner, Robert
ENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ENTION: METHODS

QUENCES: 57

CE ADDRESS:
Brown, Martin, Haller & McClain
660 Union Street

Diego

California

USA

1-2926

DABLE FORM:

E: Diskette

IBM Compatible

SYSTEM: DOS

FastSeq Version 1.5

ICATION DATA:

N NUMBER: US/08/223,305C

E: April 4, 1994

ATION DATA:

N NUMBER: 07/868,354

E: April 10, 1992

ATION DATA:

N NUMBER: US 07/745,206

E: 15-AUG-1991

ATION DATA:

N NUMBER: US 07/620,250

E: 30-NOV-1990

ATION DATA:

N NUMBER: US 07/482,384

E: 20-FEB-1990

ATION DATA:

N NUMBER: US 07/603,751

E: 04-APR-1989

ATION DATA:

N NUMBER: WO PCT/US89/01408

E: 04-APR-1989

ATION DATA:

N NUMBER: US 07/176,899

E: 04-APR-1988

NT INFORMATION:

ON NUMBER: 33,779

DOCKET NUMBER: 52516 (P519739)

ATION INFORMATION:

(619)238-0999

R SEQ ID NO: 55:

RACTERISTICS:

079 amino acids

no acid

SS: single

linear

E: protein

E: internal

98.2%; Score 5347; DB 2; Length 1079;

larity 98.7%; Pred. No. 0;

Conservative 0; Mismatches 1; Indels 12; Gaps 2;

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|||||

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|||||

YQDLYTVEPNARQLVFAARDIEKLLSNRSKALVSLALEAEKVQAAHQRFPASN 120

|||||

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Db 121 EVVYNAKODLDPKNDSEPGSQRIKPVFIEDANFGRIQSYQHAHVHIPTDIYEC
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Db 181 NEINWTSALDEVFKNREEDPSLLMQVFGSATGLARYYPASPVVDSNRTPNKIDI
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTAKLIRTSVSEMLETSLDDDDFVNVASFN
Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTAKLIRTSVSEMLETSLDDDDFVNVASFN
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Db 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLLNNYVSRANC
QY 361 FTGGBERAQEIENKYNKDKKVRVFRFSVGOHNYERGPIONMACENKGYEYIPE
Db 361 FTGGBERAQEIENKYNKDKKVRVFRFSVGOHNYERGPIONMACENKGYEYIPE
QY 421 INTOEYLDVLRPMVLGADKAKOVQNTVYLDALGLVITGTLPVFNITGQFEN
Db 421 INTOEYLDVLRPMVLGADKAKOVQNTVYLDALGLVITGTLPVFNITGQFEN
QY 481 NQLILGVMGVDVSLEDIKRLTPRTLCPNGYYEAIIDPNGVYLLHPLNLOPKKSC
Db 481 NQLILGVMGVDVSLEDIKRLTPRTLCPNGYYEAIIDPNGVYLLHPLNLOPKKSC
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRTYTWTPVNG
Db 536 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRTYTWTPVNG
QY 601 ALVLPYVSFYIYKAKLEETITQARSKKGMKDSSETLKPDNFESGYTFFIAPRDYC
Db 596 ALVLPYVSFYIYKAKLEETITQARY-----SETLKPDNFESGYTFFIAPRDYC
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Db 649 SDNNTRELLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSKQKNIK
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Db 709 FVVTGGITRVYKPEAGENQENPETEYDSFYKRSLDNDNDNYFTAPYFNKSGPGA
QY 781 MVSKAVEIYIQGLKLPAPVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDV
Db 769 MVSKAVEIYIQGLKLPAPVVGIIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDV
QY 841 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
Db 829 LDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
QY 901 GAGHSAYVPSVADILIQGWATAAAWSILQQFLLSLTFPRLLLEAVEMEDDDFTA
Db 889 GAGHSAYVPSVADILIQGWATAAAWSILQQFLLSLTFPRLLLEAVEMEDDDFTA
QY 961 SCITEQTQYFFDNDKSPSGVLDGCGNCSRI FHGKELMNTNLIIFIMVESKGTCPD
Db 949 SCITEQTQYFFDNDKSPSGVLDGCGNCSRI FHGKELMNTNLIIFIMVESKGTCPD
QY 1021 QAEQTSQGNPCDMVK 1036
Db 1009 QAEQTSQGNPCDMVK 1024

RESULT 15

US-08-435-675B-5

; Sequence 5, Application US/08435675B

; Patent No. 5710250

; GENERAL INFORMATION:

; APPLICANT: Ellis, Steven Bradley

; APPLICANT: Williams, Mark E.

; APPLICANT: Harpold, Michael Miller

; APPLICANT: Schwartz, Arnold

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February 20, 2004, 16:53:09 ; Search time 17.3096 Seconds
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10-090-827-13

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8717 seqs, 42310858 residues

ts satisfying chosen parameters: 328717

gth: 0

gth: 2000000000

Minimum Match 0%

Maximum Match 100%

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/cgn2_6/prodata/1/1aa/backfiles1.pep:*

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or than or equal to the score of the result being printed,
red by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
10.0	1091	1	US-07-745-206A-25	Sequence 25, Appl
10.0	1091	1	US-08-455-543A-52	Sequence 52, Appl
10.0	1091	2	US-08-223-305C-52	Sequence 52, Appl
10.0	1091	2	US-08-311-363-25	Sequence 25, Appl
9.9	1091	3	US-08-713-118-4	Sequence 4, Appl
9.9	1091	3	US-09-452-007-4	Sequence 4, Appl
9.3	1086	1	US-08-455-543A-54	Sequence 54, Appl
9.3	1086	2	US-08-223-305C-54	Sequence 54, Appl
8.9	1084	1	US-08-455-543A-56	Sequence 56, Appl
8.9	1084	2	US-08-223-305C-56	Sequence 56, Appl
8.6	1103	1	US-08-455-543A-53	Sequence 53, Appl
8.6	1103	2	US-08-223-305C-53	Sequence 53, Appl
8.2	1079	1	US-08-455-543A-55	Sequence 55, Appl
8.2	1079	2	US-08-223-305C-55	Sequence 55, Appl
6.1	1106	1	US-08-435-675B-5	Sequence 5, Appl
5.8	1106	1	US-08-336-257A-8	Sequence 8, Appl
1.9	1086	6	5386025-8	Patent No. 5386025
13.7	1145	4	US-09-470-443-2	Sequence 2, Appl
13.7	1145	4	US-09-470-443-4	Sequence 4, Appl
13.3	1076	4	US-09-470-443-6	Sequence 6, Appl
18.3	508	1	US-08-435-675B-6	Sequence 6, Appl
3.4	885	3	US-09-074-579-5	Sequence 5, Appl
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44	152.5	2.9	789	3	US-09-300-529-32	Sequence
45	152.5	2.9	789	3	US-09-233-336A-4	Sequence

ALIGNMENTS

RESULT 1
US-07-745-206A-25
Sequence 25, Application US/07745206A
Patent No. 5439921

GENERAL INFORMATION:

APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-206A-25

Query Match 100.0%; Score 5346; DB 1; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTTLFQSLIGSPSPFSAVITIKSWVDKMOEDLVTLAKTAGVNN
DB 1 MAAGCLLALTTLFQSLIGSPSPFSAVITIKSWVDKMOEDLVTLAKTAGVNN

Application US/08455543A

046
ATION:
Harpold, Michael
Ellis, Steven
Williams, Mark

```

1 APPLICANT: Feldman, Daniel
2 APPLICANT: McCue, Ann
3 APPLICANT: Brenner, Robert
4 TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
5 TITLE OF INVENTION: METHODS
6 NUMBER OF SEQUENCES: 57
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Brown, Martin, Haller & McClain
9 STREET: 1660 Union Street
10 CITY: San Diego
11 STATE: California
12 COUNTRY: USA
13 ZIP: 92101-2926
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette
16 COMPUTER: IBM Compatible
17 OPERATING SYSTEM: DOS
18 SOFTWARE: Fast-SEQ Version 1.5
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/455,543A
21 FILING DATE: May 31, 1995
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/223,305
24 FILING DATE: April 4, 1994
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 07/868,354
27 FILING DATE: April 10, 1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/745,206
30 FILING DATE: 15-AUG-1991
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/620,250
33 FILING DATE: 30-NOV-1990
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 07/482,384
36 FILING DATE: 20-FEB-1990
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 07/603,751
39 FILING DATE: 04-APR-1989
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: WO PCT/US89/01408
42 FILING DATE: 04-APR-1989
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: US 07/176,899
45 FILING DATE: 04-APR-1988
46 ATTORNEY/AGENT INFORMATION:
47 NAME: Seidman, Stephanie L.
48 REGISTRATION NUMBER: 33,779
49 REFERENCE/DOCKET NUMBER: 6362-52517
50 TELECOMMUNICATION INFORMATION:
51 TELEPHONE: (619)238-0999
52 TELEFAX: (619)238-0062
53 INFORMATION FOR SEQ ID NO: 52:
54 SEQUENCE CHARACTERISTICS:
55 LENGTH: 1091 amino acids
56 TYPE: amino acid
57 STRANDEDNESS: single
58 TOPOLOGY: linear
59 MOLECULE TYPE: protein
60 FRAGMENT TYPE: internal
61
62 US-08-455-543A-52
63
64 Query Match 100.0%; Score 5346; DB 1; Length 1091;
65 Best Local Similarity 100.0%; Pred. No. 0;
66 Matches 1018; Conservative 0; Mismatches 0; Indels 0;
67

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Db	1	MAAGCLLALTUTLFSLLIGSSSEPPPSAVTTKSWVDKQOBDLVTLAKTASGVN
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Db	61	YKYQDLVTYVEFPNNARQIWEAAARDIEKLLSNASKALVSLAEAKVQAAHAWRE

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location US/08223305C
24
arion:
arold, Michael
llis, Steven
illiams, Mark
eldman, Daniel
cCue, Ann
renner, Robert

TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
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COUNTRY: USA
ZIP: 92101-2926
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
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FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/603,751
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 52516 (P519739)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-223-305C-52

Query Match 100.0%; Score 5346; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; C

Qy 1 MAAGCLLALTLTLFQSLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNC
Db 1 MAAGCLLALTLTLFQSLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGVNC
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Db 61 YEKYQDLYTTEPNNAQVETAAARDIEKLLSNRSKALVSLAEAKVQAARHWEI
Qy 121 EVVYVNAKDDLDPEKNDSEPGSQRKPVFIIDANFGROI SYOHAHVHIPTDIYEGS
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plication_US/08311363

958

ATION:

Harbold, Michael

Ellis, Steven

Williams, Mark

Feldman, Daniel

McCue, Ann

Brenner, Robert

ENTION: Human Calcium Channel Compositions and

ENTION: Methods

QUENCES: 32

CE ADDRESS:

Brown, Martin, Haller & McClain

660 Union Street

CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/311,363
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,206
 FILING DATE: 15-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-51506
 TELEPHONE: (619) 238-0999
 TELEFAX: (619) 238-0062
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1091 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-311-363-25

Query Match 100.0%; Score 5346; DB 2; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1018; Conservative 0; Mismatches 0; Indels 0;

QY 1 MAAGCLLALTTLFQSLILGPSSEPPPSAVTIKSWDKMQEDLVLTAKTASGVN
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 DB 181 NELNWTLSALDEVFKKREEDPSLLWVFGSATGLARYYPASPVVDSRTPNKIDL
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 DB 241 RPYIIGGAASPKMDLILVDVSGVSGTLKLIKRTSVSEMLETSDDDFVNVSFNFN
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 DB 301 VSCFQHLVQANVRKVKLDVANNITAKGITDYKKGFSFAFEQLLNVSFRANCN
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 DB 361 FTDGGERAQEIIFNKYNKDKKVRFRPSVQHNHYERGPIQWMAKCNKGYIYEIPIPS
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 DB 481 NQLILGVMGVDSLEDIKELTPRTLCNPGYYPALDPNGVYLLHPLNLPKPKSQ
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 DB 541 DFLDAELNDIKVEIRNKMDIGESGKTFRTLKVSQDERYIDKGNRTYTWTPVNG

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ication US/08713118

36

tion:

Ango, Rodrigo

un Chen, Ai Ru

uey, David J.

NTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

NTION: CALCIUM CHANNEL SUBUNITS

UENCES: 6

E ADDRESS:

Hamilton, Brook, Smith & Reynolds, P.C.

o Militia Drive

ngton

SA

-4799

ABLE FORM:

: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

CATION DATA:

NUMBER: US/08/713,118

: 16-SEP-1996

ION: 435

T INFORMATION:

, Elizabeth W.

N NUMBER: 38,236

CKET NUMBER: ACC96-01

TION INFORMATION:

617-861-6240

17-861-9540

: SEQ ID NO: 4:

ACTERISTICS:

91 amino acids

o acid

linear

: protein

Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1017; Conservative 0; Mismatches 1; Indels 0;
 QY 1 MAAGCLLALTTLTFLPSLLIGSSSEPPSPSAVTIKSMVDKMOEDLVTLAKTASGVN
 Db 1 MAAGCLLALTTLTFLPSLLIGSSSEPPSPSAVTIKSMVDKMOEDLVTLAKTASGVN
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 Db 61 YEKYQDLTVTPNNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREI
 QY 121 EYVYNKODLDPEKNDSEPSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG:
 Db 121 EYVYNKODLDPEKNDSEPSQRIKPVFIEDANFGROI SYOHAHVHIPTDIYEG:
 QY 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASVWVNSRTPNKIDL:
 Db 181 NELNWTSSALDEVFKKNREEDPSLLWQVFGSATGLARYYPASVWVNSRTPNKIDL:
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLI RTSVSEMLETLDSDDDFVNVASFN:
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGTLKLI RTSVSEMLETLDSDDDFVNVASFN:
 QY 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIITDYKKGFSFAFEQLLNYNVSRANCNI
 Db 301 VSCFOHLVQANVRNKKVLKDAVNNTAKGIITDYKKGFSFAFEQLLNYNVSRANCNI
 QY 361 PTDGGEERAQELFNKYNDKKVRVFRFSVGOHNYERGPIQWMACENKGYTYEIPS:
 Db 361 PTDGGEERAQELFNKYNDKKVRVFRFSVGOHNYERGPIQWMACENKGYTYEIPS:
 QY 421 INTQBYLDVLGRPMVLADGKAKQVQNTNVYLDALBLGLVITGTLPVFNITQGFENI
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 QY 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNLQPKPKPSQI
 Db 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNLQPKPKPSQI
 QY 541 DFLDAELENLKVIRRNKWDGSEKTFRTLKVSQDERYIDKGNRTYTWTPVNG'
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 Db 901 GAGRSAYVPSVADILQIGWATAAASILQOFLLSLTPRLLLEAVEMEDDDFTAS
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 Db 961 SCITEQYQYFFNDKSGSGVLDCGNCRSRIFHGKLMNTNLIFIMVESKGTCPCDI

lication US/09452007

485

ATION:

Franco, Rodrigo

Sun Chen, Ai Ru

Suey, David J.

ENTION: NUCLEIC ACID ENCODING HUMAN NEURONAL

ENTION: CALCIUM CHANNEL SUBUNITS

QUENCES: 6

CE ADDRESS:

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ington

USA

3-4799

DABLE FORM:

E: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patentin Release #1.0, Version #1.30

ICATION DATA:

N NUMBER: US/09452,007

E:

ATION:

N NUMBER: US/08/713,118

E: 16-SEP-1996

NT INFORMATION:

a. Elizabeth W.

ON NUMBER: 38,236

DOCKET NUMBER: ACC96-01

ATION INFORMATION:

617-861-6240

617-861-9540

R SEQ ID NO: 4:

091 amino acids

no acid

linear

E: protein

99.9%; Score 5342; DB 3; Length 1091;

larity 99.9%; Pred. NO. 0;

Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GCLALATLTLFQSLIGPSSREPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

GCLALATLTLFQSLIGPSSREPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

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YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

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YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

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YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

YQDLTYVEPNARQIVEIARDIEKLLNSRKALVSLALEAEKVQAAHQMREDFASN 120

361 FTGGGERAQEI FNKYNKDKKVRFRPSVQGHNYERGPQIOMACENKGYIETPE
421 INTQEVLDVLRPMVLGAKAKQVQNTNVYLDALGLGLVITGLPVENITQGFEN
421 INTQEVLDVLRPMVLGAKAKQVQNTNVYLDALGLGLVITGLPVENITQGFEN
481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPADIPNGVLLHPLNLPKPKSC
481 NQILGVMGVDVSLIEDIKRLTPRFTLCPNGYYPADIPNGVLLHPLNLPKPKSC
541 DFLDALENDIKVEIRNKMDGSGEKTFTLVKSODERYIDKGNRTYTWTPVNG
541 DFLDALENDIKVEIRNKMDGSGEKTFTLVKSODERYIDKGNRTYTWTPVNG
601 ALVLPYTFYIKAKLEETITQARSKKGMKQSETLKPDNFEESGYTFIAPRDYC
601 ALVLPYTFYIKAKLEETITQARSKKGMKQSETLKPDNFEESGYTFIAPRDYC
661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVYWSKQKNIK
661 SDNTEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNVLQVYWSKQKNIK
721 FVVTGSGITRVYKPEAGENQENPETVEDSFYKRSLDNDNYVFTAPYFNKSGPGP
721 FVVTGSGITRVYKPEAGENQENPETVEDSFYKRSLDNDNYVFTAPYFNKSGPGP
781 MVSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDPCAGPVCDCKRNSDY
781 MVSKAVEIYIQGLKLPVAVGKIDVNSWNIENFTKTSIRDPCAGPVCDCKRNSDY
841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPC
901 GAGHRSAYVPSVADIIQIGWATAAASWIIQQFLLSLTFFPRLLAEVEMEDDDFTF
901 GAGHRSAYVPSVADIIQIGWATAAASWIIQQFLLSLTFFPRLLAEVEMEDDDFTF
961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLI FIMVESKGTCPCI
961 SCITEQTQYFFDNDKSFSGVLDGCGNCSRFHGEKLMNTNLI FIMVESKGTCPCI

RESULT 7
US-08-455-543A-54
Sequence 54, Application US/08455543A
Patent No. 5792846
GENERAL INFORMATION:
APPLICANT: Harpold, Michael
APPLICANT: Ellis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995

TION DATA:
 : NUMBER: 08/223,305
 : April 4, 1994
 TION DATA:
 : NUMBER: 07/868,354
 : April 10, 1992
 TION DATA:
 : NUMBER: US 07/745,206
 : 15-AUG-1991
 TION DATA:
 : NUMBER: US 07/620,250
 : 30-NOV-1990
 TION DATA:
 : NUMBER: US 07/482,384
 : 20-FEB-1990
 TION DATA:
 : NUMBER: US 07/603,751
 : 04-APR-1989
 TION DATA:
 : NUMBER: WO PCT/US89/01408
 : 04-APR-1989
 TION DATA:
 : NUMBER: US 07/176,899
 : 04-APR-1988
 TION DATA:
 : INFORMATION: Lman, Stephanie L.
 : IN NUMBER: 33,779
 : SOCKET NUMBER: 6362-52517
 : TION INFORMATION:
 : (619)238-0999
 : 619)238-0062
 : SEQ ID NO: 54:
 : 86 amino acids
 : co acid
 : S: single
 : linear
 : : protein
 : : internal

99.3%; Score 5306.5; DB 1; Length 1086;
 arity 99.5%; Pred. No. 0;
 conservative 0; Mismatches 0; Indels 5; Gaps 1;
 KLLALTLTLPQSLIGPSSPPFPSPAVTIKSWDKQEDLVLTAKTASGVNQLVDI 60
 KLLALTLTLPQSLIGPSSPPFPSPAVTIKSWDKQEDLVLTAKTASGVNQLVDI 60
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 WTSALDEVPKKNREEDPILLQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
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 TQGAASPKDMLILVDVSGVSLTLKLRITSVSEMLETLSDDDFVNVAASFNSNAQD 300
 QHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAPQLNINYNVSRANCNKIIML 360
 QHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAPQLNINYNVSRANCNKIIML 360
 XGEERAQEIENKYNKDKVYRFRFSVQGNHYERGPQIOWMACENKGYIYIPISGAIR 420
 XGEERAQEIENKYNKDKVYRFRFSVQGNHYERGPQIOWMACENKGYIYIPISGAIR 420

421 INTQYLDVLGRPMVLADGKAKQVOMTVNYLDALGLVITGTLFVFNITQGFEN
 421 INTQYLDVLGRPMVLADGKAKQVOMTVNYLDALGLVITGTLFVFNITQGFEN
 481 NQLILGVNGVDVSLSDIIRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKPKSQ
 481 NQLILGVNGVDVSLSDIIRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKPKSQ
 541 DFLDAELENDIKVEIRNMIDGESGKFTLTKSQDERYIDKGNRTYTWTPVNG
 536 DFLDAELENDIKVEIRNMIDGESGKFTLTKSQDERYIDKGNRTYTWTPVNG
 601 ALVLPYSFYIKAKLEETITQARKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCI
 596 ALVLPYSFYIKAKLEETITQARKKGMKDSKSETLKPDPNFEESGYTFTAPRDYCI
 661 SDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNKIK
 656 SDNTEFLLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNKIK
 721 FVTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGGA
 716 FVTDGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSPGGA
 781 MVSKAVYIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCCKRNSDVI
 776 MVSKAVYIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCCKRNSDVI
 841 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPG
 836 LDDGGFLMANHDDYTNQIGRFFGEIDPSLMRHLNIVSYAFNKSVDYQSVCEPG
 901 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLRAVEMEDDDFTAI
 896 GAGHSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLRAVEMEDDDFTAI
 961 SCITEQTYFFDNDKSPSGVLDGNCNCSRIHFGEKLMNTNLIFIMVESKGTGCPD
 956 SCITEQTYFFDNDKSPSGVLDGNCNCSRIHFGEKLMNTNLIFIMVESKGTGCPD

RESULT 8

US-08-223-305C-54
 : Sequence 54, Application US/08223305C
 : Patent No. 5851824

: GENERAL INFORMATION:
 : APPLICANT: Harpold, Michael
 : APPLICANT: Ellis, Steven
 : APPLICANT: Williams, Mark
 : APPLICANT: Feldman, Daniel
 : APPLICANT: McCue, Ann
 : APPLICANT: Brenner, Robert
 : TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 : TITLE OF INVENTION: METHODS
 : NUMBER OF SEQUENCES: 57
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Brown, Martin, Haller & McClain
 : STREET: 1660 Union Street
 : CITY: San Diego
 : STATE: California
 : COUNTRY: USA
 : ZIP: 92101-2926
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSeq Version 1.5
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/223,305C
 : FILING DATE: April 4, 1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/868,354
 : FILING DATE: April 10, 1992

ATION DATA: US 07/745,206
 N NUMBER: 15-AUG-1991
 ATION DATA: US 07/620,250
 N NUMBER: 30-NOV-1990
 ATION DATA: US 07/482,384
 N NUMBER: 20-FEB-1990
 ATION DATA: US 07/603,751
 N NUMBER: 04-APR-1989
 ATION DATA: WO PCT/US89/01408
 N NUMBER: 04-APR-1989
 ATION DATA: US 07/176,899
 N NUMBER: 04-APR-1988
 NT INFORMATION:
 dman, Stephanie L.
 ON NUMBER: 33,779
 DOCKET NUMBER: 52516 (P519739)
 ATION INFORMATION:
 (619)238-0999
 R SEQ ID NO: 54:
 RACTERISTICS:
 086 amino acids
 no acid
 SS: single
 linear
 E: protein
 E: internal

99.3%; Score 5306.5; DB 2; Length 1086;

larity 99.5%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 5; Gaps 1;
 GCLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
 GCLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
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 NWTSALEVFCKNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTPNKIDLYDVR 240
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 YIQGAASPDKMLIIVDYSVSGSLTKLIRTSVSEMLETISDDDFVNVASNSNAQD 300
 FOHLVQANVRNKKVLDVANNITAKGITDYKKGFSPAFQQLNYSRANCKLIIML 360
 FOHLVQANVRNKKVLDVANNITAKGITDYKKGFSPAFQQLNYSRANCKLIIML 360
 GGEERAQEIFNKYNKKKVRVFRFSVQGHNYERGPQIOMMACENKGYIYEIPSGAIR 420
 GGEERAQEIFNKYNKKKVRVFRFSVQGHNYERGPQIOMMACENKGYIYEIPSGAIR 420
 QEYLDVLRPNVLADKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFENKTNLK 480
 QEYLDVLRPNVLADKAKQVQWNTNVYLDALGLVITGTLPVFNITQGFENKTNLK 480
 ILGVMGVDVSLIEDIKRLTPRTLCPNGYFAIDPNGVYLLHPNLQPKNSQEPVTL 540

Db 481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYFAIDPNGVYLLHPNLQPK
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTTWTPVK
 Db 536 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTTWTPVK
 QY 601 ALVLPTYSFYIYIKAKLBETITQARSKKGKMDSETLKPDPFESGYTFIAPRDY
 Db 596 ALVLPTYSFYIYIKAKLBETITQARSKKGKMDSETLKPDPFESGYTFIAPRDY
 QY 661 SDNTEFLNPNFIDRKTNNPSCNADLNRLVLLDAGFTNELLVQNYWSKQKNI
 Db 656 SDNTEFLNPNFIDRKTNNPSCNADLNRLVLLDAGFTNELLVQNYWSKQKNI
 QY 721 FVVTGGITRVPYKAGENQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPG
 Db 716 FVVTGGITRVPYKAGENQENPETYEDSFYKRSNDNDNYVFTAPYFNKSGPG
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 Db 776 MVSKAVEIYIQGKLLKPAVVGIIKIDVNSWIENFTKTSIRDPCAGPVCDCRNSD
 QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPC
 Db 836 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPC
 QY 901 GAGHRSAYVPSVADILQIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTY
 Db 896 GAGHRSAYVPSVADILQIGWATAAASWILQOFLLSLTPRLLLEAVEMEDDDFTY
 QY 961 SCITEQTYEFDNDKSPSGVLDGCGNCSRFHGEKLMNTNLIIFIMVESKGTCPCI
 Db 956 SCITEQTYEFDNDKSPSGVLDGCGNCSRFHGEKLMNTNLIIFIMVESKGTCPCI

RESULT 9

US-08-455-543A-56
 ; Sequence 56, Appellation US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,543A
 ; FILING DATE: May 31, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/223,305
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991

TION DATA:
NUMBER: US 07/620,250
: 30-NOV-1990
TION DATA:
NUMBER: US 07/482,384
: 20-FEB-1990
TION DATA:
NUMBER: US 07/603,751
: 04-APR-1989
TION DATA:
NUMBER: WO PCT/US89/01408
: 04-APR-1989
TION DATA:
NUMBER: US 07/176,899
: 04-APR-1988
T INFORMATION:
man, Stephanie L.
N NUMBER: 33,779
OCKET NUMBER: 6362-52517
TION INFORMATION:
(619)238-0999
SEQ ID NO: 56:
ACTERISTICS:
84 amino acids
o acid
S: single
linear
: protein
: internal

98.9%; Score 5289.5; DB 1; Length 1084;
arity 99.2%; Pred. No. 0;
onservative 0; Mismatches 1; Indels 7; Gaps 1;
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CLLALTTLFSLGLIPSEPPFSAVTKSWVDKMQEDLVTLAKTASGVNQLVDI 60
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QDLVTEPNNAQLVEIARIDIEKLLSNRKALVSLAEAEKVQAAHQWRDFAFN 120
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YNAKDDLPKNDSPGSRQIKPVFIEDANFGRLSYOHAHVHPTDIYEGSTIVL 180
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WTSALDEVFKKNREDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
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TQGAASPKDMLILVDVSGVSGLTUKLIRTSVSEMLETLSDDDDFNVNASFNSNAQD 300
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EYLDVGLRPMVLAKGAKQVQWNTVYLDALGLVITGTLVPVFNITGQFENKTNLK 480
LGVMGVDSLEDIKELTFRFTLCPNGYYFAIDPNGYVLLHNPQKNPKSPEPVTL 540
LGVMGVDSLEDIKELTFRFTLCPNGYYFAIDPNGYVLLHNPQKNPKSPEPVTL 540
DALENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDSL 600

Db 541 DFLDALENDIKVEIRNKMIDGESGEKTFRTLKVSQDERYIDKGNRTYTWTPVNGT
QY 601 ALVLPYTSFYIKAKLBETITQARSKKGMKDSSETLKPDNFEESGYTFIAPRDYCI
Db 601 ALVLPYTSFYIKAKLBETITQARY-----SETLKPDNFEESGYTFIAPRDYCI
QY 661 SDNTEFLNENEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIK
Db 654 SDNTEFLNENEFIDRKTNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIK
QY 721 FVVDGGITRVYPKEAGENWOENPETYEDSFYKSLDNDNTVFTAPYFNKSGPGAI
Db 714 FVVDGGITRVYPKEAGENWOENPETYEDSFYKSLDNDNTVFTAPYFNKSGPGAI
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCCKENSDV
Db 774 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGPVCCKENSDV
QY 841 LDDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGI
Db 834 LDDGGFLMANHDDVTNOIGRFFGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGI
QY 901 GAGHRSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFPRLLEAVEMEDDDFTAI
Db 894 GAGHRSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFPRLLEAVEMEDDDFTAI
QY 961 SCITEQTYFFDNDKSPSGVLDGNCNRIFHGEKLMNTNLIIFIMVESKGTGCPCDI
Db 954 SCITEQTYFFDNDKSPSGVLDGNCNRIFHGEKLMNTNLIIFIMVESKGTGCPCDI

RESULT 10
US-08-223-305C-56
; Sequence 56, Application US/08223305C
; Patent No. 5851824
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/223,305C
; FILING DATE: April 4, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/868,354
; FILING DATE: April 10, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/620,250
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/482,384
; FILING DATE: 20-FEB-1990

ATION DATA:
 1 NUMBER: US 07/603,751
 2: 04-APR-1989
 ATION DATA:
 1 NUMBER: WO PCT/US89/01408
 2: 04-APR-1989
 ATION DATA:
 1 NUMBER: US 07/176,899
 2: 04-APR-1988
 AT INFORMATION:
 1 man, Stephanie L.
 2 NUMBER: 33,779
 3 SOCKET NUMBER: 52516 (P519739)
 ATION INFORMATION:
 1 (619)238-0999
 2 (619)238-0062
 3 SEQ ID NO: 56:
 4 CHARACTERISTICS:
 5 84 amino acids
 6 10 acid
 7 SS: single
 8 linear
 9 3: protein
 10 3: internal

98.9%; Score 5289.5; DB 2; Length 1084;

Identity 99.2%; Pred. No. 0;
 Conservative 0; Mismatches 1; Indels 7; Gaps 1;

3CLLALTLTFSQILLGPSSEPPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
 3CLLALTLTFSQILLGPSSEPPPSAVTIKSWDKQEDLVTLAKTASGVNQLVDI 60
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 YQDLYTVEPNNAQLVEIARDTEKLSNRSKALVSLALEAEKVQAAHOREDPASN 120
 YNAKDDLPKNDSEFGSQRIPKFVIEDANFRQISYQHAHVHPTDIYEGSTIVL 180
 YNAKDDLPKNDSEFGSQRIPKFVIEDANFRQISYQHAHVHPTDIYEGSTIVL 180
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 YIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300
 YIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETISDDDFVNVASFNSNAQD 300
 FOHLVQANVRNKKVLDKAVNNITAKGITDYKGFSPAFEQLLNVTNSRANCNKIIML 360
 FOHLVQANVRNKKVLDKAVNNITAKGITDYKGFSPAFEQLLNVTNSRANCNKIIML 360
 GGEERAQEIENKYNKKVVRFRPSVQCHNYERGPQIOMACENKGYIYEIPSGAIR 420
 GGEERAQEIENKYNKKVVRFRPSVQCHNYERGPQIOMACENKGYIYEIPSGAIR 420
 QEYLDVIGRPMVLADGKAKQVMTNVVLDLLEGLVITGTLVPVNTIGQFENKTNLK 480
 QEYLDVIGRPMVLADGKAKQVMTNVVLDLLEGLVITGTLVPVNTIGQFENKTNLK 480
 ILGVMGVDSVLEDKRLTPRTFLCPNGYIFAIDPENGVLHLPNLPKPKSQBPVTL 540
 ILGVMGVDSVLEDKRLTPRTFLCPNGYIFAIDPENGVLHLPNLPKPKSQBPVTL 540
 DAELNDIKVEIRNMIDGESGEKTRFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 DAELNDIKVEIRNMIDGESGEKTRFLVKSQDERYIDKGNRTYTWTPVNGTDYSL 600
 LPTYSFYIKAKLETITQARSKKGMKDSITLKPDPNFEESGYTFIAPRYCNDLKI 660
 LPTYSFYIKAKLETITQARY-----SETLKPDPNFEESGYTFIAPRYCNDLKI 653

661 SDNTEFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 654 SDNTEFLINFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK
 721 FVTDGGITRVTPKEAGNWNQENPETYEDSFYKRSILDNDNYTFTAPYFNKSGPGA
 714 FVTDGGITRVTPKEAGNWNQENPETYEDSFYKRSILDNDNYTFTAPYFNKSGPGA
 781 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWIENTFTKTSIRDPCAGPVCDCRNSDV
 774 MYSKAVEIYIQGLKLPKPAVVGKIDVNSWIENTFTKTSIRDPCAGPVCDCRNSDV
 841 LDDGGFLLMANHDDVTNQIGRFFGEBIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 834 LDDGGFLLMANHDDVTNQIGRFFGEBIDPSLMRHLVNI SVYAFNKSVDYQSVCEPG
 901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPRLLEAVEMEDDDFTA
 894 GAGHSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPRLLEAVEMEDDDFTA
 961 SCITETQYFFDNDKSPSGVLDGCGNCSRI FHGEKLMNTNLIFIMVESKGTCPCD
 954 SCITETQYFFDNDKSPSGVLDGCGNCSRI FHGEKLMNTNLIFIMVESKGTCPCD

RESULT 11

US-08-455-543A-53
 ; Sequence 53, Application US/084555543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,543A
 ; FILING DATE: May 31, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/223,305
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,250
 ; FILING DATE: 30-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/482,384
 ; FILING DATE: 20-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 04-APR-1989

TION DATA:

NUMBER: WO PCT/US89/01408

: 04-APR-1989

TION DATA:

NUMBER: US 07/176,899

: 04-APR-1988

T INFORMATION:

man, Stephanie L.

N NUMBER: 33,779

CKET NUMBER: 6362-52517

(619)238-0999

TION INFORMATION:

619)238-0062

SEQ ID NO: 53:

ACTERISTICS:

03 amino acids

o acid

S: single

linear

: protein

: internal

98.6%; Score 5270; DB 1; Length 1103;

arity 97.4%; Fred. No. 0;

onservative 0; Mismatches 1; Indels 26; Gaps 2;

CLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60

|||||

CLLALTLTLFQSLIGSPSEPPPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDI 60

|||||

QDLTVTPNNARQVLVEIARIEKLLNSRKALVSLALEAEKQAAHQWREDFASN 120

|||||

QDLTVTPNNARQVLVEIARIEKLLNSRKALVSLALEAEKQAAHQWREDFASN 120

|||||

YNAKDDLDPEKNDSEPSQRIKPFIEDANFGROI SYOHAHVHIPTDIYEGSTIVL 180

|||||

YNAKDDLDPEKNDSEPSQRIKPFIEDANFGROI SYOHAHVHIPTDIYEGSTIVL 180

|||||

WTSALDEVKKNREDSPLLQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240

|||||

WTSALDEVKKNREDSPLLQVFGSATGLARYYPASPDVNSRTPNKIDLYDVR 240

|||||

IQGAASPKOMLILVDVSGVSGLTCLKLIRTSVSEMLTSLDDDFNVASFNNAQD 300

|||||

IQGAASPKOMLILVDVSGVSGLTCLKLIRTSVSEMLTSLDDDFNVASFNNAQD 300

|||||

OHLVQANVRNKKVLKDAVNNITAKGITDYKKGSPFAFQELLNVNVRANCNKIIML 360

|||||

OHLVQANVRNKKVLKDAVNNITAKGITDYKKGSPFAFQELLNVNVRANCNKIIML 360

|||||

GEERAQEIFNKYNKKVVRPFRSVGQHYRGPQIWMACENKGYIYEIPIGAI 420

|||||

GEERAQEIFNKYNKKVVRPFRSVGQHYRGPQIWMACENKGYIYEIPIGAI 420

|||||

EYLDVLRPMVLADKAKQVQWNTVYLDALBLGLVITGTLVPVNIQTGFENKTNL 480

|||||

EYLDVLRPMVLADKAKQVQWNTVYLDALBLGLVITGTLVPVNIQTGFENKTNL 480

|||||

LGVMGVDSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOK----- 530

|||||

LGVMGVDSLEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOKPIGVGIPTIN 540

|||||

-----NPKSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTFRTLKSDERYI 581

|||||

RPNLQNPQSQBPVTLDFDLAELENDIKVEIRNKMIDGESGKTFRTLKSDERYI 600

|||||

RTYTWTPVNGTDSLALVLPYTFYFIKAKLEETITQARKSGKXKMOSETLKPONF 641

|||||

RTYTWTPVNGTDSLALVLPYTFYFIKAKLEETITQARY-----SETLKPONF 653

|||||

YTFITAPRDYCNLKLISDNTEFLNFNEFIDRKTPNPNPCNADLINRVLLDAGTN 701

|||||

Db 654 BESGYTFIAPRDYCNLKLISDNTEFLNFNEFIDRKTPNPNPCNADLINRVLLD

Qy 702 ELVQNYMSKQKNIKGVKARFVVTGDTTGGITRVYPKEAGENWQENPETYEDSFYKRSLL

Db 714 ELVQNYMSKQKNIKGVKARFVVTGDTTGGITRVYPKEAGENWQENPETYEDSFYKRSLL

Qy 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQKLLKPAVVGIKIDVNSWIENFTKTS

Db 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIQKLLKPAVVGIKIDVNSWIENFTKTS

Qy 822 CAGPVCCCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPRLMRHLVNI

Db 834 CAGPVCCCKRNSDVMDCVILDDGGFLMANHDDYTNQIGRFFGEIDPRLMRHLVNI

Qy 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAWSILOQFLLSI

Db 894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAWSILOQFLLSI

Qy 942 LLEAVEMEDDDFTASLSKQSCITEQTQYFFNDNSKSPSGVLDGNCNCRIFHGEKLA

Db 954 LLEAVEMEDDDFTASLSKQSCITEQTQYFFNDNSKSPSGVLDGNCNCRIFHGEKLA

Qy 1002 IFIMVESKGTCPCDTRL 1018

Db 1014 IFIMVESKGTCPCDTRL 1030

RESULT 12

US-08-223-305C-53

; Sequence 53: Application US/08223305C

; Patent No. 5851824

; GENERAL INFORMATION:

; APPLICANT: Harpold, Michael

; APPLICANT: Ellis, Steven

; APPLICANT: Williams, Mark

; APPLICANT: Feldman, Daniel

; APPLICANT: McCue, Ann

; APPLICANT: Brenner, Robert

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; NUMBER OF SEQUENCES: 57

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92101-2926

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/223,305C

; FILING DATE: April 4, 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/868,354

; FILING DATE: April 10, 1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/745,206

; FILING DATE: 15-AUG-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/620,250

; FILING DATE: 30-NOV-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/482,384

; FILING DATE: 20-FEB-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/603,751

; FILING DATE: 04-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US89/01408

3: 04-APR-1989
 ATION DATA:
 1 NUMBER: US 07/176,899
 3: 04-APR-1988
 AT INFORMATION:
 man, Stephanie L.
 ON NUMBER: 33,779
 OCKET NUMBER: 52516 (P519739)
 ATION INFORMATION:
 (619)238-0999
 (619)238-0062
 2 SEQ ID NO: 53:
 ACTERISTICS:
 103 amino acids
 10 acid
 38: single
 linear
 3: protein
 3: internal

98.6%; Score 5270; DB 2; Length 1103;
 larity 97.4%; Pred. No. 0;
 Conservative 0; Mismatches 1; Indels 26; Gaps 2;

3CLLALTTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
 3CLLALTTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60
 QDLTYVEPNARQLVEIARDIEKLLSNRKSALVSLAEAKVQAAHQWREDFASN 120
 QDLTYVEPNARQLVEIARDIEKLLSNRKSALVSLAEAKVQAAHQWREDFASN 120
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 YNAKDDLDPEKNDSEPGSRQIKPVFTEDANFGRQISYQAAVHIPTDIYEGSTIVL 180
 WTSALDEVKQKREEDPSLLMQVFGSATGLARYYPASPVWDSRTPNKIDLYDVR 240
 WTSALDEVKQKREEDPSLLMQVFGSATGLARYYPASPVWDSRTPNKIDLYDVR 240
 IQGAASPKDMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 IQGAASPKDMLILVDVSGSVGLTKLRTSVSEMLETLSDDDFVNVSFNSNAQD 300
 QHLVQANVKKVLDKADAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKNIIML 360
 QHLVQANVKKVLDKADAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKNIIML 360
 QGERAQEIPNKYNKKVRVFRPSVQOHNYERGPIQWMAKNGYIYEIPSGAIR 420
 QGERAQEIPNKYNKKVRVFRPSVQOHNYERGPIQWMAKNGYIYEIPSGAIR 420
 QYLDVLRPMVLGAKAKOVMTNVYLDALGLVITGLPVFNITGPENKTNLK 480
 QYLDVLRPMVLGAKAKOVMTNVYLDALGLVITGLPVFNITGPENKTNLK 480
 ILGVMGVDSLEDIKRLTPRTFLCPNGYIYFAIDPNGYVLLHPNLQPK----- 530
 ILGVMGVDSLEDIKRLTPRTFLCPNGYIYFAIDPNGYVLLHPNLQPKIGVGPIPTIN 540
 -----NPKSQEPVTLDFLDAELNDIKVEIRNMIDGESGEKTFRTLKVSQDERYI 581
 RRPNIQPKSQEPVTLDFLDAELNDIKVEIRNMIDGESGEKTFRTLKVSQDERYI 600
 YRTYTWTPVNGTDYSALVLPTTYSFYIYKAKLEETITQASKKGKMDSETLKPDPF 641
 YRTYTWTPVNGTDYSALVLPTTYSFYIYKAKLEETITQARY-----SETLKPDPF 653
 YRTYFIAPROYCNDLKISDNNTEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTN 701
 YRTYFIAPROYCNDLKISDNNTEFLNPFNEIDRKTNNPNSCNADLINRVLLDAGFTN 713

QY 702 ELVQYNSKQKNIGVKARFVVTDGIIITRVYPKEAGENWQENPETYEDSFYKRSI
 DB 714 ELVQYNSKQKNIGVKARFVVTDGIIITRVYPKEAGENWQENPETYEDSFYKRSI
 QY 762 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWLENFTKT
 DB 774 VFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGIIKIDVNSWLENFTKT
 QY 822 CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRPFGEIDPSSLMRHLVN
 DB 834 CAGPVCDCCKRNSDVMDCVILDDGGFLLMANHDDYTNQIGRPFGEIDPSSLMRHLVN
 QY 882 FNKSYDYQSVCEPGAAPKQAGHRSAIYVPSVADIIQIGWATAAAWSILQQFLLS
 DB 894 FNKSYDYQSVCEPGAAPKQAGHRSAIYVPSVADIIQIGWATAAAWSILQQFLLS
 QY 942 LLEAVEMEDDDFTASLSKQSCITEQYFFDNDSKSFSGVLDCGNCRIFFHGEKLI
 DB 954 LLEAVEMEDDDFTASLSKQSCITEQYFFDNDSKSFSGVLDCGNCRIFFHGEKLI
 QY 1002 IFIMVESKGTCPCDTRL 1018
 DB 1014 IFIMVESKGTCPCDTRL 1030

RESULT 13
 US-08-455-543A-55
 ; Sequence 55, Application US/08455543A
 ; Patent No. 5792846
 ; GENERAL INFORMATION:
 ; APPLICANT: Harpold, Michael
 ; APPLICANT: Ellis, Steven
 ; APPLICANT: Williams, Mark
 ; APPLICANT: Feldman, Daniel
 ; APPLICANT: McCue, Ann
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/455,543A
 ; FILING DATE: May 31, 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/223,305
 ; FILING DATE: April 4, 1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/868,354
 ; FILING DATE: April 10, 1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/745,206
 ; FILING DATE: 15-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/620,250
 ; FILING DATE: 30-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/482,364
 ; FILING DATE: 20-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 04-APR-1989
 ; PRIOR APPLICATION DATA:

98.2%: Score 5250; DB 1; Length 1079;

RESULT 14

REASON: 1
 US-08-223-305C-55
 Sequence 55, Application US/08223305C
 Patent No. 5851824
 GENERAL INFORMATION:
 APPLICANT: Harpold, Michael
 APPLICANT: Ellis, Steven
 APPLICANT: Williams, Mark
 APPLICANT: Feldman, Daniel
 APPLICANT: McQue, Ann
 APPLICANT: Brenner, Robert
 TITLE OF INVENTION: HUMAN CALCIUM
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Brown, Martin, Halle
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92101-2926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/223,3
 FILING DATE: April 4, 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/868,354
 FILING DATE: April 10, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/745,2
 FILING DATE: 15-AUG-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/620,2
 FILING DATE: 30-NOV-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/482,3
 FILING DATE: 20-FEB-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/603,7
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US89
 FILING DATE: 04-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/176,8
 FILING DATE: 04-APR-1988
 ATTORNEY/AGENT INFORMATION:

dman, Stephanie L.
 ON NUMBER: 33,779
 DOCKET NUMBER: 52516 (P519739)
 ATION INFORMATION:
 (619)238-0999
 (619)238-0062
 R SEQ ID NO: 55:
 RACTERISTICS:
 079 amino acids
 no acid
 SS: single
 linear
 E: protein
 E: internal

98.2%; Score 5250; DB 2; Length 1079;

larity 98.7%; Pred. No. 0;
 Conservative 0; Mismatches 1; Indels 12; Gaps 2;

GCLLALTLTQLSLLIGSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 GCLLALTLTQLSLLIGSSSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
 YODLYTEPNARQVLEIARDDIEKLNSRKALVSLALEAEKQVAAHQWREDFASN 120
 YODLYTEPNARQVLEIARDDIEKLNSRKALVSLALEAEKQVAAHQWREDFASN 120
 YNNAKDLDPEKNDESGSQRIKPVFIEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180
 YNNAKDLDPEKNDESGSQRIKPVFIEDANFGRIQISYQHAHVHPTDIYEGSTIVL 180
 NWSALDVFVKKNREEDPSLLQWFGSATGLARYYPASPVWDSNRTKPKIDLYDVR 240
 NWSALDVFVKKNREEDPSLLQWFGSATGLARYYPASPVWDSNRTKPKIDLYDVR 240
 YIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDPVNVASNSNAQD 300
 YIOGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETSLDDDPVNVASNSNAQD 300
 FQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKIIML 360
 FQHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAFEQLLNVNVRANCKIIML 360
 GGEERAQEIFNKYNKKVVRFSVQGNHYERGPIONMACENKGYEIPISGAIR 420
 GGEERAQEIFNKYNKKVVRFSVQGNHYERGPIONMACENKGYEIPISGAIR 420
 QEYLDVLRPMVLADGKAKOVMTNVYLDLDELGLVITGTLPVENITQGFENKTNLK 480
 QEYLDVLRPMVLADGKAKOVMTNVYLDLDELGLVITGTLPVENITQGFENKTNLK 480
 ILVGMGVDSLEDIKRLTPRTLCFNGYFFAIDPNGYVLLHPNLPKPKQEPVTL 540
 ILVGMGVDSLEDIKRLTPRTLCFNGYFFAIDPNGYVLLHPNLPKPKQEPVTL 540
 DAELNDIKVIRNMIDGESGKTPRLVKSQDERYIDKGNRYVTWTPVNGTDSL 600
 DAELNDIKVIRNMIDGESGKTPRLVKSQDERYIDKGNRYVTWTPVNGTDSL 600
 LPTYSFYIKAKLETITQARKKGMKDSSETLKPDPNEESGYTFIAPRDYCNDLKI 660
 LPTYSFYIKAKLETITQARKKGMKDSSETLKPDPNEESGYTFIAPRDYCNDLKI 660
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 INTEFLNFNEFIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
 TDGGITRVYPKEAGNWNQENPETEYDSYKSKSLNDNDNVFTAPYFNKSGPGAYESGI 780
 TDGGITRVYPKEAGNWNQENPETEYDSYKSKSLNDNDNVFTAPYFNKSGPGAYESGI 780
 KAVEYIIOGKLLKPAVVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCCKRNSDY

Db 769 MVS KAVEYIIOGKLLKPAVVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCCKRNSDY
 QY 841 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNSVYAFNKS YDYQSVCEPK
 Db 829 LDDGGFLMANHDDYTNQIGRPFGEIDPSLMRHLVNSVYAFNKS YDYQSVCEPK
 QY 901 GAGHSAYVPSVADILQIGWATAAAMSILQQFLLSLTFFPRLLLEAVEMEDDDFTF
 Db 889 GAGHSAYVPSVADILQIGWATAAAMSILQQFLLSLTFFPRLLLEAVEMEDDDFTF
 QY 961 SCITEQTYFFDNDKSKSPSGVLDGCGNSRIFPHGEKLMNTNLIIFIMVESKGTCPCI
 Db 949 SCITEQTYFFDNDKSKSPSGVLDGCGNSRIFPHGEKLMNTNLIIFIMVESKGTCPCI

RESULT 15

US-08-435-675B-5
 ; Sequence 5, Application US/08435675B
 ; Patent No. 5710250
 ; GENERAL INFORMATION:
 ; APPLICANT: Ellis, Steven Bradley
 ; APPLICANT: Williams, Mark E.
 ; APPLICANT: Harpold, Michael Miller
 ; APPLICANT: Schwartz, Arnold
 ; APPLICANT: Brenner, Robert
 ; TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,675B
 ; FILING DATE: 05-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/314,083
 ; FILING DATE: 28-SEP-1994
 ; APPLICATION NUMBER: US 07/914,231
 ; FILING DATE: 13-JUL-1992
 ; APPLICATION NUMBER: US 07/603,751
 ; FILING DATE: 08-NOV-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-53193
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1106 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-08-435-675B-5

Query Match 96.1%; Score 5137.5; DB 1; Length 1106;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 986; Conservative 13; Mismatches 12; Indels 29;

:CLALTLTLTLOS--LLIGPSSBPPPSANTIKSWDKQEDLVITLAKTASGVNQLV 58
 :RPLAWITLTLQWMLILIGPSSBPPPSAVTIKSWDKQEDLVITLAKTASGVNQLV 60
 :KYQDLYTVEPNNARQLVEIARIDIKLLNSRKALVSLALBAEKVQAAHQWREDA 118
 :KYQDLYTVEPNNARQLVEIARIDEKLLNSRKALVRLALEBAEKVQAAHQWREDA 120
 :VYVYNAKODLDPKXNDSEPGSQRIKPVFIIDANFGRQISYQHAHVHIPTDIYEGSTI 178
 :VYVYNAKODLDPKXNDSEPGSQRIKPVFIIDANFRRQVSYQHAHVHIPTDIYEGSTI 180
 :LNWTSALDVEYFKKXREDPSSLWQVGSATGLARYYPASPWDVNSRTPNKLDLXD 238
 :LNWTSALDVEYFKKXREDPSSLWQVGSATGLARYYPASPWDVNSRTPNKLDLXD 240
 :WYIQGAASPXMOMLILVDVSGSVSGLTKLIRTSVSSEMLETTSDDDFVNVASFNSA 298
 :WYIQGAASPXMOMLILVDVSGSVSGLTKLIRTSVSSEMLETTSDDDFVNVASFNSA 300
 :CFQHLVQANVRNKKVLKDAVNNITAKGIITDYKKGSPFAPEQLLNVNVRANCKII 358
 :CFQHLVQANVRNKKVLKDAVNNITAKGIITDYKKGSPFAPEQLLNVNVRANCKII 360
 :DGGEERAQEIFNKYNKDKKVRVRFVSGQHNTERGPIOWMACENKGYIYEIPSIGA 418
 :DGGEERAQEIFAKYNKDKKVRVRFVSGQHNTERGPIOWMACENKGYIYEIPSIGA 420
 :TQEYLDVILGRPMVLADGKAKQVQWTVNYLDALDELGLVITGTLPVNIITQGFENKTN 478
 :TQEYLDVILGRPMVLADGKAKQVQWTVNYLDALDELGLVITGTLPVNIITQGFENKTN 480
 :LILGWMDVDSLEDIKRLTRPRTLCPNGYFYFADPNGYVLLHPNLQPK----- 530
 :LILGWMDVDSLEDIKRLTRPRTLCPNGYFYFADPNGYVLLHPNLQPKDVGPIPT 540
 :-----NPKSQBPVTLDFLDAELENDIKVEIRNRMIDGSEGEKTRTLVKSQDER 579
 :KRPNVQNPKSQBPVTLDFLDAELENDIKVEIRNRMIDGSEGEKTRTLVKSQDER 600
 :GNRTYTWTPVNGTGY-SLALVLPYTSFYIYKAKLBETITQARSKGKQWDSBTLKP 638
 :GNRTYTWTPVNGTGYSSLALVLPYTSFYIYKAKIBETITQARY-----SETLKP 653
 :ESGYTFIAPRDYCNDLKI SDNNTFLLNPNBEI DRKTPNPNNSCNADLINRVLLDAG 698
 :ESGYTFIAPREDYCSDLKPSDNNTFLLNPNBEI DRKTPNPNNSCNTDLINRVLLDAG 713
 :LVQNTYSKQKNIKGVKARFVVTDDGGITRVYPKEAGENQENPETVBSFYKRSLDN 758
 :LVQNTYSKQKNIKGVKARFVVTDDGGITRVYPKEAGENQENPETVBSFYKRSLDN 773
 :FTAPYFNKSGPAYESGIMVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSI 818
 :FTAPYFNKSGPAYESGIMVSKAVEIYIQGLLKPAVVGIKIDVNSWIENFTKTSI 833
 :AGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSIMRHLNVNIS 878
 :AGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTNOIGRFFGEIDPSIMRHLNVNIS 893
 :NKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGHWATAAASWILQOFLSLT 938
 :NKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGHWATAAASWILQOFLSLT 953
 :LEAVDEDDDDFTASISKQSCITEQTYQFFDNDKSGFSVGLDGCNCSRIFTGEKLN 998
 :LEAVDEDDDDFTASISKQSCITEQTYQFFDNDKSGFSVGLDGCNCSRIFTGEKLN 1013
 :FIMVESKGTCPCDTRL 1018
 :FIMVESKGTCPCDTRL 1033

GenCore version 5.1.6
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in search, using sw model

bruary 20, 2004, 16:51:31 ; Search time 36.5788 Seconds
(without alignments)
7181.696 Million cell updates/sec

3-10-090-827-13

346

MAAGCLLALTILFQSLIG.....TNLIPIVMSKGTCPDTRL 1018

OSUMG2

ipop 10.0 , Gapext 0.5

30525 seqs, 258052604 residues

its satisfying chosen parameters: 830525

lght: 0

lght: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

3PTREMBL 23:*

: sp_archaea.*

: sp_bacteria.*

: sp_fungi.*

: sp_human.*

: sp_invertebrate.*

: sp_mammal.*

: sp_mhc.*

: sp_organelle.*

: sp_phage.*

: sp_plant.*

: sp_rodent.*

: sp_virus.*

: sp_vertebrate.*

: sp_unclassified.*

: sp_rvirus.*

: sp_bacteriap.*

: sp_archaeap.*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
red by analysis of the total score distribution.

SUMMARIES

Entry	Length	DB	ID	Description
19.4	1110	4	Q9UIU0	Q9uiuo homo sapien
18.9	1091	6	O77773	O77773 sus scrofa
17.3	1091	11	Q9ERS3	Q9ers3 rattus norv
16.2	1084	11	Q8CFG7	Q8cfg7 rattus norv
16.0	1103	11	Q8B532	Q8b532 mus musculu
15.5	1079	11	Q8VH59	Q8vhs9 rattus norv
16.8	745	4	Q9UDQ3	Q9udq3 homo sapien
14.2	1150	4	Q9NY47	Q9ny47 homo sapien
14.0	1157	11	Q8CFG6	Q8cfg6 rattus norv
13.9	1156	11	Q9EQG2	Q9eqg2 mus musculu
13.7	1143	4	Q9NY48	Q9ny48 homo sapien
13.7	1145	4	Q9Y268	Q9y268 homo sapien
13.7	1148	11	Q8C8R8	Q8c8r8 mus musculu
13.5	1098	11	Q8CHE9	Q8che9 mus musculu
13.5	1084	11	Q920H6	Q920h6 mus musculu
13.3	1076	4	Q9UEW0	Q9uew0 homo sapien

17	2682	50.2	975	4	Q9NSA6	Q9nsa6 hom
18	1090	20.4	1085	11	Q8CFG5	Q8cfg5 ra
19	1085	20.3	1091	11	Q921L5	Q921l5 mu
20	1084	20.3	1091	4	Q8IZS8	Q8izs8 hom
21	1061.5	19.9	1120	4	Q8IZS9	Q8izs9 hom
22	1015	19.0	997	4	Q9NY16	Q9ny16 hom
23	1000.5	18.7	1218	5	Q9V6T7	Q9v6t7 drc
24	982.5	18.4	1170	5	Q8IP22	Q8ip22 drc
25	929.5	17.4	2190	5	Q9VJM0	Q9vjm0 drc
26	884	16.5	1255	5	Q9NK83	Q9nk83 drc
27	875	16.4	170	4	Q9UDL7	Q9udl7 hom
28	875	16.4	1120	5	Q9VJN7	Q9vjn7 drc
29	738.5	13.8	519	4	Q9NY18	Q9ny18 hom
30	658	12.3	317	11	Q920H5	Q920h5 mu
31	569.5	10.7	1148	5	Q17517	Q17517 cae
32	533	10.0	842	5	Q95R75	Q95r75 dro
33	526.5	9.8	394	13	Q8AVY7	Q8avy7 xe
34	514.5	9.6	104	4	Q9UD81	Q9ud81 hom
35	506	9.5	100	6	Q9GLH1	Q9glh1 bos
36	498.5	9.3	121	4	Q9UD82	Q9ud82 hom
37	482	9.0	98	4	Q9UDU5	Q9udus hom
38	465	8.7	97	4	Q9UD80	Q9ud80 hom
39	459	8.6	100	11	Q8C6Y3	Q8c6y3 mu
40	402	7.5	77	4	Q95026	Q95026 hom
41	337.5	6.3	1185	4	Q9HCJ9	Q9hcj9 hom
42	317.5	5.9	223	11	Q9R142	Q9r142 mu
43	231	4.3	978	6	Q95KE0	Q95ke0 mac
44	227	4.2	43	6	Q8HYX0	Q8hyx0 bos
45	222	4.2	1449	5	Q9V917	Q9v917 dro

ALIGNMENTS

RESULT 1						
Q9UIU0						
ID	Q9UIU0	PRELIMINARY;	PRT;	1110	AA.	
AC	Q9UIU0;					
DT	01-MAY-2000 (TREMBLrel. 13, Created)					
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT	01-MAY-2002 (TREMBLrel. 20, Last annotation update)					
DE	Dihydropyridine receptor alpha 2 subunit.					
GN	CACNA2D1.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=20005942; PubMed=10534405;					
RA	Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;					
RT	"Genomic structure and functional expression of a human alpha(2).					
RT	calcium channel subunit gene (CACNA2).";					
RL	Genomics 61:201-209(1999).					
DR	EMBL; AF083854; AAF03259.1; JOINED.					
DR	EMBL; AF083817; AAF03259.1; JOINED.					
DR	EMBL; AF083818; AAF03259.1; JOINED.					
DR	EMBL; AF083819; AAF03259.1; JOINED.					
DR	EMBL; AF083820; AAF03259.1; JOINED.					
DR	EMBL; AF083821; AAF03259.1; JOINED.					
DR	EMBL; AF083822; AAF03259.1; JOINED.					
DR	EMBL; AF083823; AAF03259.1; JOINED.					
DR	EMBL; AF083824; AAF03259.1; JOINED.					
DR	EMBL; AF083825; AAF03259.1; JOINED.					
DR	EMBL; AF083826; AAF03259.1; JOINED.					
DR	EMBL; AF083827; AAF03259.1; JOINED.					
DR	EMBL; AF083828; AAF03259.1; JOINED.					
DR	EMBL; AF083829; AAF03259.1; JOINED.					
DR	EMBL; AF083830; AAF03259.1; JOINED.					
DR	EMBL; AF083831; AAF03259.1; JOINED.					
DR	EMBL; AF083832; AAF03259.1; JOINED.					
DR	EMBL; AF083833; AAF03259.1; JOINED.					
DR	EMBL; AF083834; AAF03259.1; JOINED.					

Db	601	DKGNRTYTPVNGTDYSLALVLPYTFYIKALEETITQARSKGKGMKDS
Qy	642	EESGYTFIAPRDYCNDLKTSNDNTEFLNENEFIDRKTNNPNSCNADLINRVLL
Db	661	EESGYTFIAPRDYCNDLKTSNDNTEFLNENEFIDRKTNNPNSCNADLINRVLL
Qy	702	ELVQNTWSQKNIKGVKARFVVTDGGITRVVYPKBAGENWQENPETYEDSPFKRSI
Db	721	ELVQNTWSQKNIKGVKARFVVTDGGITRVVYPKBAGENWQENPETYEDSPFKRSI
Qy	762	VFTAPYFNKSGPGAYESGIMWSKAVEIYIOQKLLKPAVVGIKIDVNSWIENFTKI
Db	781	VFTAPYFNKSGPGAYESGIMWSKAVEIYIOQKLLKPAVVGIKIDVNSWIENFTKI
Qy	822	CAGPVCDCRNSDVMDCVLLDDGGFLMANHDDYTNQIGRPFGEIDPSLARHLV
Db	841	CAGPVCDCRNSDVMDCVLLDDGGFLMANHDDYTNQIGRPFGEIDPSLARHLV
Qy	882	FNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAWSTILOQFLL
Db	901	FNKSVDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAAWSTILOQFLL
Qy	942	LLEAVEMEDDDFTASLSQSCITETQYFFNDNSKSGSVGLDCGNCRSRIFHGKI
Db	961	LLEAVEMEDDDFTASLSQSCITETQYFFNDNSKSGSVGLDCGNCRSRIFHGKI
Qy	1002	IFIMVESKGTCPDTRL 1018
Db	1021	IFIMVESKGTCPDTRL 1037
RESULT 2		
077773		
ID	077773	PRELIMINARY; PRT; 1091 AA.
AC	077773;	
DC	01-NOV-1998 (TremBLrel. 08, Created)	
DT	01-NOV-1998 (TremBLrel. 08, Last sequence update)	
DT	01-OCT-2002 (TremBLrel. 22, Last annotation update)	
DE	Voltage-dependent calcium channel alpha-2 delta subunit precursor.	
OS	Sus scrofa (Pig).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OX	NCBI_TaxID=9823;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Brain cortex;	
RC	MEDLINE=98411353; PubMed=9738015;	
RA	Brown J.P., Gee N.S.;	
RT	"Cloning and deletion mutagenesis of the alpha2 delta calcium ch	
RT	subunit from porcine cerebral cortex. Expression of a soluble fo	
RT	the protein that retains [3H]gabapentin binding activity."	
RL	J. Biol. Chem. 273:25458-25465 (1998).	
DR	EMBL; AF077665; AAC36289.1; -	
DR	InterPro; IPR004010; Cache.	
DR	InterPro; IPR002035; VWF_A.	
DR	Pfam; PF02743; Cache; 1.	
DR	Pfam; PF00092; vwa; 1.	
DR	SMART; SM00327; VWA; 1.	
DR	DR PROSITE; PS50234; VWFA; 1.	
KW	SIGNAL.	
FT	FT SIGNAL.	1 24
FT	FT CHAIN	25 1091
FT		POTENTIAL..
FT		VOLTAGE-DEPENDENT CALCIUM CHANNEL A
FT		DELTA SUBUNIT.
FT		SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EB60E CRC64;
Qy	1	MAAGCLALTLTFLQSLIGPSEPPPSAVTIKSWVDKMOEDVLTAKTASGVN
Query Match		98.9%; Score 5288; DB 6; Length 1091;
Best Local Similarity		98.8%; Pred. No. 0;
Matches 1006; Conservative		5; Mismatches 7; Indels 0;


```

|||||NTSEFLNFEIDRKTNPSCNTDLINRIILLDAGFTNELVQNTWSQKNTKGVKAR 720
|||||TDGGITRVYPKEAGENWQENPETYEDSYKESLNDNDNVFTAPYFNKSGPGAYESGI 780
|||||TDGGITRVYPKEAGENWQENPETYEDSYKESLNDNDNVFTAPYFNKSGPGAYESGI 780
|||||KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
|||||KAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
|||||GGFLLMANHDDYTNQIGRFFGEIDPSLMHVLNIVSVYAFNKSVDYQSVCEPAGAPKQ 900
|||||GGFLLMANHDDYTNQIGRFFGEIDPSLMHVLNIVSVYAFNKSVDYQSVCEPAGAPKQ 900
|||||HRSAYVPSVADILQIGMWATAAASIIQQFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
|||||HRSAYVPSITDILQIGMWATAAASIIQQFLLSLTFFPRLLEAVEMEDDDFTASLSKQ 960
|||||TEQTYQFFNDKSFSGVLDGCGNSRIFPHGEKLANNTNLIFIMVESKGTCPDCTRL 1018
|||||TEQTYQFFNDKSFSGVLDGCGNSRIFPHGEKLANNTNLIFIMVESKGTCPDCTRL 1018

PRELIMINARY; PRT; 1084 AA.

(TREMBLrel. 23, Created)
(TREMBLrel. 23, Last sequence update)
(TREMBLrel. 23, Last annotation update)
nel alpha-2 delta-1 subunit isoform e.
gicus (Rat).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;

M N.A.
ue-Dawley; TISSUE=Heart atrium;
est P.M.;
egicus voltage-dependent calcium channel alpha-2 delta-1
orm e (CACNA2D1e) mRNA.
EB-2002) to the EMBL/GenBank/DBJ databases.
76; ARO14652.1; -.
084 AA; 122711 MW; 6269E92D8F1657FF CRC64;

66.2%; Score 5141.5; DB 11; Length 1084;
larity 95.7%; Pred. No. 2.6e-313;
Conservative 21; Mismatches 16; Indels 7; Gaps 1;

3CLLALTTLTQSLIIGPSSEPPPSAVTIKSWYDKMQEDLVTLAKTAGVNLVDI 60
3CLLALTTLTQSLIIGPSSEPPPSAVTIKSWYDKMQEDLVTLAKTAGVNLVDI 60
YQDLYTVPEPNNARQLVEIARDTEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
YQDLYTVPEPNNARQLVEIARDTEKLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
YNAKDDLPEDKNDSPSGRIKPVFTEDANFGRIQISYQAAVHIPTDIYEGSTIVL 180
YNAKDDLPEDKNDSPSGRIKPVFTEDANFGRIQISYQAAVHIPTDIYEGSTIVL 180
WNTSALDEVFKNRDEPDLWQVFGSATGLARYYPASPVNDSRTPNKNIDLYDVR 240
WNTSALDEVFKNRDEPDLWQVFGSATGLARYYPASPVNDSRTPNKNIDLYDVR 240
YIOGAAPKDMILLVDSVSGVSLGTLKLTISVSEMLETLSDDDFNVVASFNSNAQ 300
YIOGAAPKDMILLVDSVSGVSLGTLKLTISVSEMLETLSDDDFNVVASFNSNAQ 300
FOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLNLYNVSRAKCNKIIML 360
FOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAFEQLNLYNVSRAKCNKIIML 360

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QY 361 FTGGERAQEIENKYNKDKKVRVFRFSVQHNVERGPIOMMACENKGYVYEIP
DB 361 FTGGERAQEIENKYNKDKKVRVFRFSVQHNVERGPIOMMACENKGYVYEIP
QY 421 INTQEYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITQSEN
DB 421 INTQEYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITQSEN
QY 481 NQILGVMGVDVSLSDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPLNLPKPKSC
DB 481 NQILGVMGVDVSLSDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPLNLPKPKSC
QY 541 DFLDDELNDIKVEIRNKMIDGESGKTPRLVKSODERYIDKGNRTYTWTPVNC
DB 541 DFLDDELNDIKVEIRNKMIDGESGKTPRLVKSODERYIDKGNRTYTWTPVNC
QY 601 ALVLPYVSFYIIKAKLEETITQARSKKGMDSITLKPONFEESGYTFTIAPDYC
DB 601 ALVLPYVSFYIIKAKLEETITQARSKKGMDSITLKPONFEESGYTFTIAPDYC
QY 661 SDNTEFLNFEFIDRKTNPNSCNADLINRVLLDAGFTNELVQNTWSQKNTKG
DB 661 SDNTEFLNFEFIDRKTNPNSCNADLINRVLLDAGFTNELVQNTWSQKNTKG
QY 721 FVVTGCGITRVYPKEAGENWQENPETYEDSYKESLNDNDNVFTAPYFNKSGPGA
DB 721 FVVTGCGITRVYPKEAGENWQENPETYEDSYKESLNDNDNVFTAPYFNKSGPGA
QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDV
DB 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDV
QY 841 LDGSGFLLMANHDDYTNQIGRFFGEIDPSLMHVLNIVSVYAFNKSVDYQSVCEP
DB 841 LDGSGFLLMANHDDYTNQIGRFFGEIDPSLMHVLNIVSVYAFNKSVDYQSVCEP
QY 901 GAGHSAYVPSVADILQIGMWATAAASIIQQFLLSLTFFPRLLEAVEMEDDDFT
DB 901 GAGHSAYVPSITDILQIGMWATAAASIIQQFLLSLTFFPRLLEAVEMEDDDFT
QY 961 SCITETQTYQFFNDKSFSGVLDGCGNSRIFPHGEKLANNTNLIFIMVESKGTCPD
DB 961 SCITETQTYQFFNDKSFSGVLDGCGNSRIFPHGEKLANNTNLIFIMVESKGTCPD

RESULT 5
O08532 PRELIMINARY; PRT; 1103 AA.
AC O08532; O08533; O08534; O08535; O08536;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
GN CACNA2D1 OR CACNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97113514; PubMed=8955374;
RA Angelotti T. Hofmann F.;
RL FEBS Lett. 397:331-337(1996).
CC -!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R
CC EXCITATION-CONTRACTION COUPLING.
CC -!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU
CC ALPHA-1, ALPHA-2, BETA AND GAMMA.
CC -!- SUBUNIT: ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULF
CC LINKED.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

```

VE PRODUCTS: 5 ISOFORMS; 2A (SHOWN HERE), 2B, 2C, 2D AND PRODUCED BY ALTERNATIVE SPLICING.

ECIFICITY: ISOFORM 2A IS EXPRESSED IN SKELETAL MUSCLE AND IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN ISCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE ICULAR SYSTEM.

IA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM IOR FORM.

Y; TO OTHERS SPECIES ALPHA-2 SUBUNIT.

AA50139.1; -

AA50140.1; -

AA50138.1; -

AA50141.1; -

AA50142.1; -

5; Caca2d1.

004010; Cache.

002035; WVF_A.

; Cache; 1.

; vwa; 1.

; VWA; 1.

0234; WVEA; 1.

; Transmembrane; Ion transport; Voltage-gated channel; el; Glycoprotein; Phosphorylation; Signal; plicing.

1 24

25 957

58 1103

46 469

18 942

79 1098

POTENTIAL.

L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT.

L-TYPE CALCIUM CHANNEL DELTA SUBUNIT.

POTENTIAL.

POTENTIAL.

PHOSPHORYLATION (BY CAPK) (POTENTIAL).

PHOSPHORYLATION (BY CAPK) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

CC

CC

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[illegible]

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|APRDYCNDLKISDNNTTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGTNELVN 360
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|VCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPPRLLEAV 946
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|RELIMINARY; PRT; 1150 AA.
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|TREMELrel. 15, Created)
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|TREMELrel. 23, Last annotation update)
|el, alpha 2/delta subunit 2.
|
|(Human).
|tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
|heria; Primates; Catarrhini; Hominidae; Homo.
|06;
|N.A.
|d;
|C-1999) to the EMBL/GenBank/DBJ databases.
|N.A.
|d;
|S., Marais E., Lacinova L.;
|tribution and functional characterization of the calcium
|delta-2 subunit.";
|R-2000) to the EMBL/GenBank/DBJ databases.
|8; CAB86193.1;
|004010; Cache.
|002035; VWF A.
|; Cache; 1.
|; vwa; 1.
|7; VWA; 1.
|234; VWA; 1.
|50 AA; 129876 MW; 37875F687AF5E73C CRC64;
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|onservative 164; Mismatches 273; Indels 30; Gaps 13;
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|QY 127 AKDDL---DPEKNDSBPQS--RIKPVFIEDANFGRIQISYQAAVHIPTDIYEGS
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|DB 224 ELNWTLEALENVFWRNRQDFTLLMQVFGSATGVTRYTPATPW----RAPKIDLY
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|QY 242 PWYIQGAASPDKMLILVDVSGSVGLTLKLIRTSSEMLETILSDDDFVNVSFNS
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|
|QY 421 INTQBYLDVLRPMVLADGKAKQVQWNTVNYLDALBLGLVITGTLPVFNITQFENI
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|DB 518 NOLILGVWGVDSLEDIIRLTPRFTLCPNGYFPAIDPNGYVLLHNLNLPNPKSQ
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|QY 601 ALVLPYTFYIYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCI
|
|DB 638 GLVLPYTFYIYIKAKLEETITQARSKGKMDSETLKPDPNFEESGYTFIAPRDYCI
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|QY 661 SDNNTPEFLNFEFDIRKTPNNPNSCNADLINRVLLDAGTNELVQNTYWSKQK-NII
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|QY 720 RPYVTDGGITRVTPKXGAGENQENPETYEDSFYKSLDNDNYVFTAPYENK-SGRK
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|DB 758 VFAATDGGITRVTPKXGAGENQENPETYEDSFYKSLDNDNYVFTAPYENK-SGRK
|
|QY 779 ---GIMVSKAVEIYIOGKLKPAVVGIKIDVNSWIENTFTKSTEDPCAGPV---CA
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|DB 818 DTVGILVSTAVELSLGRRTLRPAVVGKLDLEAWAEKPKVLASNRTHQDQPKC-
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|QY 826 -VCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMHRLVNI SV
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|DB 877 CEMDCEVNNEDLLCVLIDDDGGFLVLSNQHNQWQDQVGRFFSEVDANLMLALYNSF
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|QY 885 SYDYQSCVCEPAAKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPI
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|
|QY 945 AVEMEDDDFTASLSKQSCITQTOYFFDNDKSGVLDGCGNCSRI FHGEXKLMNT
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|DB 997 ADPAEAEQ-SPTRESSCWKQTOYFSGVNSVNAIIDCGNCSRLFHAQRULTNT
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|DB 1056 VAEKPLCSQCE 1066
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|RESULT 9
|Q8CFG6
|ID Q8CFG6 PRELIMINARY; PRT; 1157 AA.
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[illegible]

RC	TISSUE=Heart;
RA	Klugbauer N.;
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Heart;
RA	Hobom M., Dai S., Marais E., Lacinova L.;
RT	"Neuronal distribution and functional characterization of the ca channel alpha(delta)-2 subunit.";
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AJ251367; CAB86192.1; --
DR	InterPro; IPR004010; Cache.
DR	InterPro; IPR002035; VWF A.
DR	Pfam; PF02743; Cache; 1.
DR	Pfam; PF00092; vwa; 1.
DR	SMART; SM00327; VWA; 1.
DR	PROSITE; PS0234; VWFA; 1.
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Query Match	53.7%; Score 2872.5; DB 4; Length 1143;
Best Local Similarity	54.5%; Pred. No. 3.8e-171;
Matches 562; Conservative 162; Mismatches 270; Indels 37;	

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QY	67	LYTVEPNNAOLVIAARDTEKLSNRSKALVSIALAEAKVOAAHQRWDPSFNS'
Db	104	LFEVENEFQKLVEKVAGDIESLLDRVKQLKKLADAANFOKAHRWQNTKEED
QY	127	AKDDL---DPKNDSPEGSQ--RIKPVFIEDANFGKQISYQHAAVHIPTDIYEGS'
Db	164	AKADAELEDPESEDVERGSKASTLRLDLFIEDPNFKKNVSYAAVQIPTDIYKGS'
QY	182	EINWTISALDEYFKONREDPSLLWQVFGSATGLARYYPASPWVDSNRSPTNKIDLY
Db	224	EINWTEALENFENRRQDPTLLWQVFGSATGVTRYYPATPW---RAPKKIDLYI
QY	242	PWYIQGAASPDMILLVDVSGSVSLTKLIRTSVSEMLETLSDDDDFNVVASFNSEI
Db	280	PWYIQGAASSPDWIIIVDVSGSVSLTKMKITSVCCEMLDTLSDDDDYNVASFNEI
QY	302	SCFQHLVQANYRNKVKILKDANNITAKGITDYKGKGFSAFEOLLNLYNVRANCNKJ
Db	340	SCFTHLVQANYRNKVPKEAVQGMAVGTTGYKAGFEYAFDLQNSNITRANCNK
QY	362	TDGGEERAQELFNKYN-KDKKRVFRFSVGOINYRGPIQMWACNKGGYYEIPSI
Db	400	TDGGEDRVQDYVFEEKYNPNRTVRVTFSTVGOHNVDVTPLQMWACANKGYYPEISI
QY	421	INTQEYLVDLGRPMVLADGKAKOVQNTNYLDAELGLVITGTLPVENITCOFENP
Db	460	INTQEYLDVLRPMVLGKREKQVQNTNVEDALGLGLVVTGTLPVFMLTQ--DGE
QY	481	NQLILGMVGVDVLEIDKRLTPFTLCPNGYYFAIDPNGYVLLHPNLQPKNPKSOE
Db	518	NQLILGMGIDVALNDIKLTPNYTLGANGYVFDLNGYVLLHPNLXPQTTFIRE
QY	541	DFLDAELENDIKVEIINKMIDGESGKETRTLIVSQDERYIDKGNRYTWTPVNGT
Db	578	DFLDAELENDENKEIEIRSMIDGMKHQKITLVKSLDSERYIDEVTRNYTVWPIRST
QY	601	ALVLPTYSFYVIKALEETITQARSKGWMKDSLETLPDNFEESGYTFIAPROYCN
Db	638	GLVLPPYSTYLQANLSDLIQ-----VKYFEFLPSSFESGHVFIAPREYCK
QY	661	SDNNTEFLMFNBFIDRKTPNPNPCNADLNKRLVDAGTTELNYQNYSKQ-NIK
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QY	720	RFVVTDGGITRVYKBAENWQENPETYEDSFYKRSLDNDNIYFATPYFNK-SGPQ

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 3KPLCSQCE 1059

PRELIMINARY; PRT; 1145 AA.

(TREMBlrel. 12, Created)
 (TREMBlrel. 12, Last sequence update)
 (TREMBlrel. 23, Last annotation update)
 protein KIAA0558.

(Human).
 Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Theria; Primates; Catarrhini; Hominiidae; Homo.
 1606;
 M N.A.

Latif F., Latif F., Ding J., Lin J., Mathis M.,
 new candidate human tumor suppressor gene located in the
 cell lung cancer homozygous deletion region homologous to
 ted calcium channel alpha 2/ delta subunit.";
 CT-1998) to the EMBL/GenBank/DBJ databases.

M N.A.
 atif F., Duh F.-M., Adreazoli-Angeloni D., Kashuba V.,
 Johnson B., Lerman M.I.;
 2 delta subunit of the L-type voltage gated calcium
 des in the lung cancer critical region on 3p21.3.";
 AN-1998) to the EMBL/GenBank/DBJ databases.

M N.A.
 0545; PubMed=9628581;
 shikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 of the coding sequences of unidentified human genes. IX.
 sequences of 100 new cDNA clones from brain which can
 ge proteins in vitro.";
 1-39(1998).
 09; AAC70914.1; -;
 92; AAB96913.1; -;
 30; BAA25484.1; -;
 1400; CACNA2D2.
 R004010; Cache.
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 3; Cache; 1.
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SQ SEQUENCE 1145 AA; 129268 MW; 9ADA4807C70971B CRC64;
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7 LALTLTLFQSLIGLSSSEPPFSAVTIKSWDKQEDLVTLAKTASGVNQLVDI
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 224 ELNWTALENVFENRRQDPTLLWQVFGSATGVTRYYPATPW----RAPKKIDL
 242 PWYIQGAASPDKMLILVDVSGVSGLTCLKIRTSVSEMLETSDDDDFNVASFNI
 280 PWYIQGASSPKDMVIIVDVSGVSGLTCLKMKTSCVCEMLDLSDDDYNVASFNI
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 481 NQLILGVMGVDVSLIEDIKRLTPRTLPCNGYFAIDPNGVYLLHPNLQPNPKSC
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Db	692	NASDNNTEFLKNFELMEKVPDPKQCNFNLLNHLILDITGITQQLVERVVRDQDL	
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Qy	777	ES-----GIMVSKAVEIYIQGLLKPAVVYGIKIDVNSIENF-----TKTSIRDP--	
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Qy	826	----VCDCKRSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPDSLMRHLVN	
Db	871	SHSCMDCVANNEDILLCVLIDGGFLVLSQNQHWDQVGRFFSEVDANLMLALYN	
Qy	882	FNKSYDYOSVCEPGAAPKQGAHRESAVVPSVADILQIGHWATAAASLILQQFLLS:	
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Qy	942	LLEAVEMEDDDFTASLKQSCITEQTQTFPDNDKSPSGVLDCGNCRSIFRFGKLI	
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Dt	01-WAR-2003 (TReMBLrel. 23, Last sequence update)		
Dt	01-WAR-2003 (TReMBLrel. 23, Last annotation update)		
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De	MKIAA0558.		
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Rn	[1]		
Rn	SEQUENCE FROM N.A.		
Rc	TISSUE=Brain;		
Ra	Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,		
Ra	Ohara O., Koga H.;		
Rt	"Prediction of the coding sequences of mouse homologues of KIAA 9		
Rt	1. The complete nucleotide sequences of 100 mouse KIAA-homologous		
Rt	cDNAs identified by screening of terminal sequences of cDNA clone		
Rt	randomly sampled from size-fractionated libraries."		
Rl	Submitted (OCT-2002) to the EMBL/GenBank/DBAJ databases.		
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Ft	NON TER		
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February 20, 2004, 16:58:06
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GenCore version 5.1.6
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46

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OSUM62

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1455 seqs, 209382283 residues

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aximum Match 100%

isting first 45 summaries

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r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

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0.0	0.0	1036	15	US-10-090-827-14	Sequence 14, Appl
0.0	0.0	1063	15	US-10-090-827-15	Sequence 15, Appl
0.0	0.0	1091	9	US-09-875-423-4	Sequence 4, Appl
0.0	0.0	1091	12	US-10-162-102-17	Sequence 17, Appl
0.0	0.0	1091	15	US-10-162-012-17	Sequence 17, Appl
0.0	0.0	1091	15	US-10-090-827-16	Sequence 16, Appl
9.3	9.3	1086	12	US-10-375-253-49	Sequence 49, Appl
8.9	8.9	1084	12	US-10-375-253-53	Sequence 53, Appl
8.9	8.9	1018	15	US-10-090-827-6	Sequence 6, Appl
8.9	8.9	1036	15	US-10-090-827-7	Sequence 7, Appl
8.9	8.9	1063	15	US-10-090-827-8	Sequence 8, Appl
8.9	8.9	1069	15	US-10-090-827-9	Sequence 9, Appl
8.9	8.9	1091	15	US-10-090-827-5	Sequence 5, Appl
8.6	8.6	1103	12	US-10-375-253-47	Sequence 47, Appl

16	5250	98.2	1079	12	US-10-375-253-51	Sequence
17	5219	97.6	1091	12	US-10-375-253-20	Sequence
18	2872.5	53.7	1145	15	US-10-116-949-2	Sequence
19	2872.5	53.7	1145	15	US-10-116-949-4	Sequence
20	2851.5	53.3	1076	15	US-10-116-949-6	Sequence
21	1085	20.3	1091	9	US-09-875-423-5	Sequence
22	1085	20.3	1091	12	US-10-162-102-18	Sequence
23	1085	20.3	1091	15	US-10-162-012-18	Sequence
24	1084	20.3	1091	9	US-09-875-423-2	Sequence
25	1084	20.3	1091	12	US-10-162-102-15	Sequence
26	1084	20.3	1091	15	US-10-162-012-15	Sequence
27	1049.5	19.6	1090	12	US-09-833-222A-10	Sequence
28	1049.5	19.6	1090	12	US-10-119-624-10	Sequence
29	343.5	6.4	1223	11	US-09-964-256A-2	Sequence
30	343.5	6.4	1223	12	US-10-146-733-44	Sequence
31	317.5	5.9	223	14	US-10-005-168-2	Sequence
32	286	5.3	75	12	US-10-264-049-3575	Sequence
33	272	5.1	51	9	US-09-864-761-44281	Sequence
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35	190	3.6	35	9	US-09-864-761-38318	Sequence
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38	182	3.4	885	9	US-09-828-423-5	Sequence
39	169	3.2	497	12	US-10-334-143-23	Sequence
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42	159.5	3.0	173	11	US-09-992-600A-100	Sequence
43	159.5	3.0	173	11	US-09-924-340-100	Sequence
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45	159.5	3.0	173	12	US-10-154-678-100	Sequence

ALIGNMENTS

RESULT 1

US-10-090-827-13
; Sequence 13, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-13

Query Match 100.0%; Score 5346; DB 15; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; G

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Db	1	MAAGCLLALTLTLFQSLIGPSSEPPPSAVTTKSWYDKMOEDLVTLAKTASGVNQ
Qy	61	YEKQDLYTTPNNARQLVEIARDIEKLKSNRSKALVSLALEAEKVQAAHQWRED
Db	61	YEKQDLYTTPNNARQLVEIARDIEKLKSNRSKALVSLALEAEKVQAAHQWRED
Qy	121	EWVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIEYGS
Db	121	EWVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIEYGS
Qy	181	NELNWTALDEVFKNREEDPSLLWQVFGSATGLRYTPASPDWNSRTPNKIDLY

WTSALDEVFKKREEDPSLLWQVFGSATGLARYYPASPWVDNSRTPNKIDYDVR 240

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IQGAASPKOMLILVDVSGSVGLTLKLRITSVSEMLETSLDDDFVNVASFNSAQD 300

QHLVOANVRNKKVLKDAVNNITAKGITYDYKKGPSFAFOLLNYSRANCNKIML 360

QHLVOANVRNKKVLKDAVNNITAKGITYDYKKGPSFAFOLLNYSRANCNKIML 360

SGEERAQELFNKYNKO KKVRFPRFSVQGHNYERGPIONMA CENKGYIYRIPSGAIR 420

SGEERAQELFNKYNKO KKVRFPRFSVQGHNYERGPIONMA CENKGYIYRIPSGAIR 420

JYLVLGRPMVLADGKAKQVQWNVYLDALGLVITGLPVNITGQFENKTNLK 480

JYLVLGRPMVLADGKAKQVQWNVYLDALGLVITGLPVNITGQFENKTNLK 480

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LGVMGVDSVLESDIKRLTPRFTLCPNGYYFAIDPNGYVLLHPLNKPKNKSPVTL 540

JAELENDIKVEIRNKMIDGESSEKTFRTLKVSQDERVIDKGNRTYTWTPVNGTDYSL 600

JAELENDIKVEIRNKMIDGESSEKTFRTLKVSQDERVIDKGNRTYTWTPVNGTDYSL 600

PTYSPFYIYKAKLETTIOARSKKGOMKOSETLKPDNFEEGYTFAPRDYCNDLKI 660

PTYSPFYIYKAKLETTIOARSKKGOMKOSETLKPDNFEEGYTFAPRDYCNDLKI 660

TFEFLNFEFIDRKTNNPSCNADLINRVLDDAGFTNELVQNVYSKQXNIKGVXAR 720

TFEFLNFEFIDRKTNNPSCNADLINRVLDDAGFTNELVQNVYSKQXNIKGVXAR 720

TGGITRVYVPKEAGENQENPETYEDSFYKXSLDNNDNYVTPAFYFNKSGPGAYESGI 780

TGGITRVYVPKEAGENQENPETYEDSFYKXSLDNNDNYVTPAFYFNKSGPGAYESGI 780

GAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840

GAVEIYIQGKLLKPAVGIKIDVNSWIENFTKTSIRDPACAGPVCDCRNSDVMDCVI 840

IGFLIMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYOSVCEPGAAPKO 900

IGFLIMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVTAFNKSVDYOSVCEPGAAPKO 900

IRSAVYPSVADILQIGMWATAAASILQOFLLSLTFPRLLAEVEMEDDDPTASLSQ 960

IRSAVYPSVADILQIGMWATAAASILQOFLLSLTFPRLLAEVEMEDDDPTASLSQ 960

TQOTQYFFNDNDSKSPSGVLDCGNSRIPHGKLMNTNLIFIMVESKGTGCPDTRL 1018

TQOTQYFFNDNDSKSPSGVLDCGNSRIPHGKLMNTNLIFIMVESKGTGCPDTRL 1018

Publication US/10090827
US20030073132A1

CTION:

er-Lambert
 ION: Method for the screening of alpha 2 delta-1 subunit
 ION: binding ligands

: 179

NOTES
10/11/55

ATION NUMBER: US/10/090,827

DATE: 2002-03-06

DATE: 2002-03-00
ION NUMBER: 115/00/207 E40

ION NUMBER: US/09/397,549

ATE: 1999-09-16

LC 300 01
REF: 100 00 01

ID NOS: 21

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;	ORGANISM: Homo sapiens	
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QY	61 YEKYQDLTYTVEPNNAQOLVEIAARDTEKLLSNRSKALVSLAEAKVKQAAHQWREI	
Db	61 YEKYQDLTYTVEPNNAQOLVEIAARDTEKLLSNRSKALVSLAEAKVKQAAHQWREI	
QY	121 EVVYNNAKDLDPEKNDSEPGSORIKPVFIEDANFGROI SYOAAAHVHPDIIYEG	
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QY	181 NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYTPASPWDNSRTPNKIDL	
Db	181 NELNWTLSALDEVFKONREEDPSLLMQVFGSATGLARYTPASPWDNSRTPNKIDL	
QY	241 RPWTYIQGAASPDKMLILVDVSGSVSLTKLIRTSVSEMLETSLSDDDPVNVASFNI	
Db	241 RPWTYIQGAASPDKMLILVDVSGSVSLTKLIRTSVSEMLETSLSDDDPVNVASFNI	
QY	301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSPAEQLILNYSRANCNI	
Db	301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSPAEQLILNYSRANCNI	
QY	361 FTDGGEERAQIEFNKYNKDKKVVFRFSGVQHNYERGP IQMMAACENKGYVYEIIPS	
Db	361 FTDGGEERAQIEFNKYNKDKKVVFRFSGVQHNYERGP IQMMAACENKGYVYEIIPS	
QY	421 INTQBYLDVLGRPMVLAGDKAKOVQNTNYLDALELGLVITGTLPVFMITQGFENI	
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QY	481 NQLILGWGVDDVSLDIKRLTPFTLCPNGYTPADPNQYVLLHNLQPKPKSQI	
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QY	541 DFLDAELNDIKVEIRNKMIDGESGKTRTLVKQODERYIDKGNRTYTWTPVNG	
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QY	601 ALVLPYTSFYIYIKALBETITQARSKKGWKOSETLKPDPNPEESGYTPIARDYCI	
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QY	661 SDNTEFLANFSEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIKI	
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QY	721 FVWTDGGITRYVPKEAGENQWENPETYEDSPYKRSLDNDNYYFTAPYFNKSGPGA	
Db	721 FVWTDGGITRYVPKEAGENQWENPETYEDSPYKRSLDNDNYYFTAPYFNKSGPGA	
QY	781 MYSKAVEIYIQGLLKPAVVGIIKDYNSEIENFTKTSIRDPACAGPVCDCCKNSDV	
Db	781 MYSKAVEIYIQGLLKPAVVGIIKDYNSEIENFTKTSIRDPACAGPVCDCCKNSDV	
QY	841 LDDGGFLMANHDDYTNQIGRFPGEDPSLMRHLNVNISVYAFNKS YDYQSCEPGI	
Db	841 LDDGGFLMANHDDYTNQIGRFPGEDPSLMRHLNVNISVYAFNKS YDYQSCEPGI	
QY	901 GAGHRSAYTFSVADIILOIGHWATAAAS ILQQFLLSLTFPRLLLEAVENDDDDFTAL	
Db	901 GAGHRSAYTFSVADIILOIGHWATAAAS ILQQFLLSLTFPRLLLEAVENDDDDFTAL	
QY	961 SCITEQTQYTFDNDSKSFSGLVDCGNCRSIRI FHGEKLMNTNLIFIMVESKGTCPD	

QY 961 SCITEQTYFFDNDKSFSGVDCGNCSTRIFHGEKLMNTNLI FIMVESKGTCPD:

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EQTYFFDNDKSPGVLDCGNCRIHFHGEKLMNTNLFIMVESKGTCPDTRL 1018
|||||
lication US/10090827
US20030073132A1
TON:
er-Lambert
TON: Method for the screening of alpha 2 delta-1 subunit
TON: binding ligands
179
TION NUMBER: US/10/090,827
DATE: 2002-03-06
ON NUMBER: US/09/397,549
TE: 1999-09-16
D NOS: 21
Lin Ver. 2.1
, sapiens
arity 100.0%; Score 5346; DB 15; Length 1063;
onservative 0; Mismatches 0; Indels 0; Gaps 0;
CLLALTTLTFLQSLIGSSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
CLLALTTLTFLQSLIGSSSEPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLVDI 60
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QDLTYVPNNARQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRDFA 120
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YNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHIPTDIYEST 180
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WTSALDEVKKNREDEPSSLQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
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IQGAASPKMDLILVDVSGSVSLGLTKLIRTSVSEMLETSLDSDDFVNVASFNS 300
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QHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAPEQLLNYNVSRANCNKI 360
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GEERAQELFNKYNKKVRFVSVGHYBERGPIQWMACENKGYIYEIPSIGAIR 420
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EYLDVLRGPMVLADKAKQVQWNTVYLDALSLGLVITGTLVPFNITGQFENK 480
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AELENDIKVEIRNKMIDGESKFTRLVKSQDERYIDKGNRTYTWPNVGTDSL 600
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QY 661 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIKI
Db 661 SDNTEFLLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIKI
QY 721 FVVDGGITRVYPKEAGENWQENPETYEDSFYKSLDNDNVFTAPYFNKSGPGA'
Db 721 FVVDGGITRVYPKEAGENWQENPETYEDSFYKSLDNDNVFTAPYFNKSGPGA'
QY 781 MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCCKNSDVA
Db 781 MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCCKNSDVA
QY 841 LDDGFFLLMANHDDYTNOIGRFFGRIIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGI
Db 841 LDDGFFLLMANHDDYTNOIGRFFGRIIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGI
QY 901 GAGHRSAYVPSVADILQIGMWATAAANSILOQFLSLTFPRLLRAVEMEDDDFTAI
Db 901 GAGHRSAYVPSVADILQIGMWATAAANSILOQFLSLTFPRLLRAVEMEDDDFTAI
QY 961 SCITEQTQYFFDNDKSPGVLDCGNCRIHFHGEKLMNTNLFIMVESKGTCPCDI
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RESULT 4
US-09-875-423-4
; Sequence 4, Application US/09875423
; Patent No. US20020081657A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL
; FILE REFERENCE: 10448-059001
; CURRENT APPLICATION NUMBER: US/09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,257
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-423-4

Query Match 100.0%; Score 5346; DB 9; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; C

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QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAPEQLLNYNVSRANCNK
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAPEQLLNYNVSRANCNK
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Publication US/10162102
US2003023336A1
Title: is, Rory A.J.
Inventor: los-Santiago, Immaculada
Applicant: Wei
Title: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
Publication Number: US/10/162,102
Filing Date: 2003-04-04
Priority Date: 2003-04-04
Priority Number: US 60/209,845
Priority Date: 2000-06-06
Priority Number: US 09/875,321
Priority Date: 2001-06-06
Priority Number: PCT/US01/18340
Priority Date: 2001-06-06
Priority Number: US 60/209,257
Priority Date: 2000-06-05
Priority Number: US 09/875,423
Priority Date: 2001-06-05
Priority Number: PCT/US01/18398
Priority Date: 2001-06-05
Priority Number: US 60/209,238
Priority Date: 2000-06-05
Priority Number: US 09/875,363

Prior Filing Date: 2001-06-05
Prior Application Number: PCT/US01/18247
Prior Filing Date: 2001-06-05
Prior Application Number: US 60/227,068
Prior Filing Date: 2000-08-22
Remaining Prior Application data removed - See File Wrapper or PAL
Number of Seq ID NOS: 48
Software: FastSeq for Windows Version 4.0
Seq ID NO 17
Length: 1091
Type: PRT
Organism: Homo sapiens
US-10-162-102-17
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;
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07:56:50 2004

us-10-090-827-13.rapb

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lication US/10162012
US20030051660A1
TON:
is, Rory A.J.
os-Santiago, Inmaculada
Wei
TON: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
10448-190001

ATION NUMBER: US/10162,012
DATE: 2002-06-04
ON NUMBER: US 60/209,845
TE: 2000-06-06
ON NUMBER: US 09/875,321
TE: 2001-06-06
ON NUMBER: PCT/US01/18340
TE: 2001-06-06
ON NUMBER: US 60/209,257
TE: 2000-06-05
ON NUMBER: US 09/875,423
TE: 2001-06-05
ON NUMBER: PCT/US01/18398
TE: 2001-06-05
ON NUMBER: US 60/209,238
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ON NUMBER: US 09/875,363
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TE: 2001-06-05
ON NUMBER: US 60/227,068
TE: 2000-08-22
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ON NUMBER: PCT/US01/25475
TE: 2001-08-15
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TE: 2001-08-21
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TE: 2001-08-21
ON NUMBER: US 60/279,281
TE: 2001-03-28
ON NUMBER: US 10/109,029
TE: 2002-03-28
ON NUMBER: PCT/US02/09728
TE: 2002-03-28
ON NUMBER: US 60/290,288
TE: 2001-05-11
ON NUMBER: US (not assigned)
TE: 2002-05-13
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REQ for Windows Version 4.0

sapiens

Query Match 100.0%; Score 5346; DB 15; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0;
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DB 841 LDDGFLLMANHDDYTNOIGRFFGIDPSLMRHLNVSIAFNKSYDQSVCEPGA
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publication US/10090827
 US20030073132A1
 TION:
 ner-Lambert
 TION: Method for the screening of alpha 2 delta-1 subunit
 TION: binding ligands
 : 179
 ATION NUMBER: US/10/090,827
 DATE: 2002-03-06
 TION NUMBER: US/09/397,549
 DATE: 1999-09-16
 ID NOS: 21
 ntIn Ver. 2.1

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 100.0%; Score 5346; DB 15; Length 1091;
 larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	781	MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEFTKTSIRDCACGPVCDCKRNSDI	
Qy	841	LDDGGFLLMANHDDYTNQIGRFFGIDSLSMRHLVNIISVYAFNKSXYDYSQVCEPC	
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RESULT 8			
US-10-375-253-49			
; Sequence 49, Application US/10375253			
; Publication No. US20040018510A1			
; GENERAL INFORMATION:			
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES			
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND			
; TITLE OF INVENTION: METHODS			
; FILE REFERENCE: SD9813DA			
; CURRENT APPLICATION NUMBER: US/10/375,253			
; CURRENT FILING DATE: 2003-02-27			
; PRIOR APPLICATION NUMBER: 08/450,273			
; PRIOR FILING DATE: 1995-05-25			
; PRIOR APPLICATION NUMBER: 08/404,354			
; PRIOR FILING DATE: 1995-02-15			
; PRIOR APPLICATION NUMBER: 07/914,231			
; PRIOR FILING DATE: 1992-07-13			
; PRIOR APPLICATION NUMBER: 08/314,083			
; PRIOR FILING DATE: 1994-09-28			
; PRIOR APPLICATION NUMBER: 07/914,231			
; PRIOR FILING DATE: 1992-07-13			
; PRIOR APPLICATION NUMBER: 07/603,751			
; PRIOR FILING DATE: 1990-11-09			
; PRIOR APPLICATION NUMBER: 08/290,012			
; PRIOR FILING DATE: 1994-08-11			
; PRIOR APPLICATION NUMBER: 08/149,097			
; PRIOR FILING DATE: 1993-11-05			
; PRIOR APPLICATION NUMBER: 08/105,536			
; PRIOR FILING DATE: 1993-08-11			
; PRIOR APPLICATION NUMBER: 08/149,097			
; PRIOR FILING DATE: 1993-11-05			
; Remaining Prior Application data removed - See File Wrapper or PAL			
; NUMBER OF SEQ ID NOS: 65			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 49			
; LENGTH: 1086			
; TYPE: PRT			
; ORGANISM: Human			
US-10-375-253-49			
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Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1013; Conservative 0; Mismatches 0; Indels 5;			
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21 QY 1YDGGITRVYKKEAGENQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
22 QY 1YAVEIYIQGKLLKPAVVGKIDVNSMIENFTKTSIRDPGAGPVCDCKRNSDVMDCVI 840
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1 PRIOR APPLICATION NUMBER: 08/450,273
2 PRIOR FILING DATE: 1995-05-25
3 PRIOR APPLICATION NUMBER: 08/404,354
4 PRIOR FILING DATE: 1995-02-15
5 PRIOR APPLICATION NUMBER: 07/914,231
6 PRIOR FILING DATE: 1992-07-13
7 PRIOR APPLICATION NUMBER: 08/314,083
8 PRIOR FILING DATE: 1994-09-28
9 PRIOR APPLICATION NUMBER: 07/914,231
10 PRIOR FILING DATE: 1992-07-13
11 PRIOR APPLICATION NUMBER: 07/603,751
12 PRIOR FILING DATE: 1990-11-09
13 PRIOR APPLICATION NUMBER: 08/290,012
14 PRIOR FILING DATE: 1994-08-11
15 PRIOR APPLICATION NUMBER: 08/149,097
16 PRIOR FILING DATE: 1993-11-05
17 PRIOR APPLICATION NUMBER: 08/105,536
18 PRIOR FILING DATE: 1993-08-11
19 PRIOR APPLICATION NUMBER: 08/149,097
20 PRIOR FILING DATE: 1993-11-05
21 Remaining prior Application data removed - See File Wrapper or PAL
22 NUMBER OF SEQ ID NOS: 65
23 SOFTWARE: PastSeq for Windows Version 4.0
24 SEQ ID NO 53
25 LENGTH: 1084
26 TYPE: PRT
27 ORGANISM: Human
28 US-10-375-253-53

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Query Match 98.9%; Score 5289.5; DB 12; Length 1084;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 7;

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DB 61 YEKYQDLYTVEPNNAQVLAARDIEKLLSNRSKALVSLALEAEKVQAAHQWRE
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DB 121 EYVYTNKADDDLPKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEG
QY 181 NELNWTLSALDEVEFKKREEDPSLLQVFGSATGLARYYPASPWVDSRTPNKIDL
DB 181 NELNWTLSALDEVEFKKREEDPSLLQVFGSATGLARYYPASPWVDSRTPNKIDL
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Publication US/10375253

US20040018510A1

TION:

SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

TION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

TION: METHODS

SD9813DA

ATION NUMBER: US/10375,253

DATE: 2003-02-27

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lication US/10090827

US20030073132A1

TION:

ner-Lambert

TION: Method for the screening of alpha 2 delta-1 subunit

TION: binding ligands

: 179

ATION NUMBER: US/10/090,827

DATE: 2002-03-06

ION NUMBER: US/09/397,549

ATE: 1999-09-16

ID NOS: 21

ntIn Ver. 2.1

scrofa

larity 98.9%; Score 5288; DB 15; Length 1018;

Conservative 5; Mismatches 7; Indels 0; Gaps 0;

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RESULT 11

US-10-090-827-7

; Sequence 7, Application US/10090827

; Publication No. US20030073132A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 su

; FILE REFERENCE: 179

; CURRENT APPLICATION NUMBER: US/10/090,827

; PRIOR FILING DATE: 2002-03-06

; PRIOR APPLICATION NUMBER: US/09/397,549

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 1036

; TYPE: PRT

; ORGANISM: Sus scrofa

; US-10-090-827-7

Query Match 98.9%; Score 5288; DB 15; Length 1036;

Best Local Similarity 98.8%; Pred. No. 0;

conservative	5;	Mismatches	7;	Indels	0;	Gaps	0;
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GFLLMANHDDYTNQIGRFEGEIDPSLWRHLVNI SVYAFNKSVDYQSVCEPAGAPKQ	900						
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; Sequence 8, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 su
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-8

Query Match          98.9%; Score 5288; DB 15; Length 1063;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0;

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Db 61 YEKYQDLYTVENNAQQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHOREI
Qy 121 EVVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGFSQISYQAAAVHIPTDIYEG
Db 121 EVVYNNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGFSQISYQAAAVHIPTDIYEG
Qy 181 NELNWTLSALDVEYFKKQREDEPSLLIQVFGSATGLARYYPASPWVDNSRTPNKIDL
Db 181 NELNWTLSALDVEYFKKQREDEPSLLIQVFGSATGLARYYPASPWVDNSRTPNKIDL
Qy 241 RPYITQGAASPMDMLLVDVSGSVGLTLKLRITSVSEMETLSDDDFVNVASFNI
Db 241 RPYITQGAASPMDMLLVDVSGSVGLTLKLRITSVSEMETLSDDDFVNVASFNI
Qy 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQLLNLYNVSRAVNCI
Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSFAFEQLLNLYNVSRAVNCI
Qy 361 FTDGGEERAQEIENKYNKDKQVFRFSVGOHNYTERGPIOMMAECENKGYTTEIPS
Db 361 FTDGGEERAQEIENKYNKDKQVFRFTFSVGOHNYDRGPIOMMAECENKGYTTEIPS
Qy 421 INTQBYLDVLGRPMVLADKAKQVQWNTNVLVDALGLGVITGTPVFNITGQFENI
Db 421 INTQBYLDVLGRPMVLADKAKQVQWNTNVLVDALGLGVITGTPVFNITGQFENI
Qy 481 NQLILGVMGVDSLEIDIKRLTPRTLCPNGYFAIDPNGVYLHLPNLQPKNPKSQI
Db 481 NQLILGVMGVDSLEIDIKRLTPRTLCPNGYFAIDPNGVYLHLPNLQPKNPKSQI
Qy 541 DFLDAELENDDKVEIRNKMIDGSGEKTFTTLVKSQDERYIDKGNRTYTTWTPVNGI
Db 541 DFLDAELENDDKVEIRNKMIDGSGEKTFTTLVKSQDERYIDKGNRTYTTWTPVNGI
Qy 601 ALVLPYTFYIYKAKLEETITQASRKGKMKDSETLKPNFBESGYTFIAPRDYCN
Db 601 ALVLPYTFYIYKAKLEETITQASRKGKMKDSETLKPNFBESGYTFIAPRDYCN
Qy 661 SDNNTEFLNFNFEFIDRKTNNPSCNADLNIRVLLDAGFTNELVQYNYSKQNKIK
Db 661 SDNNTEFLNFNFEFIDRKTNNPSCNADLNIRVLLDAGFTNELVQYNYSKQNKIK
Qy 721 FVVTDDGITRVYVKEAGNMQENPETTIEDSFYKRSLDNQNYYFTAPYFNKSGFGAI

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 KAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSDVMDCVI 840
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 XGFLMANHDDYTNOIGRFFGEIDPSLRHLVNIISVYAFNKSVDYQSVCEPAAPKQ 900
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 Publication US/10090827
 US20030073132A1
 TION:
 ner-Lambert
 TION: Method for the screening of alpha 2 delta-1 subunit
 TION: binding ligands
 : 179
 ATION NUMBER: US/10/090,827
 : DATE: 2002-03-06
 TON NUMBER: US/09/397,549
 ATE: 1999-09-16
 ID NOS: 21
 ntIn Ver. 2.1
 : scrofa
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 larity 98.8%; Pred. No. 0;
 Conservative 5; Mismatches 7; Indels 0; Gaps 0;
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 GCLALTLTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
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 YODLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFASN 120
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 YNNAKDDLPEKNDSEPGSQRIKPVFIEDANFGRIQISYQHAHVHPDIIYEGSTIVL 180
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 QEYLDVLRPMVLADGRKAKQVQWNTVNYLDALDELGLVITGTLPVFNITQFENKTLK 480

Db 421 INTQEVLDVLRPMVLADGRKAKQVQWNTVNYLDALDELGLVITGTLPVFNITQFENI
 QY 481 NQILTLGVMGVDVSLIEDIKRLTPRTLCPNGYVFAIDPNGYVZLHPNLQPKPKS
 Db 481 NQILTLGVMGVDVSLIEDIKRLTPRTLCPNGYVFAIDPNGYVZLHPNLQPKPKS
 QY 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERVIDKGNRTYTTWTPVK
 Db 541 DFLDAELENDIKVEIRNKMIDGESGEKTFRTLKVSQDERVIDKGNRTYTTWTPVK
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 QY 661 SDNTEFLNFNFIDRTKTPNNSCNADLNRVLLDAGFTNELLVONTWSKQKNI
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 QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNVFTAPYFNKSGPG
 Db 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSNDNDNVFTAPYFNKSGPG
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 Db 781 MVSKAIVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGVCDCKRNSD
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 Db 841 LDGGLFLMANHDDYTNOIGRFFGEIDPSLRHLVNIISVYAFNKSVDYQSVCEPK
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 RESULT 14
 US-10-090-827-5
 ; Sequence 5, Application US/10090827
 ; Publication No. US20030073132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 su
 ; FILE REFERENCE: 179
 ; CURRENT APPLICATION NUMBER: US/10/090,827
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US/09/397,549
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1091
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-10-090-827-5
 Query Match 98.9%; Score 5288; DB 15; Length 1091;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 100%; Conservative 5; Mismatches 7; Indels 0;

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 Db 1 MAAGCCLALTLTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN
 QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHQRRE
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07:56:50 2004

us-10-090-827-13.rapb

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|AVESKGTCPDTRL 1030

February 20, 2004, 17:12:01
i secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
in search, using sw model
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gth: 2000000000
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aximum Match 100%
isting first 45 summaries

TR 76: *
pir1: *
pir2: *
pir3: *
pir4: *
the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

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0.0	1091	2	JH0565		calcium channel al
6.2	1091	2	A44147		calcium channel pr
6.0	1106	1	CHBA2		calcium channel pr
0.3	1091	2	T30256		calcium channel al
1.4	734	2	S44617		C50C3.11 protein -
0.7	1148	2	T18770		probable calcium c
3.7	1450	2	C86880		hypothetical prote
3.6	886	2	S54355		inter-alpha-trypsi
3.5	885	2	S30350		inter-alpha-trypsi
3.3	1819	2	D97033		uncharacterized pr
3.1	889	2	JC5576		inter-alpha-trypsi
3.0	2706	2	T28155		variant-specific s
3.0	1984	2	A44396		P-type cation tran
2.9	575	2	D64998		hypothetical prote
2.9	918	2	E90542		lipoprotein (impor
2.9	680	2	A97331		membrane associat
2.9	1516	2	E71619		RA2 endonuclease
2.9	2364	2	I40884		cytotoxin L - Clo
2.9	946	1	IYH02		inter-alpha-trypsi
2.9	1315	2	T28679		fibrogen-binding
2.9	932	2	JC5953		inter-alpha-inhibi
2.8	1291	2	S46431		botulinum neurotox
2.8	1291	2	A97777		botulinum neurotox
2.8	420	2	S76691		hypothetical prote
2.8	1426	2	A98580		hypothetical prote
2.8	921	2	JC4625		inter-alpha-trypsi
2.8	1385	2	D89824		hypothetical prote
2.8	654	2	A96562		methyl-accepting c
2.8	1027	2	B90527		atp-binding protei

30	149	2.8	459	2	F64688	proteinase
31	149	2.8	930	2	JX0368	inter-alpha
32	148.5	2.8	2401	2	T28676	rhoptyr pr
33	148	2.8	964	2	S28855	DNA-direct
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36	146	2.7	4688	2	F82885	hypothetic
37	145.5	2.7	676	2	T47637	hypothetic
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39	145.5	2.7	1237	2	AC1583	internalin
40	145.5	2.7	2013	2	AD1129	probable p
41	145.5	2.7	3216	2	C90538	hypothetic
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43	144	2.7	1087	1	S41797	cellulose
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45	143.5	2.7	1252	2	H97178	ATP-depend

ALIGNMENTS

RESULT 1
JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug
C:Accession: JH0565
R:Williams, M.F., Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi,
Neuron 8, 71-84, 1992

Arrière: Structure and functional expression of alphas, alpha2, and b
A:Reference number: JH0564; MUID:92110010; PMID:1309651
A:Accession: JH0565
A:Molecule type: mRNA

A:Residues: 1-1091 <WIL>
A:Cross-references: GB:M76559; NID:gl79761; PIDN:AAA51903.1; PID:gl797
A:Experimental source: Basal ganglia
A:Note: Several conflicts are found between GenBank submission, author
C:Comment: This protein is a subunit of the voltage dependent calcium
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: glycoprotein; phosphoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-1067/Product: calcium channel alpha-2b chain #status predicted <
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F:91.142,250,625,817/Binding site: phosphate (Ser) (covalent) (by prot
F:92.136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/I
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kin

Query Match 100.0%; Score 5346; DB 2; Length 1091;
Best Local Similarity 100.0%; Pred. No. 1.6e-313;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; G

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Qy	181	NELNWTALDEVPKKNREEDPSLLWQVFGSATGLARYTPASPWNDSRTPNKIDLY	
Db	181	NELNWTALDEVPKKNREEDPSLLWQVFGSATGLARYTPASPWNDSRTPNKIDLY	
Qy	241	RPWYIQGAASPKDMLILVDVSGVSGVGLTLKLRITSVSEMLETISDDDFVNVASFNS	
Db	241	RPWYIQGAASPKDMLILVDVSGVSGVGLTLKLRITSVSEMLETISDDDFVNVASFNS	
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: calcium channel alpha-2 chain
: norvegicus (Norway rat)
34 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
47
H.; Lee, P.; King, R.G.; Chin, H.
Sci. U.S.A. 89, 3251-3255, 1992
1 expresses an alternatively spliced form of the dihydropyridine-sensitive
c: A44147; MUID:92228762; PMID:1314383
47
laty
mrna
1 <RIM>
3: GB:M86621; NID:G203954; PIDN:AAA1088.1; PID:G203955
cium channel alpha-2 chain
um; glycoprotein; ion channel; transmembrane protein

larity 95.8%; Score 5145; DB 2; Length 1091;
Conservative 22; Mismatches 19; Indels 2; Gaps 2;
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181 NELNWTSSALDEVFKQNRDEPSSLIMQVFGSATGLARYYPASPWVDSRTPNKIDI
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900 QGAGHRSAYVPSVADILQIGMWATAAAMSILQOFLSLTFFPRLLEAVEMEDDDFT.
960 QSCITEQTYQFFDNDKSKFSFGLDCGNCRIIPHGEKLMNTNLIFIMVESKGTCCPCI
960 QSCITEQTYQFFDNDKSKFSFGLDCGNCRIIPHGEKLMNTNLIFIMVESKGTCCPCI

```

RESULT 3

CHRB2

calcium channel protein alpha-2 chain precursor - rabbit

N:Alternate names: dihydropyridine-binding protein, 140K

C:Species: Oryctolagus cuniculus (domestic rabbit)

92 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
 79; A39518; A33409
 Williams, M.E.; Ways, N.R.; Brenner, R.; Sharp, A.H.; Leung, A.T.; Campbell
 -1664, 1988
 and expression of mRNAs encoding the alpha(1) and alpha(2) subunits of
 r: S10579; MUID:88336904; PMID:2458626
 79
 mRNA
 6 <ELL>
 9: EMBL:M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763
 06-Lys, and deletion of 620-Ser were also found
 P, A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
 6, 3287-3293, 1991
 al characterization of the dihydropyridine-sensitive calcium channel al
 r: A39518; MUID:91131638; PMID:1847144
 18
 protein
 73 <JAV>
 1 and identical molecular weights (17K) following deglycosylation
 Hawkes, M.J.; Brush, K.; Cook, R.
 7820-7828, 1989
 composition of the purified dihydropyridine binding protein from skelet
 c: A33409; MUID:90122765; PMID:2558713
 39
 lary
 protein
 'S', 46-47 <HAM>
 calcium channel alpha-2 chain
 m; disulfide bond; glycoprotein; ion channel; membrane protein; phosph
 mal sequence #status predicted <SIG>
 calcium channel alpha-2 chain #status predicted <MAT>
 150,470,477,606,615,676,697,784,827,891,898,988,1001,1081/Binding site:
 96.0%; Score 5132.5; DB 1; Length 1106;
 arity 94.7%; Pred.No. 1.1e-300;
 conservative 14; Mismatches 12; Indels 29; Gaps 4;
 KCLALTLTLFQS--LLIGPSSEPPSPSAVTKSWDKMQEDLVTLAKTASGVNQLV 58
 RPLAWTLTLQAWLILIGPSSEPPSPSAVTKSWDKMQEDLVTLAKTASGVNQLV 60
 KYQDLTYTEPNARGLVEIARDIEKLNSRSKALVLALEAEKVQAAHQWREDA 118
 KYQDLTYTEPNARGLVEIARDIEKLNSRSKALVLALEAEKVQAAHQWREDA 120
 VYNAKDDLDPKNDSEPGSQRIKPVIEDANFGRQISVQHAHVHIPTDIYEGSTI 178
 VYNAKDDLDPKNDSEPGSQRIKPVIEDANFGRQISVQHAHVHIPTDIYEGSTI 180
 LNWTLSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTNPKIDLYD 238
 LNWTLSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTNPKIDLYD 240
 WYIQGAASPDKMLILVDVSGVSGTLKIRTSVSEMLETSLDSDDDFVNVAFSNSNA 298
 WYIQGAASPDKMLILVDVSGVSGTLKIRTSVSEMLETSLDSDDDFVNVAFSNSNA 300
 CFQHLVQANVRNKKVLKDAVNIITAKGTDYKKGFSFAPEQLLNYNVSRANCKII 358
 CFQHLVQANVRNKKVLKDAVNIITAKGTDYKKGFSFAPEQLLNYNVSRANCKII 360
 DGEERAQEIIPNKNKKVRVFRFSVQGHNYERGIQWMAKNGYIYIPIPSIGA 418
 DGEERAQEIIPNKNKKVRVFRFSVQGHNYERGIQWMAKNGYIYIPIPSIGA 420
 TQEYLDVLRPWLADGKAKQVQWNTNVLDALEGLVITGTLVPVNIITQGPENKTN 478
 TQEYLDVLRPWLADGKAKQVQWNTNVLDALEGLVITGTLVPVNIITQGPENKTN 480
 LILGMVGVDVSLDIKRLTPRFTLCPNGYYPALDPNGVYLAHPNLOPK----- 530
 LILGMVGVDVSLDIKRLTPRFTLCPNGYYPALDPNGVYLAHPNLOPKIGVGIP 540

QY 531 -----NPKSQEPVTLDFLDALENDIKVEIRNKMIDGESGEKTERTLVR
 Db 541 INLRKRPVQNPQPKSEPTLDFLDALENDIKVEIRNKMIDGESGEKTERTLVR
 QY 580 YIDKGNRTYTWTPVNGTDY-SLALVLPYTSFYFIKAKLBETITQARSKKGKMDK
 Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYTSFYFIKAKLBETITQARY-----S
 QY 639 DNPEESGYTFIAPRDYCNLDIKSDNNTFLLNPNFIDRKTNNPNSCNADLINRV
 Db 654 DNPEESGYTFIAPRDYCNLDIKSDNNTFLLNPNFIDRKTNNPNSCNADLINRV
 QY 699 FTNELVQNTWSKQNKIKGVKARFVTDGGITRVYPKEAGNENQENPETVEDSFYK
 Db 714 FTNELVQNTWSKQNKIKGVKARFVTDGGITRVYPKEAGNENQENPETVEDSFYK
 QY 759 DNVFTAPYFNKSGPGAYSGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENF
 Db 774 DNVFTAPYFNKSGPGAYSGIMVSKAVEIYIQGKLLKPAVVGKIDVNSWIENF
 QY 819 RDPGAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPDLMRH
 Db 834 RDPGAGPVCDCRNSDVMDCVILDDGGFLLMANHDDYTQIGRFFGEIDPDLMRH
 QY 879 VYAFNKSVDYQSVCPGGAAPKQAGHRSAYVPSVADILQIGHWATAAASIIQQF
 Db 894 VYAFNKSVDYQSVCPGGAAPKQAGHRSAYVPSVADILQIGHWATAAASIIQQF
 QY 939 FPRLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNSRIFHG
 Db 954 FPRLEAVEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGCGNSRIFHG
 QY 999 TNLIFIMVESKGTCTCDTRL 1018
 Db 1014 TNLIFIMVESKGTCTCDTRL 1033
 RESULT 4
 T30256
 calcium channel alpha-2-delta-C chain - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun
 C:Accession: T30256
 R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, P.
 J. Neurosci. 19; 648-691, 1999
 A:Title: Molecular diversity of the calcium channel alpha2delta subun
 A:Reference number: Z20794
 A:Accession: T30256
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1091 <KLU>
 A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
 A:Experimental source: brain
 C:Superfamily: calcium channel alpha-2 chain
 Query Match 20.3%; Score 1085; DB 2; Length 1091;
 Best Local Similarity 28.7%; Pred No. 4.4e-57;
 Matches 309; Conservative 222; Mismatches 416; Indels 128; (
 QY 3 AGCLLALTLTLFQSLILIGPSSEPPSPSAVTKSWDKMQEDLVTLAKTASGVNQLV
 Db 14 ASALLA-TALLVAAALGDVVRESEQIPLSV-VKLWASAFGGBIKSIKAAKYSQSLLV
 QY 63 KYQDLTYTEPNARGLVEIARDIEKLNSRSKALVLALEAEKVQAAHQWREDA
 Db 72 EYKQDAVEEDIGLQVCKLAKIMEEMPHKKSEAVRRLVEAAEAHLKHEFDADL-
 QY 123 VYNAK--DDLDPKNDSEPGSQRIKPVIEDANFGR-QISVQHAHVHIPTDIYEG
 Db 129 EYFNAVLINERDKGNFLELGEFI---LAPNDFNNLPVNIISLSDVQVPTNMYN
 QY 180 LNELNWTLSALDEVFKKNEEDPSLLMQVFGSATGLARYYPASPWVDSNRTNPKIDI

17
nary
DNA

RESULT 6

probable calcium channel protein - *Caenorhabditis elegans*
 C1Species: *Caenorhabditis elegans*
 C1Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C1Accession: T18770; T25249
 R1Sulston, J.
 submitted to the EMBL Data Library, June 1995
 A1Reference number: Z19019
 A1Accession: T18770
 A1Status: preliminary; translated from GB/EMBL/DBJ
 A1Molecule type: DNA
 A1Residues: 1-1148 <WIL>
 A1Cross-references: EMBL:Z49907; PIDN:CAA90091.1; GSPDB:GN00020; CESP
 A1Experimental source: clone B0491


```

Qy 27 FBSAVTIKSWVDKMQEDLVTLAKTAGVNOVLVDIYEKIQDLYTVTEPNNAQLVETI
Db 98 YFQNKYEKVAQKOYERKAVSQKTAG---LVKASGRKLEKFQTVSVNVNVAAGSVVT
Qy 87 EXLLNRSKALVSLALAEKVOAAHQWREDFASNEVVYVYNAKODLDPEKNDSFEG
Db 154 EELL-KRNKGYEMVLKQPKQLVHRFEID-----AHIEP-
Qy 147 PVFIEDANFGRQISYQHAHAVHIPTDIYEGSTIVLNLNMTSALDVFVKXNREEDP
Db 190 GISMLDAE-----ASFITNDL-LGSALTQSF-
Qy 207 VFGSATGLARYYPASPWVDNSRT--PNKID-----LYDVRRP-
Db 215 -----SGKKGHVSFKPSLDQQRSCPTCTDSLNGDFTIVYDVNRESFGNVQIVNG
Qy 246 ---QG-AASPMDMLITVDVSGVSGLTLKLIRTSVSEMLETLSDDDDFVNVASFNS
Db 270 FAPQGLPVVPKNIPIVDVSGSMGRKIQTREALLKILDDVKEDDYLYNFIIPST
Qy 302 SCFO-HLVQANVRNKVLKDAVNNTAKGITYDKKGSFAFEOQLLNNVSRAN--
Db 327 TTWKDHLVQATPAULKERAKTEFVNIHPDQSMTNTDGLLKGIEML---NKAREDHT
Qy 355 NKIIMLEFDG---GEERAQBIENKYNK---DKKVRVFRFSVGHOHYERGPQIOWMA
Db 384 TSIIIMLTDGDANTGESRPEKIQENVRNAGGKFLYNLGFQ-NNLNNYFETLA
Qy 409 YYEIPSGAIRINTQEYLDVLGRPMVLADGKAKQVOMTNNVYLDALLEGL---VIT
Db 443 LARRIVEDSANLQLOQGYEYVANPLL-----TNVEVEYPENAILDLTR
Qy 467 FNITQFENKTNLKNQLILGVNGVDVLESDIKRLTPRFTLCPNGYFADDPNGYV
Db 492 F-----YQG-----SEIVVAGRLVDRMND-----FKADVKGHG
Qy 527 LQPKNPKSQEPWTLDFLDAELENDIKVEIRKMKIDGSGBK--TFRTLKVSODER
Db 524 -----DLTTEEVDMZDAALK-----BQGYIPGDYIERLWAYLITIEQLLEKR
Qy 585 NRTYTWTPVNGTDSLA--LVLPYSPYYIKAKLEETITQARSKKMKMDSET--
Db 573 DSEKENIT-AEALDLSLKHYFTPTITSMVVKPEDNEQDQTSIADNAGESEAFATTT
Qy 638 PDNFESGVTFIAPRDYCNLDLKI SDNNTFEFLNPFIDRKTNNPNSCNADLINR
Db 632 TQOQSQSPYYV-----DGPHEIIQI-----PGKNDSCIFN
Qy 698 GFTNELVQNYMSKQNIKGVKVARFVTDGGITRYPYKBAGENWQENPETYDSFY
Db 669 GTWLRLLD-----PVT--GIT-VTGOIIGD-----

```

[illegible]

```

RESULT 9
S30350
inter-alpha-trypsin inhibitor heavy chain 3 precursor - human
N;Alternate names: HC3; inter-alpha-trypsin inhibitor chain H3; pre-a
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 04-Feb-1995
C;Accession: S30350 S34123 S02141; D34245; A39079; S50133; B53642;

```

F:647/Modified site: chondroitin sulfate ester carboxyl end (Asp) (in

```
Query Match      3.5%; Score 185; DB 2; Length 885;
Best Local Similarity 20.4%; Pred. No. 0.0046;
Matches 133; Conservative 106; Mismatches 243; Indels 170; (C

QY    27 FPSAVTIKSWDKMQEDLVTLAKTAGSVNQLVDIVIEKKVQDLYTFEPPNARQVLVEL
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY    97 YPGNKKEVKAKQYEKAVSQGTAG-----
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY    87 EKLSSNRKAL---VSLALEARKVQAHHQWRBDFASNEVVYNAXDDLDPEKNDSI
DB          || | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   132 EKPTVSNNVAAAGSKVPFELYELLKRHKG-----YEMYLKVQPK-
DB          || | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   144 RIKPFVFIEDANFCRQISYCHAAVHIPTDIYESGTVILNELAMNTSALDEVFVKNEH
DB          || | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   174 LVKHFEIK-----VDIFEQGISM LDAERASFITNDLL-----
DB          || | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   204 LMQVFGSATGLARYYPASPWNDSRT-PNKID-----LYDVRRRP-
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   209 LTSFGSGKGKHGVFKPS---LQQRSCTPTCSLNGDFTITYDVNRESPGNVOIQ
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   245 I----QG-AASPCKMLILVDVSGSVGLTKLIRTSVSEMLETUSDODDFNVVASI
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   266 VHPFAPOGLPWPVKNAVFVIDISSGWAGKLGQTKEALRIULEMQESDYLNFLFI
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   299 QDVSCF-OHLVQANVRNKKYLKDANNINIAKTIDYKKGFSFAPQLNLVNSVR--
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   324 -DVSTWKEHLVQATPENLQBEAKTFVKSMEDKGMTWINDLGLRGISML---NKAREI
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   352 ANCNKIIMLTDG-----GBERAQEIFPNKYK--DKQVRFVFSVGQHNYERGPIQV
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   380 ERSTSIVIMLTGDGANVGSRPEKIOENRVNAIGKFFPLYNLGF-G-NMLATNFLEI
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   406 NKGYYEIPISGAIRINTOEYLDVLRPMVLAGDKAKQVQWTVNVYLDAL-
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   439 NHGPARIYSDSDADLOLQGFEEVANPL-LTGVEMEYPE--NALIDLQNTYQHI
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   457 GLVITGTPLVFNITGOFENKTNLK-----NQILGMVMGVDSLSLEDIKRLTFRFLIC
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   496 EIVVAGRL-VDEDMNSF--KADVKGHGATNDL---TFTEEVDMKEMEK-----ALG
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   512 YPAIDPN-----GYVLLHPNLPK---NPKSQBPVTLDLFDAELENDIKVEIRNI
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   545 IFG---NYIERLWAYITIELQLEKKRNAHGEKENLTARALDLSIKHFVFTPLTS
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   563 ESGEKTERFLVKQSDERYI-DKGNRTYTTPVN-GTDYSIALVLPPTYSFYYI 612
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   602 PE-----DNEDERALADKPGEAEATPVSPAMSYLTSYQPQNPPYYV 644
DB          :| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
D97033
Unclassified protein, probably surface-located [imported] - Clostri
C:Species: Clostridium acetobutylicum
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep
C:Accession: D97033
R:A;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A>Title: Genome Sequence and Comparative Analysis of the Solvent-Produ
A:Reference number: A96900; PMID:21359325; PMID:21359325
A:Accession: D97033
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1819 <URL>
A:Cross-references: GB:AB001437; PIDN:AAK79055.1; PID:g15023996; GSPDE
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1081

Query Match      3.3%; Score 175.5; DB 2; Length 1819;
Best Local Similarity 18.8%; Pred. No. 0.053;
```

Conservative 154; Mismatches 342; Indels 335; Gaps 51

?PSAVTIKSWVDQMQEDL-VTLAKTAGVGNQLVD-----IYEKYQDLYTVEPNNNA 75
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
IKNARTSKG-ADLTKDIEGTIIANTSDSIKGIIDRMTKGTAUVSDYQFLLIITQVNSN 191
?EIAARDIEKLISNRSKALVSLE-----AEKVQAQHQRREDPASNEVVYYNA 127
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
--LDQINSWLTKRYALISKILSTVDKIITTVASNNINNDHESDFALQI--YNV 243
..DPKRND-----SEFGSRIKPVF-----IEDANFGR-QISYQH--A 164
..VPFLNENISAANKNGSDLSSSEINTVVKDSLKLQALERINLGQTLLDYHFIG 303
[PTDIYEGSTIVLNELNWTLSALDEVFKNR--BEDPSLLMQV--FGSATGLARYPA 220
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
JENNILEDVNGWANGKW-----FERNNAIBEINSIVEPLSRINGSGDSTAADYA 356
?PWDSNRTPN-----KIDLYDVRRRPWYIQGA 248
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
XGVDDNNIDIKSVAIEAKQKGLKNLNIABIKSAVEHYKTVLFDYLKK-----GT 411
QO--MLILVDVS--GSVSGL-----TLKLI RTSVSMELETSLD-----DD 287
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
IDYNAIGLATGVTDENDVTDMNELLKNRDIKTLNKLQNINSIIKSLAKINAGDTDPD 471
?ASEFSNAODVSCF-----OHLVQANVR--NKVLKDAVNNTAK----- 328
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
J-NISSVTQNTSFIRDDIKTAQAGSDLNKGIQDSVNSNKLRLSAMDRINAGSA 530
DYK----KGFSAFEQLLNYSRANCNKIIMLFTDGEERAQBIFNKYK----- 378
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
YNLLGIEGVTSDNLTFVANNQVKSCKTIDELTKVSD--ALKLYDSYNKVNNGDA 598
QVRV-FRSVGCHNYERGP IQMACENKGY-YEIPSIG--AIRN-----422
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
YLKIGIVIKIEBVTYNG---VPKGNFYLEBLKVGGINAVRISTENIKNG 643
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
-----TOEYLDVLGRPMVLADGKAKOV-----QWTVNVL 451
?BDFTIAGTYGVTENIKYINKVIIEGGDASPEAISNIITEVNVETQSIXRMSSGV 703
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
ALELGL-VITGLPVFNITQPENKTNLIKQILGMGVGDVSDLEIKRLTPRTLCL 507
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
YKSLGLSVTEENTSYIMDRVVKNTYYSKVELIEAVEAIIKEKEIYERINLQATV 763
YFAI-----DPNGVYLLHPNLQPNPKSQEPVTLDFDLDAELENDIKVB--- 554
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
YIKVTGTSVMITSINDV-----KSGNLTTRRELQAKI--DVVIQTQS 810
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
--IRNMIDGSGSEKTFR---TLVKSODERYIDKGNRTYTTPVNGTDYSIALVL 604
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
DWIGVRNLGEBANTSDFFBMGITVYVNSFNQIVVDHLKDKDKYTTIDAIAKAATVVF 870
?PYIKAKLEBITQARSKKGMKOSSETLKPDNFESSGYTFIAPRDYCNDLKLSDNN 664
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
IY-----EEIN-----KGATL-----DYNLSLGTGVT 898
..LNPNFIIDRKTPNPNSCADLINRVLLDAGFTNELVQNYWSKQNIKGVKARFWVT 724
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
TYINLNIKESSVFNAS---DIQTKV-----NALISVVGYYEEINKGEATVDVYT 948
[TRYVPKEAGENWQENPETYESFYGRSLDNDNVYTPATPFYNGSGPGAYESGIMVSK 784
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
TGv-----TKENIIIFINTYIKE---GQYPDLTSLKS 980
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
-----YIQ--GKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGVCDCRNSD 834
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
LEEKYEAVKLTSGK---AVUG-----DYTKVGIKQDVTEENTAIYMINLID 1026
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

: 838
1030

```

RESULT 11
JC5576
inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Ma
C/Accession: JCS5576; PC4486
R/Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinochara, H.
J. Biochem. 122, 71-82, 1997
A/Title: Molecular cloning and sequencing of cDNAs encoding three hea
sin inhibitor heavy chain family.
A/Reference number: JCS5574; MUID:97420688; PMID:9276673
A/Accession: JCS5576
A/Molecule type: mRNA
A/Residues: 1-889 <NAK>
A/Cross-references: DBJB:D89287
A/Experimental source: liver
A/Accession: PC4486
A/Molecule type: protein
A/Residues: 34-53;449-475;509-526 <NA2>
C/Comment: In the plasma three inter-alpha-trypsin inhibitor heavy ch
that the complexes play important role for pancreatic cancer.
C/Superfamily: inter-alpha-trypsin inhibitor complex component II
F/236-239, 664-865/Disulfide bonds: #status predicted

```

```

Query Match      3.1%; Score 164.5; DB 2; Length 889;
Best Local Similarity 23.2%; Pred. No. 0.079;
Matches 66; Conservative 56; Mismatches 112; Indels 51;

QY      202 SLLMVFGSATGLARYYPASPVWDSRT--PNKID-----LYDVRRR--PWYI
Db       211 SALTSTSGKKGHVSPFS---LDQBSCTCTDSLINGDFIVIVDVNRESQNV
QY      249 -----ASPKMLILVDVSVSGSLTUKLIRTSVSEMLETSLDDDDFNVV.
Db       268 YFVHFAPQGLPVVPKQIVFVDISGSMAGRKIQOTRVALLKILDPMKQDDYLF.
QY      297 NAOQDVSCFQHLVQANRVNKKVLDAVNNITAKGIDYKKKGFSFAFEQLIN----VI
Db       328 GV--TTWKDSLVAQTPANLEEARTFVRSISDQGMTNIDNGLLRIGRLMTDAREQH
QY      353 NCNKIIMLFTDG-----GEERAQELFNKYNKKXKRVFRFSVG--QHNVERGPTQWMI
Db       386 STSIIIML--TDGDANTGESPEKIQENVRKAIEGRFPLYNLGFGNLNNYNFLETFM
QY      408 GYTYEIPSIGAIRINTQEYLDVLGRPMVLAGDKAKQVQWNTNYLD 452
Db       445 GYARRIVEDSDANLOLQGFVEEVANPL-----TNVEVE 478

```

RESULT 12
T28155
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)
N:Alternate names: erythrocyte membrane binding protein 1 (EMPI)
C:Species: Plasmodium falciparum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-1999
C:Accession: T28155
R:Rowe, J.A.; Moulds, J.M.; Newbold, C.I.; Miller, L.H.
Nature 388, 292-295, 1997
A:Title: Plasmodium falciparum rosetting is mediated by PfEMP1 and requires a novel protein, PfEMP4
A:Reference number: 220477; MUID:97373957; PMID:9230440
A:Accession: T28155
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2706 <ROW>
A:Cross-references: EMBL:Y13402; PIDD:CAA73831.1
A:Experimental source: strain IT 4/25/5
C:Genetics:
A:Introns: 2493/3
A:Note: R29R+var1

Query Match
3.0%; Score 161; DB 2; Length 2706;

arity 18.2%; Pred. No. 0.75;
 Conservative 137; Mismatches 345; Indels 338; Gaps 46;
 QY QDQDLVTLAKTASGVNQLVDIYKQYQDLYTVBPNNA-----RQL 78
 DQ : : : : :
 DB WAEBCFRIRKI-----KLENVKCECD-----EPNNKYCSGDHCKRYLYKDNITP 358
 QY : : : : :
 QY IARDIEKLNSRKSALVSLAEAEKVQAAHQRWEDFASNEVYVYNKADLDPEKND 138
 DB : : : : :
 DB ICPRCNACSNYTK-----WIBTQRKQFQKQK--YMEI--KIKTINISNENDK 408
 QY : : : : :
 QY -----PQSRIKPVFEDANFGQISYQAAHVHPDITYEGSTIVLNLNWTALDE 191
 DB : : : : :
 DB NLDKKGYSTIN--TFLESNLHGKQC-----DN 438
 QY QNREEDPSLLQWFGSATGLARYTASP-----WVDSNRPNKI 233
 DB : : : : :
 DB QKNTNFKNL--ETFGP-----SGYCEACPIYGVKCSNEKCTPVTEWNSNRLPTDT 493
 QY YVRRPWYIQGAASPQMDLILVDVSGSVGLTLKLRISVSEMLETSLDDDFVNVAS 293
 DB : : : : :
 DB ILM-----ATNIDMLVNDIGNAI-----515
 QY IADVSCFQHLVQAVRNK-----VLKDAVNNITAKGIDYKKGSPAPBQLL 345
 DB : : : : :
 DB ILEKNCITYGILKGIKKQKQWQOYLNNDQCKINNVMSGYPDNKAIFNVLFQWL 573
 QY 'SRANCKIIMLFTDGGERAQEIFNKYNKKVVRFRFVSQGHYERGPQIMWACE 405
 DB : : : : :
 DB 'RDHRLK-----EKIDVICIKENINENICIKCKTN-----CE 610
 QY 'YIEPSIGAIRI-----NTQEVLDVLRPMVLADKAKOVQWNTVYLDALGLVIT 461
 DB : : : : :
 DB WLEKEAEWDKINQHYNOKNHMFILIPYWTGFYEK--ITFPNDPFKALE-----DV 665
 QY 'VFNITQGFENKTNLQNLILGMGVDSLEIDKRLTPRFTLCPNGYYFAIDPBGV 521
 DB : : : : :
 DB VLDTLKECD--THCKIEKIRSI--DVDLKEIISLQNKIEVCK--HHDEDKHEYC 721
 QY NLQPNKPSQBPVTLDFDLAELENDIKVEIRNMIDGSGEKT-----PRT 571
 DB : : : : :
 DB DILPKSVDDDEED--EEVDEKEESSQTTKN--ISQKGTYSASCVKGACAIKVG 775
 QY QDERYID-----KGNRTYTW-----TPVNGTD-----YSLALVLPYSP 609
 DB : : : : :
 DB KSNGSIDCNNAKRNKKEWQCDKNTFVDSGEGVCMPPRRKSCICIHNLTLBEQTKN 835
 QY --YIKAKLEET--ITOARSKGKMDSETLK-----PDNFE--SGYTFIAPRDC--N 656
 DB : : : : :
 DB EAFIKCAAKETNLWDKYNDKNEABELLXGKIPEDFMRIMFTYFGDFRDFCLEN 895
 QY ---KISDNNTBFLNFBFIDRK-----TPNPNPC--NADLINRVLIDAGFINEL 703
 DB : : : : :
 DB DVDKVKKNINKVFNSSKRGFKKIDPENWNGPQIWNGLCALIHADTKDSIKN 955
 QY -----W-----SKQNKINGVKARFV 723
 DB : : : : :
 DB KYEKVTILAKRDSNGMTLSEFAKKPFLRWFEVYDDYCKERQKYLTEVASTCKS 1015
 QY ITRV-----YKKEAGENWQENPETYEDSFYKRSIDN-----DNTV-- 762
 DB : : : : :
 DB QLKCDRGNNKDEYKYMKXKGEWNLQDKYYKDKRENKIDGKPIGIIIVKDYVL 1075
 QY -----FTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKDVSNI-- 810
 DB : : : : :
 DB EYLKXKFTASCVTSSGKAQNSATBEVKKNIELLEEY-----YDADQYCGC 1126
 QY ---ENFTKTSIBDPGAGVCDCK-----RNSDVMDCVIL 841
 DB : : : : :
 DB HDDKYSKISGRSNCGLNSDAKKNKIKWRNSDEKDYAFL 1169

A44396
 P-type cation translocating ATPase - malaria parasite (Plasmodium fal
 C:Species: plasmodium falciparum
 C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Ju
 C:Accession: A44396
 R:Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; R
 J. Cell Biol. 120, 385-398, 1993
 A:Title: A family of cation ATPase-like molecules from Plasmodium fal
 A:Reference number: A44396; MUID:93132070; PMID:8421054
 A:Accession: A44396
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-1984 <KRI>
 A:Note: sequence extracted from NCBI backbone (NCBIP:122678)

Query Match 3.0%; Score 159; DB 2; Length 1984;
 Best Local Similarity 17.1%; Pred. No. 0.6; Mismatches 366; M
 Matches 179; Conservative 144; Indels 359; Indels 366;
 QY 58 VDIYEKYQDLYTVBPNNAQQLVEIAARDIEKLLSNR-----SKALVSLA
 DB 128 INVY-RYNTSYIISSS-----ELVPGDIYEIKNNWTIPCDTIIILSGSVTSEHM
 QY 107 VQAAHQWREDFASNEVYVYNKADLDPEKND-----SEPGSQRIKPVFIEDANF
 DB 181 V-PIHKERLPPEGNAIINKNNKYDSNDEKDDYLRYYNNHASINMIKRNHLIBETL
 QY 161 YQAAVHIPTDIYEGSTIVLNLN--TSALDEVFKKNEEDPSLLWQVFGSATGL
 DB 240 EYKSWTH-----DLCSMNKLCYNNYDDVHKKNRMD-----
 QY 220 ASPWVDNSRTNPKIDLYDVRPRPWIYQGA--ASPQMDLILVDVSGSVGLTLKLR
 DB 273 ---YNNNNNNKKKKINLN---PVKGYINSNDLLY-----
 QY 279 MLETSLDDDFVNVASFNNAQDVSCFQHLVQAVNRNKKVLKDAVNNITAKGIDYI
 DB 304 -----DDKIGVNIPE--DDVNNMKH--KFNQNRINYYNKKDTNNL-----EY
 QY 339 PAFEOALLNNVNSRANCKIIMLFTDGGERAQEIFNKYNKKVVRFRFVSQGHN
 DB 346 YIYDCLLKKVFAISQKKIY-----SNEDINKY-----
 QY 399 IQMWACENKGYHYIPIPSIGAIRINTQBYLDVLRPMVLG-----DI
 DB 375 ---MLYGGTVVLSLYNINKIKYNNKEENRILGL-VIKTGFITTKGKIVNNLIYH
 QY 445 QWTVYLDALDELGLVITGTLFVFNITQGFENKTNLKNQILG-----
 DB 430 NLINDSVYKFLII-LIYALPFSVFIILYITLSNNEYTHIIKCLDIITDAIPALI
 QY 488 MGVDSVLEIDIKRLTPRFTLCPNGYYFA-----IDPNGYVLLHPNLQ-----PK
 DB 489 VQISIASRLKKSISCLCPHKINIAGQINTWVFDKGTG-TLTENNLOFIIIGITQ
 QY 536 BPVTLDFDLAELENDIKVEIRNMIDGSGEKTFRTLVKSQDERYIDKGNRTYTW
 DB 548 NWLS-DFTHIK-----EMNTESYIHSKDDNMIHNKN-----
 QY 596 TDYSIALVLPYSPYIYKAKLEETITQARSKGGKKO-----SETLKPDNE
 DB 578 -----SIISYYIKDNMKNLHTSSK-KKSITKERSNLFVQTIKSCLLKDHVI
 QY 646 YTFIAPRDNDLKISNN--TEFLN-----FNEP--IDRKTPNNSCNADLINE
 DB 628 KEYTNNYTCNDLHNDSTCSYLLNSETKDAYCEYNNIDH-----LCD---INK
 QY 697 AGFTNELVQNTWSQKNIKGVKARFVVTDDGITRVYPKAGENWQENPETYEDSFY
 DB 679 INSKNELMGKYSKVELMGKTIKNELM-----GKYS
 QY 757 DNDNVYTFAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVG-----IKTIDV

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QY 502 PRFTLCPNGYYFAIDPNGYVILLHPNLPKPKSQB 536
Db   ||| ||||| :|::| |::|
448 LLFELTLNQKASIDKLRYA--PDNKLAISKTKXE 480
      ||| ||||| :|::| |::|

RESULT 15
E90542
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aa
C;Accession: E90542
R;Chabaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissier, C.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen M. pulmonis
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90542
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-918 <CUR>
A;Cross-references: GB:AL44566; PID:g14089658; PIDN:CACI3418.1; GSP:
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU 2450
A;Genetic code: GSC3

Query Match          2.9%; Score 156.5; DB 2; Length 918;
Best Local Similarity 20.0%; Pred. No. 0.25;
Matches 122; Conservative 99; Mismatches 229; Indels 161;

QY 305 QHLQVANRNKKV---LKDAVNNTAKGTYDKGPSAPAFEQQLNNVSRANC
Db   ||| ||||| :|::| |::|
91 KRILPSNVNRNLDFNSLUKITKDNTLIGKNIPKNYTVAFSIDPN-SVENASAI
      ||| ||||| :|::| |::|

QY 361 FTDGEERAQAIFNFKYNKKKV---RVRFPSVGQHNYERGPIONMACENKGYYFI
Db   ||| ||||| :|::| |::|
146 -TGG-----SMNIIVSLKKONGVFLEKFKIT-----GLLSIE

QY 418 AIRINTQBYLDVLGRPMVLADKKAQQWNTNVYLDALDELGLVITGTLP-----
Db   ||| ||||| :|::| |::|
182 DQNLIK----VDVPKNKEILASSIVEVEQITNE-----KISLSQGKVPSTFDLTN

QY 468 NITGFENKTNLKNQLILGVWG-----VDVSLEDIKR--LTPRFTL-CPNGYYFF
Db   ||| ||||| :|::| |::|
233 HVLSHDDKSGSKIRVLSLAKSKTKSKDFTYIEFGFQSFLDRISLAKAQGVNRV

QY 519 GYVLLHPNLPKPKSQBPVTLPDLDAELENDIKVEIRNNKMIDGESGEKTFRLTV
Db   ||| ||||| :|::| |::|
292 --LIKSLLQPSSASED--KLNVLKSAYDISVPDGKLFNFVFEAKQGTFF-----

QY 579 RYIDKGNRTYTWPVNGTDSLALVPTYSFYVIKAKLEETIQARSKKGMKDS
Db   ||| ||||| :|::| |::|
339 ---DKGVLYTFLTGINGTRRETEVKDIQTFFNIKKGYLDDETLIKDISV--VLKEN

QY 638 --PONFRESGYTFIAPDQCNDLKISDNNTPELLNFNER-IDRKTPNNPSCNADL
Db   ||| ||||| :|::| |::|
394 SLPELVENKEI----ENWQNEIELDSSKAKINVKNFQOVSVTSANPEYN-----

QY 695 LDAGFTNE-----LVQNTWSQRQNIKGYKARF--VVTDGGGITRYP---KEAG
Db   ||| ||||| :|::| |::|
443 IDGSINLEVRIISDGIYQKVTKRSLGLTKLDANLFDVAVAKANVSNQLPGNLKAKO

QY 743 NPETYE-DSP-----YKRSLDN---DNVVTFTAPY---FNKSGPG
Db   ||| ||||| :|::| |::|
503 GEKTFSTDSEFLKPFKNKAKENNSTLNLYKLSLENVCLNFSGQVSFDVKETRAGTG

QY 780 IMWSKAVEIYIOGKLL-----KPAAVVGIKIDVNSMLENFTKITSIR
Db   ||| ||||| :|::| |::|
563 VTISKKITNFKXDVLPDQQRRYPDENDEHFHKALTAULTWTMTREFIK-----

QY 825 PVEDCKNSDV 835
Db   ||| ||||| :|::| |::|
611 -IVDARENDOL 620

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07:56:51 2004

us-10-090-827-13.rpr

se
jc

February 20, 2004, 16:59:22
3 BECB

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

ein search, using sw model

February 20, 2004, 16:48:25 ; Search time 11.1043 Seconds
(without alignments)
4311.242 Million cell updates/sec

S-10-090-827-13

346

MAAGCLLALTLTLFQSLILG.....TNLIFIMVSKGTCPCDTRL 1018

LOSUM62

apop 10.0 , Gapext 0.5

27863 seqs, 47026705 residues

its satisfying chosen parameters: 127863

lgth: 0

lgth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

MissProt_41.*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
red by analysis of the total score distribution.

SUMMARIES

Entry	Length	DB	ID	Description
10.0	1091	1	CIC2 HUMAN	P54289 homo sapien
6.2	1091	1	CIC2 RAT	P54290 rattus norv
6.0	1106	1	CIC2 RABIT	P13806 cynoetholagus
3.4	1249	1	UN36 CAEL	P34374 caenorhabdi
3.6	886	1	ITH3 MOUSE	Q61704 mus musculu
3.4	885	1	ITH3 HUMAN	Q06033 homo sapien
3.4	887	1	ITH3 RAT	Q63416 rattus norv
3.1	886	1	ITH3 MESAU	P97280 mesocricetu
3.0	1829	1	DPOL_THEST	O33845 thermococcu
3.0	1956	1	ATX1_PLAPA	Q04956 plasmodium
2.9	575	1	YFBK_ECOLI	P76481 escherichia
2.9	946	1	ITH2 HUMAN	P19823 homo sapien
2.8	1290	1	BXCI_CLOBO	P18640 clostridium
2.8	420	1	Y103 SYN3	Q55874 synecocyst
2.8	921	1	ITH4_PIG	P79263 sus scrofa
2.8	554	1	MCPC_BACSU	P54576 bacillus su
2.8	930	1	ITH4 HUMAN	Q14624 h inter-alp
2.8	964	1	DPOL_CBBEPV	P30319 choriastoneu
2.7	1087	1	YXNX_CLOTM	P38535 clostridium
2.7	946	1	ITH2 MESAU	P97279 mesocricetu
2.7	1169	1	SMC_METJA	Q59037 methanococc
2.6	1251	1	RBF2_PLAVB	Q00799 plasmodium
2.6	935	1	ITH2_PIG	O02668 sus scrofa
2.6	2710	1	TOXA_CLODI	P16154 clostridium
2.6	3305	1	APLP_MANGE	Q25490 manduca aex
2.6	764	1	PAG_BACAN	P13423 bacillus an
2.6	1513	1	STUL_YEAST	P38198 saccharomyc
2.6	1180	1	CANA_EACTI	P16480 bacillus th
2.6	3063	1	CAIC_HUMAN	Q99715 homo sapien
2.5	946	1	ITH2 MOUSE	Q61703 mus musculu
2.5	2077	1	TEGU_HSV6U	P52340 human herpe
2.5	862	1	MUTS_BOREU	O51737 borrelia bu
2.5	1323	1	ADRI_YEAST	P07248 saccharomyc

34 132.5 2.5 547 1 SYM_BUCAL P57210 buc
35 132.5 2.5 929 1 CALC_NOTVI Q91145 not
36 132.5 2.5 1679 1 YIO9_YEAST P40457 bac
37 132 2.5 697 1 YE9C_SCHPO O13773 bcl
38 131 2.5 1634 1 YD94_METJA Q58295 met
39 130.5 2.4 987 1 YD94_METJA Q58789 met
40 130.5 2.4 1018 1 YC14_METJA Q58611 met
41 130.5 2.4 1036 1 Y946_ARCFU Q29316 arc
42 129.5 2.4 1658 1 YM67_YEAST Q03661 sac
43 129 2.4 1244 1 Y307_MYCPN P75342 myc
44 128.5 2.4 1254 1 UBPC_YEAST P39538 sac
45 128 2.4 1113 1 Y140_MYCPN P75033 myc

ALIGNMENTS

RESULT 1
CIC2_HUMAN
ID CIC2_HUMAN STANDARD; PRT; 1091 AA.
AC P54289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.
DE CACNA2D1 OR CACNL2A OR CCHL2A.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=92110010; PubMed=1309651;
RA Williams M.E., Feldman D.H., McCue A.F., Brenner R.,
RA Velicelebi G., Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype";
RL Neuron 8:71-84(1992).
CC FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R
CC EXCITATION-CONTRACTION COUPLING.
CC SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC SUBCELLULAR LOCATION: Integral membrane protein.
CC TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE;
CC AORTA TISSUES.
CC PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE
CC A PRECURSOR FORM (BY SIMILARITY).
CC SIMILARITY: TO OTHER SPECIES, ALPHA-2 SUBUNIT.
CC SIMILARITY: Contains 1 VWFA domain.

CC This SWISS-PROT entry is copyright. It is produced through a coll
CC between the Swiss Institute of Bioinformatics and the EMBL out
CC the European Bioinformatics Institute. There are no restriction
CC use by non-profit institutions as long as its content is ir
CC modified and this statement is not removed. Usage by and for c
CC entities requires a license agreement (see <http://www.isb-sib.ch/>
CC or send an email to license@isb-sib.ch).

CC EMBL; M76559; AAA51903.1; -;
CC PIR; JH0565; JH0565.
CC Genew; HGNC:1399; CACNA2D1.
CC MIW; 114204; -;
CC GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
CC GO; GO:0015270; F: dihydropyridine-sensitive calcium channel a.
CC GO; GO:0006832; P: small molecule transport; TAS.
CC InterPro; IPR004010; Cache.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF02743; Cache; 1.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00327; VWA; 1.
CC PROSITE; PS50234; VWFA; 1.

QY	601	ALVLPTYGYIYIKAKLETTITQARSKGKWKDSETLXPDNFESGYFTFIAPRDYC
Dd	601	ALVLPTYGYIYIKAKLETTITQARSKGKWKDSETLXPDNFESGYFTFIAPRDYC
QY	661	SDNNTEFLINNEFIDRKTNNPNSCNADLNIRVLLDAGFTNELVONYWSKKNIK
Dd	661	SUNNTEFLINNEFIDRKTNNPNSCNADLNIRVLLDAGFTNELVONTWWSKKNIK
QY	721	FVVTDDGGITRVYPKEAGENMOENPETEYDSFYKRSLDNNDNYVTAPYFNKSGPGA
Dd	721	FVVTDDGGITRVYPKEAGENMOENPETEYDSFYKRSLDNNDNYVTAPYFNKSGPGA
QY	781	MYSKAVEIYIQGLLKPAVGIGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDV
Dd	781	MYSKAVEIYIQGLLKPAVGIGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDV
QY	841	LDDCGFLMANHDDYTQIGRFGEIDPSLMRHLVNISVAFNKSVDYQSVCPEPG
Dd	841	LDDCGFLMANHDDYTQIGRFGEIDPSLMRHLVNISVAFNKSVDYQSVCPEPG
QY	901	GAGHSAYVPSVADIQLIGMWATAAASILLQQFLLSLTFPRLEAVEMEDDDFTA
Dd	901	GAGHSAYVPSVADIQLIGMWATAAANSILLQQFLLSLTFPRLEAVEMEDDDFTA
QY	961	SCITEQTQYFFDNDKSFSGVLDGCNGSRIFHGHEKLMNTNLIFIMVESKGTCTCPD
Dd	961	SCITEQTQYFFDNDKSFSGVLDGCNGSRIFHGHEKLMNTNLIFIMVESKGTCTCPD
RESULT 2		
CIC2 RAT		STANDARD; PRT; 1091 AA.
ID	CIC2 RAT	
AC	P54290;	
DT	01-OCT-1996 (Rel. 34, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.	
DE	GN	CACNA2D1 OR CACNL2A OR CCHL2A.
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ra	
NCBI TaxID=10116;	[1]	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=92228762; PubMed=1314383;	
RA	Kim H.L., Kim H., Lee P., King R.G., Chin H.;	
RT	"Rat brain expresses an alternatively spliced form of the dihydropyridine-sensitive L-type calcium channel alpha 2 subunit Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).	
RL	-!- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R	
CC	-!- EXCITATION-CONTRACTION COUPLING.	
CC	-!- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU	
CC	ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS	
CC	HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).	
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.	
CC	-!- ALTERNATIVE PRODUCTS:	
CC	Event=Alternative splicing; Named isoforms=1;	
CC	Comment=2 isoforms are produced;	
CC	Name=1;	
CC	IsoId=P54290-1; Sequence=Displayed;	
CC	-!- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE	
CC	A PRECURSOR FORM (BY SIMILARITY).	
CC	-!- SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.	
CC	-!- SIMILARITY: Contains 1 VMFA domain.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a col.	
CC	between the Swiss Institute of Bioinformatics and the EMBL ou	
CC	the European Bioinformatics Institute. There are no restriction	
CC	use by non-profit institutions as long as its content is i	
CC	modified and this statement is not removed. Usage by and for	
CC	entities requires a license agreement (see http://www.isb-sib.ch	

51 2004

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38.1; --

Cache.

VWF A.

; 1.

1.

FA; 1.

membrane; Ion transport; Voltage-gated channel;

coprotein; Phosphorylation; Signal;

POTENTIAL.

L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT

(BY SIMILARITY).

L-TYPE CALCIUM CHANNEL DELTA SUBUNIT

(BY SIMILARITY).

POTENTIAL.

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POTENTIAL.

POTENTIAL.

96.2%; Score 5145; DB 1; Length 1091;

Y 95.8%; Pred. No. 3.8e-300; Indels 2; Gaps 2;

rative 22; Mismatches 19; Indels 2; Gaps 2;

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

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LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

LTLTLFQSLALGPSSPPPSAVTIKSWVDQMDLVTLAKTASGVNQLVDI 60

51-975; 992-1000 AND 1033-1050.
 535; PubMed=2168391;
 Warner C., Catterall W.A.;
 purified calcium channels. Alpha 2 and delta are encoded
 inge.;
 . 265:14738-14741(1990).
 CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
 N-CONTRACTION COUPLING.
 THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:
 ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
 IERS THAT ARE DISULFIDE-LINKED.
 AR LOCATION: Integral membrane protein.
 RE PRODUCTS:
 ernative splicing; Named isoforms=1;
 =2 isoforms are produced;
 13806-1; Sequence=Displayed;
 ICIFICITY: Skeletal muscle.
 A-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM
 OR FORM.
 f: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
 f: Contains 1 VWFA domain.

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 profit institutions as long as its content is in no way
 this statement is not removed. Usage by and for commercial
 ices a license agreement (See <http://www.isb-sib.ch/announce/>
 ail to license@isb-sib.ch).

 AAA81562.1; -;
 ZHRBA2.
 004010; Cache.
 002035; VWF_A.
 ; Cache; 1.
 ; vwa; 1.
 7; VWFA; 1.
 234; VWFA; 1.
 al; Transmembrane; Ion transport; Voltage-gated channel;
 al; Glycoprotein; Phosphorylation; signal;
 plicing.
 1 26
 27 960
 51 1106
 18 471
 21 945
 32 1101
 35 432
 34 94
 38 138
 36 186
 26 326
 50 350
 77 477
 36 606
 15 615
 78 678
 34 784
 27 827
 31 891
 98 898
 88 988
 01 1001
 03 503
 48 848
 06 AA; 125042 MW, B00DE7F3C877B618 CRC64;
 96.0%; Score 5132.5; DB 1; Length 1106;
 arity 94.7%; Pred. No. 2.2e-299;
 onservative 14; Mismatches 12; Indels 29; Gaps 4;
 CLALTLTLFQS--LLIGPSEPPPSAVTIKSWDKQEDLVTLAKTASGVQLV 58

Db 1 MAAGRPLAWTLTLQAWLILIGPSEPPPSAVTIKSWDKQEDLVTLAKTASGV
 Qy 59 DIYEKYQDLTYTFEPNNARQVETAAARDIEKLLSNRSKALVSLALEAKVQAAHQR
 Db 61 DIYEKYQDLTYTFEPNNARQVETAAARDIEKLLSNRSKALVSLALEAKVQAAHQR
 Qy 119 SNEVYVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGROIISYQHAHVHPTDIYE
 Db 121 SNEVYVYNAKDDLPKNDSEPGSQRIKPVFIEDANFGROIISYQHAHVHPTDIYE
 Qy 179 VLNELNWTSSALDEVFKKREEDPSLLWQVFGSATGLARYYPASPWVDSNSTPKKID
 Db 181 VLNELNWTSSALDEVFKKREEDPSLLWQVFGSATGLARYYPASPWVDSNSTPKKID
 Qy 239 RREPWTYOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASE
 Db 241 RREPWTYOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASE
 Qy 299 QDVSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLINYNVSRANC
 Db 301 QDVSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLINYNVSRANC
 Qy 359 MLFTDGGEEARAQEIFKNKNDKKVRFRFSVGQHYNTGERGPIQWMAENKGYTYEIP
 Db 361 MLFTDGGEEARAQEIFAKYNKDKKVRFTFSVGQHYNTDRGPIQWMAENKGYTYEIP
 Qy 419 IRINTQBYLDVLRPMVLADGKAKQVQNTVNYLDLDELGLVITGLTPVFNITQOFE
 Db 421 IRINTQBYLDVLRPMVLADGKAKQVQNTVNYLDLDELGLVITGLTPVFNITQOFE
 Qy 479 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYYPFADPNPGYVLLHPNLQPK ----
 Db 481 LKNQLILGVMGVDVSLIEDIKRLTPRTFLCPNGYYPFADPNPGYVLLHPNLQPKPIGV
 Qy 531 -----NEKQEPVTLDFDAELENDEIKVEIRNKMIDGESGEKTRTLVKS
 Db 541 INLRKRPNVONPKSQSPVTLDFDAELENDEIKVEIRNKMIDGESGEKTRTLVKS
 Qy 580 YIDKGNRTYTWTPVNGTDY-SLALVLPYTSFYIKAKLEETITQARSKKGKMDSE
 Db 601 YIDKGNRTYTWTPVNGTDYSSALVLPYTSFYIKAKLEETITQARY-----SE
 Qy 639 DNFEESGYTFIAPRDYCNLDKISDNNTEFLINPNEFIDRKTNNPNSCNADLINRVL
 Db 654 DNFEESGYTFIAPRDYCSLDKPSDNNTEFLINPNEFIDRKTNNPNSCNTDLINRVL
 Qy 699 FTNELVQNYWSKQNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKR
 Db 714 FTNELVQNYWSKQNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKR
 Qy 759 DNTVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFT
 Db 774 DNTVFTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFT
 Qy 819 RDCAGPVCCKNSVDMDCVILDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHL
 Db 834 RDCAGPVCCKNSVDMDCVILDDGGFLMANHDDYTNOIGRPFGEIDPSLMRHL
 Qy 879 VYAFNKSVDYQSVCEPCAPKQAGHRSVVPVADILQIGWATAAASILQOFL
 Db 894 VYAFNKSVDYQSVCEPCAPKQAGHRSVVPVADILQIGWATAAASILQOFL
 Qy 939 FPRLLAEVEMDDDDFTASLSKQSCITEQTQYFFDNDKSKPSGVLDCGNCGRIFHGEI
 Db 954 FPRLLAEVEMDDDDFTASLSKQSCITEQTQYFFDNDKSKPSGVLDCGNCGRIFHGEI
 Qy 999 TNLIFIMVESKGTGTCPCDTRL 1018
 Db 1014 TNLIFIMVESKGTGTCPCDTRL 1033

RESULT 4

STANDARD; PRT; 1249 AA.
P34373;
el. 28, Created)
el. 42, Last sequence update)
el. 42, Last annotation update)
el. 42, Last annotation update) (Uncoordinated
precursor (Uncordinated
channel unc-36 precursor
calcium channel

-72 OR C50C3.9/C50C3.10/C50C3.11.
C. elegans.
Chromadorea; Rhabditida; Rhabditoidea;
Peloderinae; Caenorhabdittis.
339;

N.A.
1 N2;
PubMed=7906398;
nsough R., Anderson K., Baynes C., Berks M., Coulson A.,
Burton J., Connell M., Copsey T., Cooper J., Fraser A., M.,
Pear S., Du Z., Durbin R., Favello A., Frazer A., Jier M.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Jones M., Kerhaw J., Kirsten J., Laister N.,
Lightning J., Lloyd C., Mortimore B., O'Callaghan M., R.,
Percey C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
Thompson N., Smith A., Smith M., Sonhammer E., Staden K.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Watson A., Weinstock L., Wilkinson-Sproat J.,
contiguous nucleotide sequence from chromosome III of *C.*

2-38(1994).

iov-2002) to the EMBL/GenBank/DDBJ databases.

NOV TISSUE SPECIFICITY.

295; Sanchez B.M., Kenyon C.J.;
cting sensitivity to serotonin in *Caenorhabditis elegans*.";
3-1219-1230(1996).
N.N: May act as an auxiliary subunit of the UNC-2 voltage-
calcium channel which appears to trigger calcium-activated
g pathways that control the serotonin response. Inhibiting
in sensitivity of the vulval muscles results in egg laying
. May act in both neurons and muscle cells to enhance motor
Y.

SPECIFICITY: Descendants of the cells AB and AB.p (that give
nearly all nonpharyngeal neurons), descendants of p1 (that
se to body muscle) and cell lineages that give rise to the
and juvenile motor neurons.

SPECIFICITY: Contains 1 VWFA domain.

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email to license@isb-sib.ch).

333; AAA27971.3; --
7; S44617.
250C3.9; CE32168.
IPR004010; Cache.
IPR002035; VWF_A.
2743; Cache: 1.
00927; vwa; 1.
00327; VWA; 1.
P050234; VWFA; 1.
Ionic channel; Ion transport; Voltage-gated channel;
channel; Signal; Glycoprotein.
19
POTENTIAL.

[illegible]

STANDARD; PRT; 886 AA.

el. 36, Created)

el. 36, Last sequence update)
el. 41, Last annotation update)

ypsin inhibitor heavy chain H3 precursor (ITI heavy er-alpha-inhibitor heavy chain 3) (HC3).

iratus (Golden hamster).

azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Rodentia; Sciurognathi; Muridae; Cricetinae;

36.

Y.A.

38: PubMed=9276673:

Yuzuki Y., Yamamoto T., Sinohara H.;
Cloning and sequencing of cDNAs encoding three heavy-chain
of the inter-alpha-trypsin inhibitor in Syrian hamster;
for the evolution of the inter-alpha-trypsin inhibitor
family.";
2:71-82(1997).

-50; 446-472 AND 504-523, AND SUBUNITS.

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!1; PubMed=8864857;
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umamoto K., Sinohara H.;
trypsin inhibitor and its related proteins in Syrian

and plasma.¹¹

TEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, HOSE ON CELL SURFACES IN TISSUES TO REGULATE THE 'N, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE 'O CELLS UNDERGOING BIOLOGICAL PROCESSES (BY

ALPHA-I PLASMA PROTEINASE INHIBITORS ARE ASSEMBLED FROM HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, TER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2, I, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND ID, P-TER-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUTIN. CHAINS ARE INTERLINKED WITH BIKUTIN VIA A CHONDROITIN RIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY

BELONGS TO THE ITIH FAMILY.

Contains 1 VWFA domain.

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 1 to license@isb-sib.ch).

AA13940.1; -.

DR	InterPro; IPR006587; VIT.				
DR	InterPro; IPR002035; VWF_A.				
DR	Pfam; PF00992; vwa; 1.				
DR	SMART; SM00609; VIT; 1.				
DR	SMART; SM00327; VWA; 1.				
DR	PROSITE; PS05234; VWFA; 1.				
KW	Serine protease inhibitor; Repeat;				
KW	Multigene family;				
KW	Glycoprotein.	1	18		
FT	SIGNAL	19	30	POTENTIAL.	
FT	PROPEP	31	646	BY SIMILARITY.	
FT	CHAIN			INTER-ALPHA-TRYPSIN INHIBITOR HEAVY C	
FT				H3.	
FT	PROPEP	647	886	BY SIMILARITY.	
FT	DOMAIN	279	439	VWFA.	
FT	CARBHYD	88	88	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBHYD	577	577	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	BINDING	646	646	CHONDROITIN 4-SULFATE, CROSS-LINK SIT	
FT				(BY SIMILARITY).	
SQ	SEQUENCE	886 AA;	99018 MW;	AC0594C6852576B8 CRC64;	

Query Match 3.1%; Score 164.5; DB 1; Length 886;
Best Local Similarity 23.2%; Pred. No. 0.033;
Matches 66; Conservative 56; Mismatches 112; Indels 51; Ga

QY	202	SLLWQVFSATGLARYYPASPWVDSRT--PKKID-----LYDVRR--PWYIQ	
DB	208	SALTKSFGKKGHVSFKPS---LQQRSCPTCTSLLNGDFTIYVDVNRSGFNQV	
QY	249	-----ASPDKMLLDVSGSVSGLTKLRTSVSEMLETSLDSDDFVNVAS	
DB	265	YFVHFFAPQGLPVVPKNVFIIDISGWAGRKICQTRVALLKIILDMKQDDYILFIL	
QY	297	NAQDVSCQHLVQANVRNKKVLKDAVNNITAKGIDTYKKGSFAPEOLLN---YNV	
DB	325	GV--TTWKDSLQVQATPANLEEARTFVRSISDQGMTNINDGLLGRIMLTQAREQHTV	
QY	353	NCNKIIMLFTDG----GEERAQBITFNKYNDKKVRFVSVG--OHNYERGPIQWAC	
DB	393	STSIIML--TUGDANTGESRPEKIQENVRKAIEGRFLYINLFGFNINYNFLETMAL	
QY	408	GYYEYIISGAIIRINTQBYLDVLGRPMVLAGDKAKAQVQNTNYILD 452	
DB	442	GVARRIYEDSDANILQCGFYEEVANPLL-----TNVEV 475	

RESULT 9

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ail to license@isb-sib.ch).

CA073475.1; -
ITGO.
006172; DNA_pol_B.
006134; DNA_pol_B_dom.
006133; DNA_pol_B_exo.
003586; Hedgehog_hintC.
003587; Hedgehog_hintN.
006141; Intein.
006142; Intein.
004042; Intein_endonuc.
004578; Pol2.
; DNA_pol_B; 4.
; DNA_pol_B_exo; 1.
; HintC; 3.
; HintN; 3.
; POLBc; 1.
001443; intein_Cterm; 3.
001445; intein_Nterm; 3.
000592; Pol2; 2.
16; DNA_POLYMERASE_B; FALSE_NEG.
18; Intein_C TER; 3.
19; Intein_ENDONUCLEASE; 2.
17; Intein_N TER; 3.
NA-directed DNA polymerase; DNA replication;
hydrolyase; Endonuclease; Autocatalytic cleavage;
ng.
1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).
0 769 INTEIN I.
0 855 DNA POLYMERASE, 2ND PART (POTENTIAL).
6 1392 INTEIN II.
3 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).
2 1598 INTEIN III.
9 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).
9 AA; 211875 MW; A113A8BC57EB9C83 CRC64;
3.0%; Score 161; DB 1; Length 1829;
rity 20.1%; Pred.No. 0.16;
nservative 101; Mismatches 301; Indels 282; Gaps 39;
PSSEPPPS-----AVTISWV-----DKMOEDLVTLA 48
RDKEHPKPIHRMGDSFAVEIKRIHFDLPVVRRTINLPTTYLEAVYVGLKT 288
VNQLVDIYKYQDL-----YTFEPNARQLVEIAARDIEKLLSNRSKALVSLALE 103
ABETAIAWETESMKKLAQYSME--DARATYEL-----GREFFPMNEAE 334
AAHQWREFPAS--NEWVY-----NAKDDLDPEKNDSEPGSQRIKPVFI----- 150
GQSVWDVSRSTGNLVYLLRVAVERNELAPNPEDEEYRRURRTYLGIVYKE 394
GRQISYQHAHVHPTD-----IYEGSTIV-----INELNMTSALDEVFKKNREDPSL 203
WENTAYLDFRCH-PADTKVIVKGGIVNISDVKEGDIYLGIDG----- 441
GSATGLARYYPASPDWNSR---TPN-KIDLYDVRPWPYIQAASPKDMLILDV 259
-RVKKWKYHYEGKLINGLKLCTPNHKVPVVTENDRQTRI-----RDSLAKSF 491
SGLTLKLIRTSVSEMLETLSDDDDFVNVASFNSN----- 297
KG---KIITTKL-----FEKAEPKPNPSEELKGBLSGIIIAEGTL 537
SCF-----OHLVQANV-RNKKVLKDAV-----NNITAKG----- 329

Db 538 LRKDIIEFDSSRGKRIHQYVEITIGENEKELLERILYIFDKLFGIRPSVKKKG
Qy 330 --ITDYKKGFSFAFEQLLNVSFRANCKIIMLFTDGGERAQEI FNKYNKDKKVR
Db 598 LKITTAKAVYLOIEELK-NIESLYAPAVLRGF-----FERDATVN
Qy 388 SV-----GQHYRERGPIQWMACENKGY---YYEIPSIGAIRINTQEVLDVLRPMVL
Db 643 TIVVTQGTNNKWKIDIVAKLLDSIGIPYSRYEYKIENGKELTKHILEITGRD---
Qy 441 AKQVQWTVNYLDALEGLVITGLPVFNITQGF-----NKTNLKNQLILGV
Db 696 -----GLILFQTLVGFISSERKNEALEKALEVREMNRKKNNSFYNL
Qy 492 VSLEDIKRLTPFTLCPNGYVFAIDPNGVYLLHPNLPQKNPKSQEPVTLDFLDAEL
Db 740 VSSEYKGEVYDITLGNPYFA--NG-ILTHNSLYPSIIVTHN-VSPDTLRE-
Qy 552 KVEIRNMIDGESGKTFRTLVKSODERYIDKGNRTYTTVPVNGTIDYSLALVLPY.
Db 790 -----GCKNVDAPIVG--YKFCCKDFPG-
Qy 612 IKAKLEETITQARSKKGKMDSETLKPDPNPEESGY-----TFIAPRDYCNDL
Db 812 IPSILGELITMROEIKKKMK--ATIDPIEKOMLDYRQRAVKLLANSILPNW---L
Qy 663 NNTFELNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKOKNIKGVK
Db 867 NGBVKFKIGERIDRYMESQKQKRVTVNDTEVLEVDNIFAFSLNKSKEIKKVK
Qy 723 VTDGGITRVYKGEAGE 738
Db 925 -----IRHKYKGEAYE 935
RESULT 10
ATX1_PLAFA STANDARD; PRT; 1956 AA.
AC Q04956;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T9/96;
RX MEDLINE=93132070; PubMed=8421054;
RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,
RA Robson K.J.;
RT "A family of cation ATPase-like molecules from Plasmodium
falciparum";
RL J. Cell Biol. 120:385-398(1993).
CC -- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
CC -- SUBCELLULAR LOCATION: Integral membrane protein.
CC -- SIMILARITY: Belongs to the cation transport ATPases family (P-
ATPases). Subfamily V.
CC
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entitities requires a license agreement (See <http://www.isb-sib.ch/a>
or send an email to license@isb-sib.ch).
CC
CC EMBL; X65738; CAA46646.1; -
DR InterPro; IPR001757; ATPase_E1-E2.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 7.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.

234; VMFA; 1.
protein; Complete proteome.
16 394 VMFA.
5 AA; 63634 MW; 7BB6A1A77A2BE111 CRC64;
arity 2.9%; Score 157.5; DB 1; Length 575;
conservative 93; Mismatches 206; Indels 105; Gaps 25;
ARQLVEIAARDIEKLNSRKALVSLALEAEKVOAAHQWREDFASNEVYNAKDD 130
KESQOQPSPTTEQVLAQAQAAIK---EAEQSA---AKALAAQVEVQVSDKQA 75
KND-----SEPGSRIKPVFTEDANFGRIQSYQHAA---VHIPTDI 172
LOEAPTFAAAKAKATHIANPGTARYQQF---DDNPVKVAQNPLATFSLDVTGTS 132
TIVLINE-----LNWTSALDEVFKKNEEDPSLLWQVGSATGLARYY 218
RRFLNQGLPPDPDAVRVEEIVNYPSPWDI---KDKQIPASKPIPFAMRYELA--- 187
WVNSRTPNKIDLVDRRRPFWYIQGAASPKIMLILVDVSGS-VSLGLTKLIRTSVS 277
W-NEQRTLLKVDILAKDKSEELPAS---NLVFLITDSGMSISDERLPLIQSLK 241
TISDDDFVNVASFNSNAQVSCFHLVQAVNRNKKVLKDAVNNITAKGITYKKGF 337
ELREQDNIAVTYAGDSRIA-----LPSISGSHKAEINAAIDSLDARGSTNGGAGL 296
EQILNVNVRANCNKIMLFTDG-----GEERAQEIFNKVYKDKKVRVFRFVSQ 391
QOATK-GFIKGGINR-ILLATDGFNVGIDDPKSIEMSVKQRESGVTLSTFGVGN 354
RGIQWACNKGYYEIPISGAIRINTOBYLDVLRPMVL---AGDKAKQVQ--- 445
ZAMVRIADVGNYSYIDTLS-----EAQVLSNEMEQMLITVAKDVKAQIEFNP 410
LDLALGLGLVITGLPVNTGTGFENKTNKQNLILQWGVQV-VSLEDI---KRLT 501
---ROIG-----YE-----KQLRVEHFNNVDVADGIDGAGKHIT 447
JCPNGYFAIDPNGYVLLHNPLOPKPKSOE 536
JLNGQKASIDKLRYA---PDNKLAKSDKTKE 480
STANDARD; PRT; 946 AA.
; Q15484;
rel. 17, Created
rel. 17, last sequence update
rel. 42, last annotation update
Trypsin inhibitor heavy chain H2 precursor (ITI heavy
inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin
inhibitor component II) (Serum-derived hyaluronan-associated
protein 2).
[Human].
[Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Primates; Catarrhini; Hominidae; Homo.
[6];
N.A., AND PARTIAL SEQUENCE.
[37]; PubMed=2450046;
[Threimüller T., Hochstrasser K., Wachter E.,
DNA and derived amino acid sequence of the precursor
three protein components of the inter-alpha-trypsin
inhibitor.];
[63-67(1988)].
[4-865 FROM N.A.
[76; PubMed=2446322;
[14-865 FROM N.A.
[76; PubMed=2446322;

Salier J.-P., Diarra-Mehrpour M., Seeboue R., Bourguignon J.,
Benarous R., Ohkubo I., Kurachi S., Kurachi K., Martin J.P.,
"Isolation and characterization of cDNAs encoding the heavy chain
human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous
evidence for multipolypeptide chain structure of I alpha TI.";
Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
[3]
SEQUENCE OF 384-766 FROM N.A.
MEDLINE=89076497; PubMed=2462430;
Salier J.-P., Diarra-Mehrpour M., Seeboue R., Bourguignon J.,
Martin J.P.;
"Human inter-alpha-trypsin inhibitor. Isolation and characterizat
of heavy (H) chain cDNA clones coding for a 383 amino-acid sequen
of the H chain.";
Biol. Chem. Hoppe-Seyler 369:15-18(1988).
[4]
PARTIAL SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=89024442; PubMed=3663330;
Schreitmüller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
Gebhard W.;
"cDNA cloning of human inter-alpha-trypsin inhibitor discloses th
different proteins.";
Biol. Chem. Hoppe-Seyler 368:963-970(1987).
[5]
SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
MEDLINE=89380192; PubMed=2476436;
Engel J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
"Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
Polypeptide chain stoichiometry and assembly by glycan.";
J. Biol. Chem. 264:15975-15981(1989).
[6]
SEQUENCE OF 55-64.
TISSUE=Plasma;
MEDLINE=93039735; PubMed=1384548;
Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,
Tartar A., Fournet B., Mizon J.;
"The heavy chains of human plasma inter-alpha-trypsin inhibitor:
isolation, their identification by electrophoresis and partial
sequencing. Differential reactivity with concanavalin A.";
Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
[7]
SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND
CARBOHYDRATE-LINKAGE SITES THR-691.
MEDLINE=93232026; PubMed=7682553;
Engel J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
Pizzo S.V., Hefta S.A.;
"Presence of the protein-glycosaminoglycan-protein covalent cross-
in the inter-alpha-inhibitor-related proteinase inhibitor heavy c
2/bikunin.";
J. Biol. Chem. 268:8711-8716(1993).
[8]
SEQUENCE OF 67-101, AND HYALURONAN BINDING.
TISSUE=Serum;
MEDLINE=94075371; PubMed=7504674;
Huang L., Yoneda M., Kimata K.;
"A serum-derived hyaluronan-associated protein (SHAP) is the heavy
chain of the inter-alpha-trypsin inhibitor.";
J. Biol. Chem. 268:26725-26730(1993).
[9]
SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE
TISSUE=Plasma;
MEDLINE=94229087; PubMed=7513643;
Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,
Michalski C., Fournet B., Mizon J.;
"Chondroitin sulphate covalently cross-links the three polypeptide
chains of inter-alpha-trypsin inhibitor.";
Eur. J. Biochem. 221:881-888(1994).
[10]
CARBOHYDRATE-LINKAGE SITES, AND MASS SPECTROMETRY.
MEDLINE=98343966; PubMed=9677337;
Flahaut C., Capon C., Balduyck M., Ricart G., Sautiere P., Mizon J

N.A.
487; PubMed=2204031;
lund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
poff M.R., Kurazona H., Binz T., Niemann H., Gill D.M.,
sequence of Clostridium botulinum C1 neurotoxin.";
Res. 18:4924-4924 (1990).

N.A.
Stockholm / C-ST;
998; PubMed=2222445;
jii N., Tuzuki K., Murakami T., Indoh T.,
Takeshi K., Syuto B., Oguma K.;
nucleotide sequence of the gene coding for botulinum
in the C-ST phage genome.";
hys. Res. Commun. 171:1304-1311 (1990).

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Stockholm / C-ST;
072; PubMed=2450068;
Okosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
t of a monoclonal antibody recognizing an antigenic site
stridium botulinum type B, C1, D, and E toxins and
.";
. 56:898-902 (1988).

N OF SUBSTRATE.
966; PubMed=7901002;
man E.R., Yamaseki S., Binz T., Niemann H., Jahn R.;
rotoxin C1 blocks neurotransmitter release by means of
l/syntaxin.";
21-4828 (1993).

BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CASE THAT CLEAVES SYNTAXIN.
ACTIVITY: Limited hydrolysis of proteins of the
toxis apparatus, synaptobrevins, SNAP25 or syntaxin. No
action on small molecule substrates.
Binds 1 zinc ion per subunit (by similarity).
DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
IN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
N- AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL
AND TOXIN BINDING, RESPECTIVELY.
AR LOCATION: Secreted.
30US: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF
NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.
30US: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
PAGE.
/: BELONGS TO PEPTIDASE FAMILY M27.

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CAA47060.1; -
CAA51313.1; -
CAA37780.1; -
BAA14235.1; -
CAA44263.1; -
3BTA.
12; -
00395; Bontoxilysin.
06025; Zn_MTPeptide.
Peptidase_M27, 1.

DR PRINTS; PRO0760; BONTOKILYSIN.
DR ProDom: PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT INIT_MET 0
FT CHAIN 0 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN
FT CHAIN 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN
FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 229 229 BY SIMILARITY.
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 436 452 INTERCHAIN (PROBABLE).
FT CONFLICT 84 84 P -> T (IN REF. 2).
SQ SEQUENCE 1290 AA; 148734 MW; 71PBE379F97129E8 CRC64;

Query Match 2.8%; Score 152; DB 1; Length 1290;
Best Local Similarity 20.3%; Pred. No. 0.32; Indels 334; G
Matches 205; Conservative 125; Mismatches 346;

QY 106 KQAAHQRREDFASNEVVYNAKDDLDPEKNDSEPGSQRIK---PVFIEDANFGR-
DB 138 KTRQGNWVKTSINPSVIITG---PRENIIDPETSTFKLTNTNTFAAQEGFAL
QY 158 -----QISYQHAHVHIPTDIYEGS-----TIVLNLNWTSLDVEFK---
DB 193 ISPRFMLTYSNAT---NDVGEGRFSKSEFCMDPILILMHELN---HAMHNLGLAI
QY 199 EDPSLLWQVFGSATGLARYYP---ASPWVDNSRTPNKIDLYDVRPRPWYIOGAA
DB 247 TISSTVSNIFYQNVNKLVAEIVAGGPID--LIPKSARKYFEKALDYRSIA
QY 254 MLILVDVG---SVSGTLTKLR-----TSVSEMLETSLDDDFVNVVASFNSNAQD
DB 305 SITTANPSSFNKYGKYLKIRYFVVSSEGEV--TVNRKFFVEL--YNELTQI
QY 305 QHLVQANVRKKV-LKDAVNNITAK-----CITYKKGFSFAPEQL---LNNVNSR
DB 361 NYAKIYNQVRKYLNSVYTPVTANTILDNDVYDIQNGFNIPKSNLNVLFMGQNLSE
QY 352 --ANCKNIIMLFT-----DGGEERAQEIFNK-----YKND-----KKV
DB 421 RKNYPENMLYLFYKFKCHKAIDG-----RSLYKNTLDCRELLVKNVTDLPFGDISDV
QY 387 FSVQGHNYERGPQWMAKENKGYEIPISGAIRI--NTQY--LDVL-----
DB 476 FLRKDINEETEVI-----YYPDNVSDQVILSKNTSEHQDLLYPSIDSES
QY 431 GRPMWLAGKAKQOVQWVN--VYLDALGLGIVTGLTPVFNITQGFENKTN-----
DB 527 GENQVFDNRQNVYDLYNSYYLESQKL-----SDNVEDEFTFTRSI EALDNSAKVY
QY 479 -LKNQILGVMG-----VDVSLEDIKRLTPFTLCPNGYYPFADIPNGYVLLHPN
DB 583 TLANKVNAVQGGFLMWANDVVEDEFTNLKOTLDKISDVSAILP-----YIGPA
QY 531 NPKSQBPVTLDF-----LDALENDI-----KVEIRNMIDGSESEKTI
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QY 573 VKSQDERYIDKGNRTVTM-----TPVNGTDYSLALVLPYTSFYIKAKLEE
DB 693 LEQRIKRWKD-----SYEMMGVTWLSRIITQFNINISYQMYDSL-NYQAGAKAKID--
QY 623 ARSKGKMKDSETLKP--DNFESGYTFIAPRDYCNLDKISDNNTFELNFEFFI--
DB 743 LEYKYSGSDKENIKSQVENLKN-----LDVKIS-----EAMNINKFIRI
QY 676 -----DRKTPNPNPCNADLINRVLLDA-----
DB 788 TYLFKNMLPKVIDELNEFDRNT-----KAKLIN--LIDSHNIIIVGEVDKLKAKVA
QY 698 -----GFTN-----ELVQNYM-----SKQNKIKGVKARFVVTGGGITRVYPK
DB 840 QNTIPNIFSYTNNLLKDIINEYFNINNINDSKILSLQNRKNTLVDTSG-----YNAI

ENPTYEDSFYKRLDNDNYVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLIK 796
 LNP-----IF--PFPKLGSSGSDRGKIVITQNEIVNYSWYE 935
 IKIDVNSWIENTFTKSTRDPCAGVCDCKRNSVDWCVIDLDGQFLMANHD--- 853
 FWIRINKVSNLPGYTIID-----SVKNSSGMSIGIISNFIIVFTLKQNEDESEQ 988
 -DYNTOIGR-----FFGBIDPSLRHRLVNIISVYAFNKSVDYQSVCE 893
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 sl. 35, last sequence update)
 sl. 41, last annotation update)
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 sp. (strain PCC 6803).
 bacteria; Chroococcales; Synechocystis.
 3;
 3 A.
 29; PubMed=8590279;
 aka A., Sato S., Korani H., Sazuka T., Miyajima N.,
 ata S.;
 /sis of the genome of the unicellular cyanobacterium
 sp. strain PCC6803. I. Sequence features in the 1 Mb
 positions 64% to 92% of the genome.";
 .166(1995).
 : TO E. COLI YFBK.
 : Contains 1 VWFA domain.
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 : las Institute of Bioinformatics and the EMBL outstation -
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 : l to license@sib-sib.ch).
 :
 :AA10635.1; -
 :6691.
 :2035; VWFA.
 :vwa; 1.
 :4; VWFA; 1.
 :rotein; Complete proteome.
 : 215
 : VWFA.
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 :LVDVSGSGGLTKLIRTSVEMLETLSDDFNVNVSNAQDVSCFQHLVQA 310
 :NLDHSGSDGQPLETVKSAALGLIDRLBEDRLSVIAFDRAKIV-----IENQ 95
 :VLKDAVNNTAKGITDYKKGFSFAPEQLNLYNVSRAKCNKLIIMLTDCGEERAQ 370
 :AIKAIERLKAEGGTADIEGLXGLQEAAGKEDRV-----HIFLLTDGENEHD 152
 :FNKYNKDKVVRFSVQGHYRGPQIOMACENK---YYEIPISGAIKINTQ 424
 :LGTVASDYKLTVHTLIGFDH-WNQDVLEAIAASAGSLSYIENPS-EALHTFRQ 210
 :GRPWVLADKAKQVQWTVNYLDALGL-----LVITGTLFVNITGQFENKTNLK 480

211 LE-----QRMNVGITNAHL-LLELAPOAHAI--VKPVAQVSPETMDL;
 481 NQLILGVGVDSLEIDIKRLTRFTLCNPGYFFAIDPNGYVLLHNPLOKPKSQE-
 255 NQGAIEERVLGSLMTDQBRV-----LLNLVLDQLLPQGHVIGQVIRYDDPASGQJ
 537 ---PVTIDELDALENDIKVEIRNKMDIGSEKGT--PRTLKVSQDERYIDKGRK
 310 SDPLPLTIQ-VQTQVQSTDVQVQESILTLAKYRQTAETKLKAGDRQGAATMLQJ
 591 TPVNGTDSYSLALVLPYTFYIKAKLEETITQARSKKGKMDSETLKP 638
 369 TALQMGDKNGATILQTN-----TRLQSGEDLSEGRDKKTRMVKSTTLQ 413
 RESULT 15
 ITH4 PIG
 ID ITH4 PIG STANDARD; PRT; 921 AA.
 AC P79263;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy
 DE chain H4) (inter-alpha-inhibitor heavy chain 4) (inter-alpha-tryps
 DE inhibitor family heavy chain-related protein) (IHRP) (Major acute
 DE phase protein) (MAP).
 GN ITH4 OR IHRP.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.
 RC TISSUB=Liver;
 RX MEDLINE=96271024; PubMed=8830057;
 RA Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,
 RA Ozawa A., Yasue H., Tomita M.;
 RT "Primary structure of the pig homologue of human IHRP: inter-alpha
 RT trypsin inhibitor family heavy chain-related protein.";
 RL J. Biochem. 119:577-584(1996).
 RN [2]
 RP PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
 RC TISSUB=Liver;
 RX MEDLINE=90371455; PubMed=1697703;
 RA Buchman T.G., Cabin D.B., Vickers S., Deutschman C.S., Delgado E.,
 RA Sussman M.M., Bulkley G.B.;
 RT "Molecular biology of circulatory shock. Part II. Expression of fo
 RT groups of hepatic genes is enhanced after resuscitation from
 RT cardiogenic shock.";
 RL Surgery 108:559-566(1990).
 RN [3]
 RP SEQUENCE OF 28-54 AND 223-240.
 RC TISSUB=Serum;
 RX MEDLINE=96013138; PubMed=7556597;
 RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A.,
 RA Garcia-Gil A., Lampreave F., Pineiro A.;
 RT "The major acute phase serum protein in pigs is homologous to humar
 RT plasma kallikrein sensitive PK-120.";
 RL FEBS Lett. 371:227-230(1995).
 CC -1- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
 CC -1- TISSUE SPECIFICITY: Liver-specific.
 CC -1- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
 CC SHOCK.
 CC -1- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).
 CC -1- PTM: CLEAVED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA
 CC FRAGMENTS.
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: Contains 1 VWFA domain.
 CC -1- CAUTION: REF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTI
 CC SEQUENCING ERRORS.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collat

Swiss Institute of Bioinformatics and the EMBL outstation -
Bioinformatics Institute. There are no restrictions on its
profit institutions as long as its content is in no way
this statement is not removed. Usage by and for commercial
ires a license agreement (See <http://www.ieb-sib.ch/announce/>
ail to license@sib-sib.ch).

AD00024.1; -;
AAB46821.1; -;
-; NOT ANNOTATED_CDS.
JC4625.

006587; VIT.

002035; VWF_A.

; vwa; 1.

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Db 631 SRLTGGSSVD-----PVFS-----HRRGWKGQAQ-----GFEEK
Qy 648 FIAPR 652
Db 662 -LPPR 665

Search completed: February 20, 2004, 16:56:08
Job time : 24.1043 secs

1 27
28 921 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
H4.

70 428 VWF.

30 80 N-LINKED (GLCNAC. . .) (POTENTIAL).

05 205 N-LINKED (GLCNAC. . .) (POTENTIAL).

12 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

13 513 N-LINKED (GLCNAC. . .) (POTENTIAL).

77 577 N-LINKED (GLCNAC. . .) (POTENTIAL).

19 50 HT -> SK (IN REF. 3).

13 703 D -> H (IN REF. 1; AA SEQUENCE).

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2.8%; Score 150.5; DB 1; Length 921;

urity 19.9%; Pred.No.0.24;

nservative 100; Mismatches 264; Indels 265; Gaps 36;

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-----YY-----YEIPSGAIRINTQEYLDVL--GR 432

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10-090-827-13
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the number of results predicted by chance to have a
than or equal to the score of the result being printed,
l by analysis of the total score distribution.

SUMMARIES

Y	h	Length	DB	ID	Description
0	1018	14	US-10-090-827-13	Sequence 13, Appl	
0	1036	14	US-10-090-827-14	Sequence 14, Appl	
0	1063	14	US-10-090-827-15	Sequence 15, Appl	
0	1091	9	US-09-875-423-4	Sequence 4, Appli	
0	1091	14	US-10-162-012-17	Sequence 17, Appl	
0	1091	14	US-10-090-827-16	Sequence 16, Appl	
0	1091	15	US-10-162-102-17	Sequence 17, Appl	
3	1086	15	US-10-375-253-49	Sequence 49, Appl	
9	1084	15	US-10-375-253-53	Sequence 53, Appl	
9	1018	14	US-10-090-827-6	Sequence 6, Appli	
9	1036	14	US-10-090-827-7	Sequence 7, Appli	
9	1063	14	US-10-090-827-8	Sequence 8, Appli	
9	1069	14	US-10-090-827-9	Sequence 9, Appli	
9	1091	14	US-10-090-827-5	Sequence 5, Appli	
6	1103	15	US-10-375-253-47	Sequence 47, Appl	

ALIGNMENTS

RESULT 1
US-10-090-827-13
; Sequence 13, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-13

Query Match 100.0%; Score 5346; DB 14; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; Gap
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Db 1 MAAGCLLALTTLTFLSLLIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLA
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Db 121 EVVYNAKDDLDPEKNDSEFGSORIXPVFIEDANFORQISYQHAHVHIPTDIYEGSTI
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mplication US/10090827
US20030073132A1
TION:
ner-Lambert
TION: Method for the screening of alpha 2 delta-1 subunit
TION: binding ligands
3: 179
ATION NUMBER: US/10/090,827
3 DATE: 2002-03-06
TION NUMBER: US/09/397,549
DATE: 1999-09-16
ID NOS: 21
antin Ver. 2.1

TYPE: PRT
ORGANISM: Homo sapiens
US-10-090-827-14
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Best Local Similarity 100.0%; Pred. No. 0;
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:26:17 2004

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cation US/10090827

20030073132A1

N:

N: Lambert

N: Method for the screening of alpha 2 delta-1 subunit

N: binding ligands

ON NUMBER: US/10/090,827

TE: 2002-03-06

NUMBER: US/09/397,549

: 1999-09-16

NOS: 21

n Ver. 2.1

sapiens

100.0%; Score 5346; DB 14; Length 1063;

city 100.0%; Pred. No. 0;

iservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-875-423-4

; Sequence 4, Application US/09875423

; Patent No. US20020081657A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Roly A. J.

; TITLE OF INVENTION: 21784, A NOVEL HUMAN CALCIUM CHANNEL

; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

; FILE REFERENCE: 10448-059001

; CURRENT APPLICATION NUMBER: US/09/875,423

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/209,257

; PRIOR FILING DATE: 2000-06-05

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 1091

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-875-423-4

Query Match 100.0%; Score 5346; DB 9; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1016; Conservative 0; Mismatches 0; Indels 0; G

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121 EWVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHTDIIYEG
181 NELNWTSSALDEVFKQKREDEPSLLQWFGSATGLARYYPASPWNDSRTENKIDLI
181 NELNWTSSALDEVFKQKREDEPSLLQWFGSATGLARYYPASPWNDSRTENKIDLI
241 RPWYIQGAASPKMMLILVDVSGSVGLTLKIRISVSEMLETLSDDDPFVNVASFN
241 RPWYIQGAASPKMMLILVDVSGSVGLTLKIRISVSEMLETLSDDDPFVNVASFN
301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFEQLNLYNVSRANCN
301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAFEQLNLYNVSRANCN

us-10-090-827-13.rapb

:26:17 2004

PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18247
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/928,530
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: PCT/US01/25475
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/934,421
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/US01/26096
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/279,281
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 10/109,029
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US02/09728
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US (not assigned)
PRIOR FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 1091
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-012-17

Query Match 100.0%; Score 5346; DB 14; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1018; Conservative 0; Mismatches 0; Indels 0; C

QY 1 MAAGCGLLALTLTFLQSLGIGSSSEPPFSAVTIKSWVDKQEDLVTLAKTAGVGN
DB 1 MAAGCGLLALTLTFLQSLGIGSSSEPPFSAVTIKSWVDKQEDLVTLAKTAGVGN
QY 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHORE
DB 61 YEKYQDLYTVEPNARQLVEIARDIEKLLSNRSKALVSLALEAEKVQAAHORE
QY 121 EVVYINAKDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQVAAVHIPTDIYE
DB 121 EVVYINAKDLDPEKNDSEPGSQRIKPVFIEDANFGROIYQVAAVHIPTDIYE
QY 181 NELNWTSLALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKID
DB 181 NELNWTSLALDEVFKKNREEDPSLLMQVFGSATGLARYYPASPWVDSNRTPNKID
QY 241 RPYWYOGAASPKDMLLVDSVSGSLTLKLRITSVSEMLETLSDDDFVNVASF
DB 241 RPYWYOGAASPKDMLLVDSVSGSLTLKLRITSVSEMLETLSDDDFVNVASF
QY 301 VSCFQHLVQANVKNKKVLDKDAVNNITAKGITYKKGFSFAFEQLLNNVSRAN
DB 301 VSCFQHLVQANVKNKKVLDKDAVNNITAKGITYKKGFSFAFEQLLNNVSRAN
QY 361 FTGGEERAQEIENKYNKDKKVRVFRFVSGHNYERGPVGMACENKGYIYEI
DB 361 FTGGEERAQEIENKYNKDKKVRVFRFVSGHNYERGPVGMACENKGYIYEI
QY 421 INTQEYLDVLRPNVLAGDKAKQVQWNTNVYLDLLELGLVITGTLPVFNITQGF
DB 421 INTQEYLDVLRPNVLAGDKAKQVQWNTNVYLDLLELGLVITGTLPVFNITQGF
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKNPF
DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKNPF

Application US/10162012
US20030051660A1
ATTN: RORY A.J. Immaculada
ilos-Santiago, Immaculada
u. Wei
ATTN: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
E: 10448-190001
CATION NUMBER: US/10/162.012
IG DATE: 2002-06-04
ACTION NUMBER: US 60/209,845
DATE: 2000-06-06
ACTION NUMBER: US 09/875,321
DATE: 2001-06-06
ACTION NUMBER: PCT/US01/18340
DATE: 2001-06-06
ACTION NUMBER: US 60/209,257
DATE: 2000-06-05
ACTION NUMBER: US 09/875,423
DATE: 2001-06-05
ACTION NUMBER: PCT/US01/18398
DATE: 2001-06-05
ACTION NUMBER: US 60/209,238
DATE: 2000-06-05
ACTION NUMBER: US 09/875,363

RAQEIFNKYNKDKKVRVFRFVSGHNYERGPVGMACENKGYIYEIPSIGAIR 420
RAQEIFNKYNKDKKVRVFRFVSGHNYERGPVGMACENKGYIYEIPSIGAIR 420
RAQEIFNKYNKDKKVRVFRFVSGHNYERGPVGMACENKGYIYEIPSIGAIR 480
LDVLRPNVLAGDKAKQVQWNTNVYLDLLELGLVITGTLPVFNITGTQFENKTNLK 480
LDVLRPNVLAGDKAKQVQWNTNVYLDLLELGLVITGTLPVFNITGTQFENKTNLK 480
VMGVDSVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKNPSQBPVTL 540
VMGVDSVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKNPSQBPVTL 540
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VMGVDSVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKNPSQBPVTL 1018
VMGVDSVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKNPSQBPVTL 1018
VMGVDSVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOPKNPSQBPVTL 1018

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NDIKVEIRNKWIDGESGKTRTLVKSDERYIDKGNRTYTWTVPVNGTDYSL    600
NDIKVEIRNKWIDGESGKTRTLVKSDERYIDKGNRTYTWTVPVNGTDYSL    600
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SFYYIKAKLEETITQARSKKGWKMDSETLKPONFESGYTFIAPRDYCNDLKI   660
SFYYIKAKLEETITQARSKKGWKMDSETLKPONFESGYTFIAPRDYCNDLKI   720
LLANFNFEIDRKTNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNIKGVKAR  780
LLNLFNEIFDKETNNPNSCNADLINRVLLDAGFTNELVQNTWSQKNIKGVKAR  780
LITRYYPKEAGENQENPETVEDSYFKRSLDNNDNVFTAPYFNKSGPGAYESGI  780
LITRYYPKEAGENQENPETVEDSYFKRSLDNNDNVFTAPYFNKSGPGAYESGI  780
HIHYIOGKLKKPAVVGIIKDVSNIWIENFTKTSIRDPCAGPVCCKRNSDVMDCVI  840
HIHYIOGKLKKPAVVGIIKDVSNIWIENFTKTSIRDPCAGPVCCKRNSDVMDCVI  840
HIHYIOGKLKKPAVVGIIKDVSNIWIENFTKTSIRDPCAGPVCCKRNSDVMDCVI  900
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LLMANHDDVTNQIGRFHGHDPSLMRHVLNISVYAFNKSVDYQSVCEPGAAPKQ  960
AUYPSVADIILQIGMWATAAAWSILQQFLLSLTTPRLLEAVEMEDDDFTASLSKQ  960
AUYPSVADIILQIGMWATAAAWSILQQFLLSLTTPRLLEAVEMEDDDFTASLSKQ  960
AUYPSVADIILQIGMWATAAAWSILQQFLLSLTTPRLLEAVEMEDDDFTASLSKQ  1018
TYQTFFNDNSKFSFGVLDGCGNSRIFHGBKMLNTNLFIPIWVESKGTCPCDTRL  1018
TYQTFFNDNSKFSFGVLDGCGNSRIFHGBKMLNTNLFIPIWVESKGTCPCDTRL  1018
TYQTFFNDNSKFSFGVLDGCGNSRIFHGBKMLNTNLFIPIWVESKGTCPCDTRL  1018

ication US/10090827
S20030073132M1
ON: rrr-Lambert
ON: Method for the screening of alpha 2 delta-1 subunit
ON: binding ligands
179
ION NUMBER: US/10/090,827
DATE: 2002-03-06
ION NUMBER: US/09/397,549
TE: 1999-09-16
D NOS: 21
tIn Ver. 2.1

: sapiens
100.0%; Score 5346; DB 14; Length 1091;
arity 100.0%; Pred. No. 0; Indels 0; Gaps 0;
onservative 0; Mismatches

GCGLALTTLTFSLLIGPSSPEEPSAVTIKSWVDKMQEDLVTLAKTAGVNQLVDI 60
GCGLALTTLTFSLLIGPSSPEEPSAVTIKSWVDKMQEDLVTLAKTAGVNQLVDI 60
GCGLALTTLTFSLLIGPSSPEEPSAVTIKSWVDKMQEDLVTLAKTAGVNQLVDI 120
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YQDLYTEPNNAQQLVEIAARDIEKLSNRSKALVSLAEAEKVQAHHOWREDPASN 180
YYYNNAKDLDPEKNDSEPGSQRIKPVFTIEDANFGQISYQHAAVHIPTDIYEGSTIVL 180
YYYNNAKDLDPEKNDSEPGSQRIKPVFTIEDANFGQISYQHAAVHIPTDIYEGSTIVL 180
YYYNNAKDLDPEKNDSEPGSQRIKPVFTIEDANFGQISYQHAAVHIPTDIYEGSTIVL 240
LNMTSALDEVFKKNREEDPSLLQWFGSATGLARYYPASPWNDSNTPKNILDYDVR 240
NMTSALDEVFKKNREEDPSLLQWFGSATGLARYYPASPWNDSNTPKNILDYDVR 240

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RESULT 7
US-10-162-102-17
; Sequence 17, Application US/10162102
; Publication No. US2003023336A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Sillos-Santiago, Inmaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162.102
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257

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ATE: 2000-06-05
ION NUMBER: US 09/875,423
ATE: 2001-06-05
ION NUMBER: PCT/US01/18398
ATE: 2001-06-05
ION NUMBER: US 60/209,238
ATE: 2000-06-05
ION NUMBER: US 09/875,363
ATE: 2001-06-05
ION NUMBER: PCT/US01/18247
ATE: 2001-06-05
ION NUMBER: US 60/227,068
ATE: 2000-08-22
Application data removed - See File Wrapper or PALM.
ID NOS: 48
.SEQ for Windows Version 4.0

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100.0%;	Score 5346;	DB 15;	Length 1091;	
ilarity 100.0%;	Pred. No. 0;			
Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

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GENERAL INFORMATION:
APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
FILE REFERENCE: SD9813DA
CURRENT APPLICATION NUMBER: US/10/375,253
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: 08/450,273
PRIOR FILING DATE: 1995-05-25
PRIOR APPLICATION NUMBER: 08/404,354
PRIOR FILING DATE: 1995-02-15
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 08/314,083
PRIOR FILING DATE: 1994-09-28
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 07/603,751
PRIOR FILING DATE: 1990-11-09
PRIOR APPLICATION NUMBER: 08/290,012
PRIOR FILING DATE: 1994-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
PRIOR APPLICATION NUMBER: 08/105,536
PRIOR FILING DATE: 1993-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
Remaining Prior Application data removed - See File Wrapper or PA
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 1086
TYPE: PRT
ORGANISM: Human
Trs-10-375-253-49

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Query Match	Score 5306.5;	DB 15;	Length 1086
Best Local Similarity	99.5%;	Pred. No. 0;	
Matches 1013;	Conservative 0;	Mismatches 0;	Indels 5;
QY	1	MAACCLLALTLTFLQSLLIGPSSEEPFPPSAVTTIKSWDKMQEDLVTLAKTASGV	
Db	1	MAACCLLALTLTFLQSLLIGPSSEEPFPPSAVTTIKSWDKMQEDLVTLAKTASGV	
QY	61	YEKQDLYTVPEPNNARQVLEIAARDIEKLLSNRSKALVSLALEAEKQVQAHHWF	
Db	61	YEKQDLYTVPEPNNARQVLEIAARDIEKLLSNRSKALVSLALEAEKQVQAHHWF	

ICATION NUMBER: US/10
2003-02-27

[illegible]

301	QY	VSCFQHLVQANVRNKKVLKDAVNNITAKGTTDYKKGFSFAFEQLLNNVSRANCNKI
301	Db	VSCFQHLVQANVRNKKVLKDAVNNITAKGTTDYKKGFSFAFEQLLNNVSRANCNKI
361	QY	FTDGEERAQEI FNKNYKOKKVRVFRFSVG OHNVERGPIOMHACENKGYIYEPSIG
361	Db	FTDGEERAQEI FNKNYKOKKVRVFTFSVG OHNVRDRGPIOMHACENKGYIYEPSIG
421	QY	INTQBYLDVLGRPMVLADGKAKQOVWTVNYLDALGLGVITGTLVPFVNITQGFENKT
421	Db	INTQBYLDVLGRPMVLADGKAKQOVMTWTVNYLDALGLGVITGTLVPFVNITQONENKI
481	QY	NQLILGVMGVDSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLOPKNPKSOE
481	Db	NQLILGVMGVDSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLOPKNPKSOE
541	QY	DFDLDALENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRITYTWTVPNGTI
541	Db	DFDLDALENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRITYTWTVPNGTI
601	QY	ALVLPTYSFYIYI KAKUEETIQARSKKGKWKOSETLKPDPNFESGVTFTIAPRDYCN
601	Db	ALVLPTYSFYIYI KAKUEETIQARSKKGKWKOSETLKPDPNFESGVTFTIAPRDYCN
661	QY	SDNNTEFLMNFNEPIDRKTNNPNSCNADLNRVLLDAGFTNVLQNVWSKQKNIKG
661	Db	SDNNTEFLMNFNEPIDRKTNNPNSCNTLNRVLLDAGFTNVLQNVWSKQKNIKG
721	QY	FWVTDGGITRVYYPKEAGSNQWENPETYEDSFYKRSLONDNVYFTAPYFNKSGGPA
721	Db	FWVTDGGITRVYYPKEAGSNQWENPETYEDSFYKRSLONDNVYFTAPYFNKSGGPA
781	QY	MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIEINFNTKTSIRDPACAGVPCDCKNSDV
781	Db	MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIEINFNTKTSIRDPACAGVPCDCKNSDV
841	QY	LDDGGFLLMANHDDYTNQIGRFFGEIDPSLRHVNISVYAFNKSYDYQSVCEPG
841	Db	LDDGGFLLMANHDDYTNQIGRFFGEIDPSLRHVNISVYAFNKSYDYQSVCEPG
901	QY	GAGHRSAYVPSVADILOIGHWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTA
901	Db	GAGHRSAYVPSADIILHIGHWATAAAWSILOQFLLSLTFPRLLEAVEMEDDDFTA
961	QY	SCITEQTOYGFDDNDSKFSFGLVDCGNCRSRIFHGEKLMNTNLIFIMVYESKGTCPCI
961	Db	SCITEQTOYGFDDNDSKFSFGLVDCGNCRSRIFHGEKLMNTNLIFIMVYESKGTCPCI

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RESULT 11
US-10-090-827-7
; Sequence 7, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 s
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-7
Query Match          98.9%; Score 5288; DB 14; Length 1036;
Best Local Similarity 98.8%; Pred. No. 0;

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SKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVMDCVI 840
DGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
DGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
GHRSAIVPSVADIIQIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDPTASLSKQ 960
GHRSAIVPSIADILHIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDPTASLSKQ 960
TTEQTOYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018
TTEQTOYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIIFIMVESKGTCPDTRL 1018
plication US/10090827
US20030073132A1
rner-Lambert
ACTION: Method for the screening of alpha 2 delta-1 subunit
ACTION: binding ligands
E: 179
G DATE: 2002-03-06
ACTION NUMBER: US/09/397,549
DATE: 1999-09-16
ID NOS: 21
ent in Ver. 2.1
is scrofa
98.9%; Score 5288; DB 14; Length 1069;
ilarity 98.8%; Pred. No. 0;
Conservative 5; Mismatches 7; Indels 0; Gaps 0;
AGCLLALTLTFLQSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60
AGCLLALTLTFLQSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASGNQLVDI 60
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KYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDFASN 120
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VYNNAKDLDPEKNSPEGSQRIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
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3LNTWTSALDVFKNKEEDPSLLQVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
PWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDSDDFVNVASFNNAQD 300
PWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDSDDFVNVASFNNAQD 300
SCFOHLVQANVRNKKVLKDAVNNITAGKITDYKGFSAFEQLLNYSANCNKIIML 360
SCFOHLVQANVRNKKVLKDAVNNITAGKITDYKGFSAFEQLLNYSANCNKIIML 360
TDGGEERAQELFNKYNKDKVRVPFVSGVGHNYERGPQIOWMACENKGYEIEISGAIR 420
TDGGEERAQELFNKYNKDKVRVPFVSGVGHNYERGPQIOWMACENKGYEIEISGAIR 420
NTQBYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLVPVFNITQGFENKTNLK 480

Db 421 INTQBYLDVLRPMVLADGKAKQVQWNTVYLDALGLVITGTLVPVFNITQGFENKTNLK 480
QY 481 NQLIILGWGVDVSLIEDIKRLTFRFTLCBNGYVFAIDPBGVLLHPNLQPKNPKS 480
Db 481 NQLIILGWGVDVSLIEDIKRLTFRFTLCBNGYVFAIDPBGVLLHPNLQPKNPKS 480
QY 541 DFLDAELENDIKVELIRNKMIDGESGEKTFRTILVKSQDERYIDKGNRTYTWTPVN 541
Db 541 DFLDAELENDIKVELIRNKMIDGESGEKTFRTILVKSQDERYIDKGNRTYTWTPVN 541
QY 601 ALVLPITYSYIYKAKLEETITQARSKGKKMDSETLKPDPFESGYTTFIAPRDY 601
Db 601 ALVLPITYSYIYKAKLEETITQARSKGKKMDSETLKPDPFESGYTTFIAPRDY 601
QY 661 SONNTEFLNFNEFDIDRKTNNPNSCNADLINRVLLDAGFTNVLVQYWSKQKNI 661
Db 661 SONNTEFLNFNEFDIDRKTNNPNSCNADLINRVLLDAGFTNVLVQYWSKQKNI 661
QY 721 FVVTDGIIITRVYPKEAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPG 721
Db 721 FVVTDGIIITRVYPKEAGENQENPETYEDSFYKRSLDNDNYYVFTAPYFNKSGPG 721
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSI 781
Db 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSI 781
QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEI 841
Db 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEI 841
QY 901 GAGHRSAIVPSVADIIQIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDPTASLSKQ 901
Db 901 GAGHRSAIVPSVADIIQIGMWATAAAWSILQQFLSLTPRLEAVEMEDDDPTASLSKQ 901
QY 961 SCITEQTOYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIIFIMVESKGTCPD 961
Db 961 SCITEQTOYFFDNDKSFSGVLDCGNCRSRIFHVEKLMNTNLIIFIMVESKGTCPD 961
RESULT 14
US-10-090-827-5
; Sequence 5, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 ;
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-5
Query Match 98.9%; Score 5288; DB 14; Length 1091;
Best local similarity 98.8%; Pred. No. 0;
Matches 1006; Conservative 5; Mismatches 7; Indels 0;
QY 1 MAAGCLLALTLTFLQSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASG 1
Db 1 MAAGCLLALTLTFLQSLLIGPSSPEPPSAVTIKSWDKMQEDLVTLAKTASG 1
QY 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQW 61
Db 61 YEKYQDLYTVEPNNAQOLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQW 61

PRIOR FILING DATE: 1995-05-25
PRIOR APPLICATION NUMBER: 08/404,354
PRIOR FILING DATE: 1995-02-15
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 08/314,083
PRIOR FILING DATE: 1994-09-28
PRIOR APPLICATION NUMBER: 07/914,231
PRIOR FILING DATE: 1992-07-13
PRIOR APPLICATION NUMBER: 07/603,751
PRIOR FILING DATE: 1990-11-09
PRIOR APPLICATION NUMBER: 08/290,012
PRIOR FILING DATE: 1994-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
PRIOR APPLICATION NUMBER: 08/105,536
PRIOR FILING DATE: 1993-08-11
PRIOR APPLICATION NUMBER: 08/149,097
PRIOR FILING DATE: 1993-11-05
Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 1103
TYPE: PRT
ORGANISM: Human
US-10-375-253-47

Query Match 98.6%; Score 5270; DB 15; Length 1103;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1010; Conservative 0; Mismatches 1; Indels 26; G;

QY 1 MAAGCLLALTLTFLQSLLIGPSEEPFPPSAVITKSWVDXMQEDLVLTAKTAGSVNQ
DB 1 MAAGCLLALTLTFLQSLLIGPSEEPFPPSAVITKSWVDXMQEDLVLTAKTAGSVNQ
QY 61 YEKYQDLYTVPEPNNAQLVEIAARDIEKLNSRKSALVSLEAEKVQAHHWRED
DB 61 YEKYQDLYTVPEPNNAQLVEIAARDIEKLNSRKSALVSLEAEKVQAHHWRED
QY 121 EVVYNNAKDLDPEKNDSFGSQRIPKFVFIEDANFGSQISYQHAAVHIPTDIYECS
DB 121 EVVYNNAKDLDPEKNDSFGSQRIPKFVFIEDANFGSQISYQHAAVHIPTDIYECS
QY 181 NELNWTLSALDEVFKKNEEDPSLLIMOVFGSATGLARYYPASPWVDSRTPNKIDL
DB 181 NELNWTLSALDEVFKKNEEDPSLLIMOVFGSATGLARYYPASPWVDSRTPNKIDL
QY 241 RPWYTQGAASKPMILLVDVSGSVSGLTKLRITSVSSEMLETSLDDDFNVASFN
DB 241 RPWYTQGAASKPMILLVDVSGSVSGLTKLRITSVSSEMLETSLDDDFNVASFN
QY 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGITYKKGFSAFEQLLNYSVRANC
DB 301 VSCFOHLVQAVNRNKKVLKDAVNNTAKGITYKKGFSAFEQLLNYSVRANC
QY 361 FTDGGEERAQEIFPKYKNDKKVRFVSFGQHNRYERGPIQMCAENKGYYEIPS
DB 361 FTDGGEERAQEIFPKYKNDKKVRFVSFGQHNRYERGPIQMCAENKGYYEIPS
QY 421 INTQEVLDVGRPMWLADKAKQVMNTNYVLDLELGIVTGTLPVFNITGOFEN
DB 421 INTQEVLDVGRPMWLADKAKQVMNTNYVLDLELGIVTGTLPVFNITGOFEN
QY 481 NOLLILGVMGVDVSLEDIKRLTPRTLCPNGYYFAIDPNGVYLHPNLQPK-----
DB 481 NOLLILGVMGVDVSLEDIKRLTPRTLCPNGYYFAIDPNGVYLHPNLQPKIGV
QY 531 -----NPKSQEPVTLDLEALENDIKVEIRNMIDGESGEKTFTLIVSK
DB 531 LRRKRPNQNPKSQEPVTLDLEALENDIKVEIRNMIDGESGEKTFTLIVSK
QY 582 DKGNETTYTWPNGTDYSIALVLPITYSFYIIKAKLETITTOARSKGKMCKDET

Application US/10375253
US20040018510A1
INVENTOR:
SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
TITLE: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
METHODS
CLASSIFICATION: SP9813DA
PUBLICATION NUMBER: US/10375,253
PUBLICATION DATE: 2003-02-27

Application US/10375253

APPLICATION US/103
US20040018510A1

US20040010310A1

3 SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATION

CONCLUSION: HUMAN CAL

NOTATION: METE

E: SD9813DA

CATION NUMBER: US/10
2003-02-27

ISSUE DATE: 2003-02-27
 SECTION NUMBER: 08/450,273

us-10-090-827-13.rapb

6:26:17 2004

|||||
TYTWPVNGIDYSLALVLPYTSFYIRAKLEETITQARY-----SETLKPDNF 653
TFIAPROYCNDLKI SDANTEFLNFEIDRKTNNPSCNADLINRVLLDAGFTN 701
TFIAPROYCNDLKI SDNTEFLNFEIDRKTNNPSCNADLINRVLLDAGFTN 713
YWSKKNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNY 761
YWSKKNIKGVKARFVVTDDGGITRVYPKEAGENWOENPETYEDSFYKRSLDNDNY 773
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YFENKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 833
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YFENKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENFTKTSIRD 893
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YDQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTPEPR 953
VEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNL 1001
VEMEDDDFTASLSKQSCITEQTQYFFDNDKSFSGVLDGNCNCSRI FHGEKLMNTNL 1013
WESKGTCPCDTRL 1018
WESKGTCPCDTRL 1030

March 17, 2004, 20:26:51
: secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

in search, using sw model

bruary 20, 2004, 16:51:31 ; Search time 37,2255 Seconds
(without alignments)
7181.696 Million cell updates/sec

3-10-090-827-14

143 MAAGCCLLTLTLFQSLIG.....RLLIQAQTSQGNPCDMVK 1036

LOSUM62

apop 10.0 , Gapext 0.5

30525 seqs, 258052604 residues

its satisfying chosen parameters: 830525

ngth: 0

ngth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPTREMBL 23:*

:: sp_archaea:*

:: sp_bacteria:*

:: sp_fungi:*

:: sp_human:*

:: sp_invertebrate:*

:: sp_mammal:*

:: sp_mhc:*

:: sp_organelle:*

:: sp_phase:*

:: sp_plant:*

:: sp_rodent:*

:: sp_virus:*

:: sp_unclassified:*

:: sp_rv1rus:*

:: sp_bacteria:*

:: sp_archaeap:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query Match	Length	DB	ID	Description
99.4	1110	4	Q9UIU0	Q9uiuo homo sapien
98.8	1091	6	O77773	O77773 aus scrofa
97.2	1091	11	Q9ERS3	Q9ers3 rattus norv
96.1	1084	11	Q8CFG7	Q8cfg7 rattus norv
96.0	1103	11	Q08532	Q08532 mus musculu
95.4	1079	11	Q8VHS9	Q8vhs9 rattus norv
67.4	745	4	Q9UDQ3	Q9udq3 homo sapien
54.2	1150	4	Q9NY47	Q9ny47 homo sapien
53.7	1157	11	Q8CFG6	Q8cfg6 rattus norv
53.7	1143	4	Q9NY48	Q9ny48 homo sapien
53.6	1156	11	Q9EQG2	Q9eqg2 mus musculu
53.6	1148	11	Q8CGR8	Q8cgr8 mus musculu
53.4	1145	4	Q9Y268	Q9y268 mus musculu
53.2	1098	11	Q8CHE9	Q8che9 mus musculu
53.2	1084	11	Q920H6	Q920h6 mus musculu
53.0	1076	4	Q9UEW0	Q9uew0 homo sapien

17	2717	49.9	975	4	Q9NSA6	Q9nsa6 hom
18	1090	20.0	1085	11	Q8CFG5	Q8cfg5 ral
19	1085	19.9	1091	11	Q9Z1L5	Q9z1l5 mu
20	1084	19.9	1091	4	Q8IZS8	Q8izs8 hom
21	1063	19.5	1120	4	Q8IZS9	Q8izs9 hom
22	1015	18.6	997	4	Q9NY16	Q9ny16 hom
23	1007	18.5	1218	5	Q9V6T7	Q9v6t7 dro
24	982.5	18.1	1170	5	Q8IP22	Q8ip22 dro
25	929.5	17.1	2190	5	Q9VJM0	Q9vjm0 dro
26	886	16.3	1255	5	Q9NK83	Q9nk83 dro
27	877	16.1	1120	5	Q9VJN7	Q9vjn7 dro
28	875	16.1	170	4	Q9UDL7	Q9udl7 hom
29	738.5	13.6	519	4	Q9NY18	Q9ny18 hom
30	658	12.1	317	11	Q920H5	Q920h5 mu
31	572	10.5	1148	5	Q17517	Q17517 cae
32	539.5	9.9	942	5	Q9SR75	Q9sr75 dro
33	526.5	9.7	394	13	Q8AVY7	Q8avy7 xe
34	514.5	9.5	104	4	Q9UD81	Q9ud81 hor
35	506	9.3	100	6	Q9GLH1	Q9glh1 bos
36	498.5	9.2	121	4	Q9UD82	Q9ud82 hor
37	482	8.9	98	4	Q9UDU5	Q9udus hor
38	465	8.5	97	4	Q9UD80	Q9ud80 hor
39	459	8.4	100	11	Q8C6Y3	Q8c6y3 ml
40	402	7.4	77	4	Q95026	Q95026 hor
41	365.5	6.7	223	11	Q9R142	Q9r142 ml
42	337.5	6.2	1185	4	Q9HCJ9	Q9hcj9 hor
43	231	4.2	978	6	Q95KE0	Q95ke0 mac
44	227	4.2	43	6	Q8HYX0	Q8hyx0 bot
45	223	4.1	1449	5	Q9V917	Q9v917 dr

ALIGNMENTS

RESULT 1

Q9UIU0 PRELIMINARY; PRT: 1110 AA.

AC Q9UIU0; TREMBLrel. 13, Created

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 20, Last annotation update)

DE Dihydropyridine receptor alpha 2 subunit.

GN CACNA2D1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]_

RP SEQUENCE FROM N.A.

RX MEDLINE=2005942; PubMed=10534405;

RA Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;

RT "Genomic structure and functional expression of a human alpha(2

RT calcium channel subunit gene (CACNA2).";

RL Genomics 61:201-209(1999).

DR EMBL; AF083854; AAF03259.1; JOINED.

DR EMBL; AF083817; AAF03259.1; JOINED.

DR EMBL; AF083818; AAF03259.1; JOINED.

DR EMBL; AF083819; AAF03259.1; JOINED.

DR EMBL; AF083820; AAF03259.1; JOINED.

DR EMBL; AF083821; AAF03259.1; JOINED.

DR EMBL; AF083822; AAF03259.1; JOINED.

DR EMBL; AF083823; AAF03259.1; JOINED.

DR EMBL; AF083824; AAF03259.1; JOINED.

DR EMBL; AF083825; AAF03259.1; JOINED.

DR EMBL; AF083826; AAF03259.1; JOINED.

DR EMBL; AF083827; AAF03259.1; JOINED.

DR EMBL; AF083828; AAF03259.1; JOINED.

DR EMBL; AF083829; AAF03259.1; JOINED.

DR EMBL; AF083830; AAF03259.1; JOINED.

DR EMBL; AF083831; AAF03259.1; JOINED.

DR EMBL; AF083832; AAF03259.1; JOINED.

DR EMBL; AF083833; AAF03259.1; JOINED.

DR EMBL; AF083834; AAF03259.1; JOINED.

[illegible]

D	b	601	DKGNRTVTVTVEVNGTDYSLALVLPETSYFYLKAKLLELL..
O	7	642	EESGYTIAPRDYCNDLKISDNNTTEFLNFNEFDIKRTPNPNPCNADLINRVLLDAG
O	Y	661	EESGYTIAPRDYCNDLKISDNNTTEFLNFNEFDIKRTPNPNPCNADLINRVLLDAG
D	b	702	ELVQNYTKSKQNIKGVKARFVVTDGGITRVYPKEAGENWOENPETYEDSFYKGSLDN
O	Y	721	ELVQNYMSKQNIKGVKARFVVTDGGITRVYPKEAGENWOENPETYEDSFYKRSLDN
D	b	762	VPTATYFNKSGPGAYESGIMWSKAWEIYIOGKLKPAVVGIKIDVNSWIENTFTKTSI
O	Y	781	VPTATYFNKSGPGAYESGIMWSKAWEIYIOGKLKPAVVGIKIDVNSWIENTFTKTSJ
D	b	822	CAGPVCDCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRPFGEDIPSLMRHLVNMI
O	Y	841	CAGPVCDCCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRPFGEDIPSLMRHLVNMI
D	b	882	FNKSYDYQSVCERGAAPKOGAHRSAVPVSADIILQIGMWATAAAWSIIQQOFLLSL
O	Y	901	FNKSYYDYQSVCERGAAPKOGAHRSAVPVSADIILQIGMWATAAAWSIIQQOFLLSL
D	b	942	LLEAVEMEDDDFTASLSKSCITEQTQYFPDNDKSFSGVLDCGCNCSRIFPHGEKLM
O	Y	961	LLEAVEMEDDDFTASLSKSCITEQTQYFPDNDKSFSGVLDCGCNCSRIFPHGEKLM
D	b	1002	IFIMVESKGTCPCDTRLIIQAETSQDPNPCDMVK 1036
O	Y	1021	IFIMVESKGTCPCDTRLIIQAETSQDPNPCDMVK 1055
D	b		
O	7	RESULT 2	
O	7	07773	PRELIMINARY; PRT; 1091 AA.
I	D	07773	
A	C	07773;	
D	T	01-NOV-1998 (TREMBLrel. 08, Created)	
D	T	01-NOV-1998 (TREMBLrel. 08, Last sequence update)	
D	T	01-OCT-2002 (TREMBLrel. 22, Last annotation update)	
D	E	Voltage-dependent calcium channel alpha-2 delta subunit precursor.	
D	S	Sus scrofa (Pig).	
O	C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
O	C	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
O	X	NCBI_TaxID=9823;	
R	N	[1]	
R	P	SEQUENCE FROM N.A.	
R	C	TISSUE=Brain cortex;	
R	C	MEDLIN=98411353; PubMed=9738015;	
R	X	Brown J.P., Gee N.S.;	
R	A	"Cloning and deletion mutagenesis of the alpha2 delta calcium c	
R	T	subunit from porcine cerebral cortex. Expression of a soluble f	
R	T	the protein that retains [3H]gabapentin binding activity.";	
R	T	J. Biol. Chem. 273:25458-25465(1998).	
R	L	EMBL; AF077665; AAC36289.1; -.	
D	R	InterPro; IPR004010; Cache.	
D	R	InterPro; IPR002035; VWF A.	
D	R	Pfam; PF02743; Cache; 1.	
D	R	Pfam; PF00092; vwa; 1.	
D	R	SMART; SM00327; VWA; 1.	
D	R	PROSITE; PS50234; VWFA; 1.	
K	M	Signal.	
F	T	SIGNAL	
F	T	CHAIN	
F	T	1 24	POTENTIAL
F	T	25 1091	VOLTAGE-DEPENDENT CALCIUM CHANNEL
F	T		DELTA SUBUNIT
F	T		293DDC7EBE9EE60E CRC64;
F	T	SEQUENCE 1091 AA; 123150 MW; 293DDC7EBE9EE60E CRC64;	
F	T		
S	Q		
		Query Match 98.8%; Score 5380; DB 6; Length 1091;	
		Best local Similarity 98.7%; Pred. No. 0;	
		Matches 1023; Conservative 7; Mismatches 7; Indels 0;	
O	Y	1 MAACIALATLTTFQSLICPGSSEPPPSAVTIKSWVDKKQEDIVTLAKTAGS	

7:56:54 2004

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1AALTITLTLFQSLIGSSQEPSPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
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1LYTVENPNARQVEIAARDIEKLLNSRKALVSLALEAEKVQAAHOMREDFASN 120
1YAKDDLPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGSTIVL 180
1NAKDDLPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGSTIVL 180
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1JHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQQLNNVNSRANCKIIML 360
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1LQWGVDSLEDIKELTLPRTFLCPNGYVFAIDPNGYVLLHNPLOKPNKSEPTVL 540
1LQWGVDSLEDIKELTLPRTFLCPNGYVFAIDPNGYVLLHNPLOKPNKSEPTVL 540
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1AELENDIKVEIRNKMIDGESGKTRFTLVKSDERYIDKGNRTYTWTPVNGTDSL 600
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1XGFFLLMANHDDVTNOLGRFFGIDPSLMHLVNI SVYAFNKSIDYQSVCEPAAKQ 900
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1EQTSQGNPCDMVK 1036
1EQTSQGNPCDMVK 1036

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ID Q9ERS3 PRELIMINARY; PRT; 1091 AA.
 AC Q9ERS3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Voltage-gated calcium channel alpha2/delta-1 subunit.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratt
 OX NCBI_TaxID=10116;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Superior cervical ganglion;
 RA Lin Y., Lipscombe D.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF286488; AAG28164.1; --
 DR InterPro: IPR004010; Cache.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam; PF02743; Cache; 1.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00234; VWF_A; 1.
 FT VARIANT 209 212 GSAT -> AADR.
 FT VARIANT 338 338 S -> T.
 FT VARIANT 599 600 SL -> RY.
 FT VARIANT 869 869 S -> R.
 SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;
 Query Match 97.2%; Score 5291; DB 11; Length 1091;
 Best Local Similarity 96.4%; Pred. No. 0;
 Matches 999; Conservative 22; Mismatches 15; Indels 0; C

QY 1 MAAGCLLALTITLQSLIGSSQEPSPSAVTIKSWVDKMQEDLVTLAKTASGVN
 Db 1 MAAGCLLALTITLQSLIGSSQEPSPSAVTIKSWVDKMQEDLVTLAKTASGVN
 QY 61 YEKYQDLYTVENPNARQVEIAARDIEKLLNSRKALVSLALEAEKVQAAHOMRE
 Db 61 YEKYQDLYTVENPNARQVEIAARDIEKLLNSRKALVSLALEAEKVQAAHOMRE
 QY 121 EVVYNNAKDDLPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEG
 Db 121 EVVYNNAKDDLPEKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEG
 QY 181 NELNWTLSALDEVFKKREEDPSILLMQVFGSATGLARYYPASPVWNSRTPNKIDI
 Db 181 NELNWTLSALDEVFKKREEDPSILLMQVFGSATGLARYYPASPVWNSRTPNKIDI
 QY 241 RPWYIQGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDDFVNVASF
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDDFVNVASF
 QY 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQQLNNVNSRANCI
 Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQQLNNVNSRANCI
 QY 361 FTDGGEERAQBIENKYNKKVVRFRFSVQHNTERGPIQWMAKNGYIYIPI
 Db 361 FTDGGEERAQBIENKYNKKVVRFRFSVQHNTERGPIQWMAKNGYIYIPI
 QY 421 INTQBYLDVLRGPMVLADKAKQVQNTVNYLDALGLVITGTLPVFNITGQF
 Db 421 INTQBYLDVLRGPMVLADKAKQVQNTVNYLDALGLVITGTLPVFNITGQF
 QY 481 NQILILGWGVDSLEDIKELTLPRTFLCPNGYVFAIDPNGYVLLHNPLOKPNKPS
 Db 481 NQILILGWGVDSLEDIKELTLPRTFLCPNGYVFAIDPNGYVLLHNPLOKPNKPS
 QY 541 DFLLDAELNDIKVEIRNKMIDGESGKTRFTLVKSDERYIDKGNRTYTWTPV
 Db 541 DFLLDAELNDIKVEIRNKMIDGESGKTRFTLVKSDERYIDKGNRTYTWTPV
 QY 601 ALVLPITYFYIKAKLEETITQARSKKGMKQSETLKPONFESGYTFIAPRDC

241	QY	RPHYIOGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETISDDDFVNVAFSNFI
241	Db	RPHYIOGAASPKDMLILVDVSGSVSGLTKLIRTSVSEMLETISDDDFVNVAFSNFI
301	QY	VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSAFEOQLLNNYTSRANCKN
301	Db	VSCFOHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSAFEOQLLNNYTSRANCKN
361	QY	PTDQGEERAQEIENKNNKKVVRPRFSVGQHYNERGPIONMACEKNGYYIEIPSI
361	Db	PTDQGEERAQEIENKNNKKVVRPRFSVGQHYNERGPIONMACEKNGYYIEIPSI
421	QY	INTQEYLDVLGRPMVLADGAKAKOVMTNYLDALDELGLVITGTLPVFNITGQFENK
421	Db	INTQEYLDVLGRPMVLADGAKAKOVMTNYLDALDELGLVITGTLPVFNITGQFENK
481	QY	NQLILGVNGVDVSLIEDIKRUTPFTLCPNGYFAIDPNNGYVLLHPNLQPKPKSQI
481	Db	NQLILGVNGVDVSLIEDIKRUTPFTLCPNGYFAIDPNNGYVLLHPNLQPKPKSQI
541	QY	DFDLAELENDIKVEIRNNKWDGSGEKTFTLVKSQDERYIDKGNRTYTWTPVNG
541	Db	DFDLAELENDIKVEIRNNKWDGSGEKTFTLVKSQDERYIDKGNRTYTWTPVNG
601	QY	ALVLPYSPYYIKAKLETTIOAQRSSKKGMKQSETLKPDNFEESGYTFIAPDYCI
601	Db	ALVLPYSPYYIKAKLETTIOAQRSSKKGMKQSETLKPDNFEESGYTFIAPREYC
661	QY	SDNNTFELNPFNEFIDRKTNNPNSCNADLNRLDAGFTNELVONWYSKQNNIK
654	Db	SDNNTFELNPFNEFIDRKTNNPNSCNTDLINRLDAGFTNELVONWYSKQNNIK
721	QY	FVVTGCGITRVYPKEAGENQBNPTYESDYPYKKSLONDNIVFTAPYFNKSGPGA
714	Db	FVVTGCGITRVYPKEAGENQBNPTYESDYPYKKSLONDNIVFTAPYFNKSGPGF
781	QY	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTWTSIRDPACAGPVCDCRNSD
774	Db	MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTWTSIRDPACAGPVCDCRNSD
841	QY	LDDGGFLLMANHDDYTNQIGRPFGEIDPSLMHRLVNI SVYAFNKSXYDYSQVCEP
834	Db	LDDGGFLLMANHDDYTNQIGRPFGEIDPSMHRHLVNI SLVAFNKSXYDYSQVCDP
901	QY	GAGHRSAYVPSVADILQIGWATAAASLQOQFLSLTFPRLLLEAVEMEDDDFT
894	Db	GAGHRSAYVPSITDILQIGWATAAASLILQQLLSLTFPRLLLEAVEMBEDDFT
961	QY	SCITBQTOYFPDNDKSPGVLDGNCNSRI FHEGKLMNTNLJFI MVBSKGTGCP
954	Db	SCITEQTQYFFKNDTKSPGLLDGNCNSRI FHEKLMNTLVFI MVBSKGTGCP
1021	QY	QABQTSIDGPNPCDMWK 1036
1014	Db	QABQTSIDGPDPCDMWK 1029

RESULT	5	PRT:	1103	AA.
008532	PRELIMINARY;	008532		
008533	008533; 008534; 008535; 008536;			
AC	008332; 008533; 008534; 06, Created)			
DT	01-JUN-1998 (TREMELrel. 06, Last sequence update)			
DT	01-JUN-1998 (TREMELrel. 06, Last annotation update)			
DT	01-MAR-2003 (TREMELrel. 23, Last annotation update)			
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta			
DE	subunits precursor.			
DE	subunits precursor.			
GN	CACNA2D1 OR CACNA2.			
OS	Mus musculus (Mouse).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosteo			
OC	Fish; Actinopterygii; Cyprinodontiformes; Cyprinodontidae; Poeciliidae; Murinae;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
OX	NCBI_TaxID=10090;			
PN	[1]			

[illegible]

61	YKYLQDLYTVEPNARQLVEIAARDIEKLKSNRSKALVSLALEAEKVQAAHQRRED	QY	61	YKYLQDLYTVEPNARQLVEIAARDIEKLKSNRSKALVSLALEAEKVQAAHQRRED
61	YKYLQDLYTVEPNARQLVEIAARDIEKLKSNRSKALVSLALEAEKVQAAHQRRED	Db	61	YKYLQDLYTVEPNARQLVEIAARDIEKLKSNRSKALVSLALEAEKVQAAHQRRED
121	EVVYNAKDDLDPEKNDSPGSRQIKPVFIEDANFGQRQISYQAAVHIPTDIEGGS	QY	121	EVVYNAKDDLDPEKNDSPGSRQIKPVFIEDANFGQRQISYQAAVHIPTDIEGGS
121	EVVYNAKDDLDPEKNDSPGSRQIKPVFIEDANFGQRQISYQAAVHIPTDIEGGS	Db	121	EVVYNAKDDLDPEKNDSPGSRQIKPVFIEDANFGQRQISYQAAVHIPTDIEGGS
181	NELNWTALDEVPKKNREDDPSLLMQVFGSATGLARYYPASPMVDNSTRNKIDLY	QY	181	NELNWTALDEVPKKNREDDPSLLMQVFGSATGLARYYPASPMVDNSTRNKIDLY
181	NELNWTALDEVPKKNREDDPSLLMQVFGSATGLARYYPASPMVDNSTRNKIDLY	Db	181	NELNWTALDEVPKKNREDDPSLLMQVFGSATGLARYYPASPMVDNSTRNKIDLY
241	RPWYIQGAASPDKMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVSFNS	QY	241	RPWYIQGAASPDKMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVSFNS
241	RPWYIQGAASPDKMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVSFNS	Db	241	RPWYIQGAASPDKMLILVDVSGSVGLTLKLRISVSEMLETLSDDDFVNVSFNS
301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNNVSRANCK	QY	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNNVSRANCK
301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNNVSRANCK	Db	301	VSCFQHLVQANVRNKKVLDKAVNNITAKGTDYKKGFSFAPEQLLNNVSRANCK
361	FTDGGEEARAQEIFNKYNKOKKVRFRFSVQGNRYERGPIOMMACENKGYIIEPSI	QY	361	FTDGGEEARAQEIFNKYNKOKKVRFRFSVQGNRYERGPIOMMACENKGYIIEPSI
361	FTDGGEEARAQEIFNKYNKOKKVRFRFSVQGNRYERGPIOMMACENKGYIIEPSI	Db	361	FTDGGEEARAQEIFNKYNKOKKVRFRFSVQGNRYERGPIOMMACENKGYIIEPSI
421	INTQBYLDVLRPMVLADGKAKQVQNTNVDLDELGLVITGTLPVFNITQGFENI	QY	421	INTQBYLDVLRPMVLADGKAKQVQNTNVDLDELGLVITGTLPVFNITQGFENI
421	INTQBYLDVLRPMVLADGKAKQVQNTNVDLDELGLVITGTLPVFNITQGFENI	Db	421	INTQBYLDVLRPMVLADGKAKQVQNTNVDLDELGLVITGTLPVFNITQGFENI
481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOK-----	QY	481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOK-----
481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOK-----	Db	481	NOLILGVNMGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHNPLOK-----
531	-----NPKSQBPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSO	QY	531	-----NPKSQBPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSO
541	LKRKRPVQNPQSQBPVTLDFLDAELENEIKVEIRNKMIDGESGKTFRTLVKSO	Db	541	LKRKRPVQNPQSQBPVTLDFLDAELENEIKVEIRNKMIDGESGKTFRTLVKSO
582	DIGNRTYTWPNVNGTDYSALVLPYVSYFYIKAKLEETITQARSKKMKDSSETL	QY	582	DIGNRTYTWPNVNGTDYSALVLPYVSYFYIKAKLEETITQARSKKMKDSSETL
601	DIGNRTYTWPNVNGTDYSALVLPYVSYFYIKAKLEETITQARY-----SETL	Db	601	DIGNRTYTWPNVNGTDYSALVLPYVSYFYIKAKLEETITQARY-----SETL
642	ESGTYTPIAPRDYCNLKI SDNNTFELNFEFIDRKTNNPNSCNADLINRVLLD	QY	642	ESGTYTPIAPRDYCNLKI SDNNTFELNFEFIDRKTNNPNSCNADLINRVLLD
654	ESGTYTPIAPREYCNLKP SDNNTFELNFEFIDRKTNNPNSCNTDLINRILLD	Db	654	ESGTYTPIAPREYCNLKP SDNNTFELNFEFIDRKTNNPNSCNTDLINRILLD
702	ELVQNTWSKQKNIKGVKARFVVTDDGITRVYPKEAGENQENPETTEDSDPYKRSI	QY	702	ELVQNTWSKQKNIKGVKARFVVTDDGITRVYPKEAGENQENPETTEDSDPYKRSI
714	ELVQNTWSKQKNIKGVKARFVVTDDGITRVYPKEAGENQENPETTEDSDPYKRSI	Db	714	ELVQNTWSKQKNIKGVKARFVVTDDGITRVYPKEAGENQENPETTEDSDPYKRSI
762	VFTAPYFNKSGPGAYESGIMVSKAVIYIQGLKPAVVGIKIDVNSWIENFTKI	QY	762	VFTAPYFNKSGPGAYESGIMVSKAVIYIQGLKPAVVGIKIDVNSWIENFTKI
774	VFTAPYFNKSGPGAYESGIMVSKAVIYIQGLKPAVVGIKIDVNSWIENFTKI	Db	774	VFTAPYFNKSGPGAYESGIMVSKAVIYIQGLKPAVVGIKIDVNSWIENFTKI
822	CAGPVDCCKNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGFEIDPSLMRHLVA	QY	822	CAGPVDCCKNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGFEIDPSLMRHLVA
834	CAGPVDCCKNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGFEIDPSLMRHLVA	Db	834	CAGPVDCCKNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGFEIDPSLMRHLVA
882	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADTLOIGMWATAAASILQOFLIF	QY	882	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADTLOIGMWATAAASILQOFLIF
894	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADTLOIGMWATAAASILQOFLIF	Db	894	FNKSYDYQSVCEPGAAPKQAGHRSATVPSVADTLOIGMWATAAASILQOFLIF
942	LLEAVEHEDDDFTASLSKQSCITQOTVFFDNDSKSPSGVLDCGNCRSRIFHGEKI	QY	942	LLEAVEHEDDDFTASLSKQSCITQOTVFFDNDSKSPSGVLDCGNCRSRIFHGEKI
954	LLEAVEHEDDDFTASLSKQSCITQOTVFFDNDSKSPSGVLDCGNCRSRIFHGEKI	Db	954	LLEAVEHEDDDFTASLSKQSCITQOTVFFDNDSKSPSGVLDCGNCRSRIFHGEKI
1002	IFIMVSKGTCPCTRLLIQAEQTSDFGNPCDMVK 1036	QY	1002	IFIMVSKGTCPCTRLLIQAEQTSDFGNPCDMVK 1036
1014	IFIMVSKGTCPCTRLLIQAEQTSDFGNPCDMVK 1048	Db	1014	IFIMVSKGTCPCTRLLIQAEQTSDFGNPCDMVK 1048
RESULT 6				
QVHS9	PRELIMINARY;	PRT;	1079	AA.
ID	QVHS9			

N.A.

14; PubMed=8955374;

Hofmann F.J.

331-337(1996).

CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN I-CONTRACTION COUPLING.

THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS: ALPHA-2, BETA AND GAMMA.

ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-AR LOCATION: INTEGRAL MEMBRANE PROTEIN.

VE PRODUCTS: 5 ISOFORMS; 2A (SHOWN HERE), 2B, 2C, 2D AND REDUCED BY ALTERNATIVE SPLICING.

IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN SKELETAL MUSCLE AND IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN SCL. ALL FIVE ISOFORMS ARE EXPRESSED IN THE CULAR SYSTEM.

A-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM OR FORM.

Y: TO OTHERS SPECIES ALPHA-2 SUBUNIT.

AAB50139.1; -

AAB50140.1; -

AAB50138.1; -

AAB50141.1; -

AAB50142.1; -

5; Caca2d1.

004010; Cache.

002035; WVF.A.

Cache; 1.

WVF; 1.

WVF; 1.

1234; WVF.A. 1.

Transmembrane; Ion transport; Voltage-gated channel; hel; Glycoprotein; Phosphorylation; Signal; splicing.

1 24

POTENTIAL.

25 957

358 1103

446 469

918 942

079 1098

501 501

845 845

136 136

184 184

324 324

348 348

475 475

604 604

613 613

675 675

781 781

824 824

888 888

985 985

985 985

998 998

531 549

531 554

644 644

1103 AA; 124629 MW; 103773BA735120D4 CRC64;

96.0%; Score 5223; DB 11; Length 1103;

ilarity 94.1%; Pred. No. 0;

Conservative 22; Mismatches 14; Indels 26; Gaps 2;

AGCLLALTLFQSLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVQLVDI 60

AGCLLALTLFQSLIGPSEEPFSAVTIKSWDKMQEDLVTLAKTASGVQLVDI 60

(Tremblrel. 20, Created)
 (Tremblrel. 20, Last sequence update)
 (Tremblrel. 21, Last annotation update)
 am channel alpha2/delta subunit.
 gicus (Rat).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 cheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 0116;
 M N.A.
 r; TISSUE=Heart;
 1730; PubMed=11604404;
 agashima M., Tautauru M., Kobayashi T., Seki S.,
 orio Y., Tohse N.;
 a functional splice variant of L-type calcium channel
 t from rat heart.*;
 m. 276:47163-47170(2001).
 62; AAL47093.1; -.
 R004010; Cache.
 R002035; VWF_A.
 i3; Cache; 1.
 i2; vwa; 1.
 i27; VWA; 1.
 i0234; VWA; 1.
 .079 AA; 122172 MW; DC4A3641195B546C CRC64;
 95.4%; Score 5195; DB 11; Length 1079;
 ilarity 95.2%; Pred. No. 5.7e-317; Indels 12; Gaps 2;
 Conservative 22; Mismatches 16; Indels 12; Gaps 2;
 AGCLLALTLFQSLIGPSEPPFPSPVAVIKSWVDKMQEDLVLTAKTAGVGNQVLDI 60
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 AGCLLALTLFQSLIGPSEPPFPSPVAVIKSWVDKMQEDLVLTAKTAGVGNQVLDI 60
 |||||
 KYQDLYTVEPNNAQLVEIAARDIEKLLNSKALVSLALEAKVQAAHQWRDEPASN 120
 |||||
 KYQDLYTVEPNNAQLVEIAARDIEKLLNSKALVSLALEAKVQAAHQWRDEPASN 120
 |||||
 VYTNAKDDLDPKNDSPGSRQIKPVIEDANFGRIQSYQAAVHIPTDIYEGSTIVL 180
 |||||
 VYTNAKDDLDPKNDSPGSRQIKPVIEDANFGRIQSYQAAVHIPTDIYEGSTIVL 180
 |||||
 LNWTSAIDVFKKREDDPSPVLLQVFGSATGLARYYPASPMVDNSRTNPKIDLYDVR 240
 |||||
 LNWTSAIDVFKKREDDPSPVLLQVFGSATGLARYYPASPMVDNSRTNPKIDLYDVR 240
 |||||
 WYIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVASFNSAQD 300
 |||||
 WYIQGAASPKDMLILVDVSGSVGLTLKIRTSVSEMLETLSDDDFVNVASFNSAQD 300
 |||||
 CFQHLVQANVRNKKVLDKAVNNITAKGTTDYKGFSAFAEQLLNYSRANCNKIIML 360
 |||||
 CFQHLVQANVRNKKVLDKAVNNITAKGTTDYKGFSAFAEQLLNYSRANCNKIIML 360
 |||||
 DGGERAQEIIFKNYKDKKRVFRPSVQGHNYERGIQWMAKCNKGYIYEPISGAIR 420
 |||||
 DGGERAQEIIFKNYKDKKRVFRPSVQGHNYERGIQWMAKCNKGYIYEPISGAIR 420
 |||||
 JTOEYLDVLRPMVLAGDKAKQVQWNTNVDLDALEGLVITGTLPVENITGQENKTNLK 480
 |||||
 JTOEYLDVLRPMVLAGDKAKQVQWNTNVDLDALEGLVITGTLPVENITGQENKTNLK 480
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 JTLIGVWGVDVSLIEDIKRLTPRFLCPNGYFFAIDPNGYVLLHPNLPKPKSQBPVTL 540
 |||||
 JTLIGVWGVDVSLIEDIKRLTPRFLCPNGYFFAIDPNGYVLLHPNLPKPKSQBPVTL 540
 |||||
 FLDALENDIKVEIRNWKIDGESSEKTFRTLVKSQDRIYDKGNRTYTPVNGTDYSL 600
 |||||
 FLDALENDIKVEIRNWKIDGESSEKTFRTLVKSQDRIYDKGNRTYTPVNGTDYSL 595
 |||||
 LVLPTYSFYIYKAKLEETITQARY-----SETLKPDNFEESGYTFTIAPREYC
 |||||

Db 596 ALVLPYSFYIYKAKLEETITQARY-----SETLKPDNFEESGYTFTIAPREYC
 QY 661 SNNTEFLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELLVONYWSKQKNIK
 Db 649 SNNTEFLNFEFTDRKTPNPNPCNADLINRVLLDAGFTNELLVONYWSKQKNIK
 QY 721 FVVTDCGIIITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 Db 709 FVVTDCGIIITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
 QY 781 MVS KAVEIYIQGKLLKPAVVGIIKIDNSWIENFTKTSIRDPKAGPVCDCCKRNSDV
 Db 769 MVS KAVEIYIQGKLLKPAVVGIIKIDNSWIENFTKTSIRDPKAGPVCDCCKRNSDV
 QY 841 LDGGFLLMANHDDYTNQIGRPFGEIDPSLRHLVNIISVYAFNKSVDYQSVCEPC
 Db 829 LDGGFLLMANHDDYTNQIGRPFGEIDPSLRHLVNIISVYAFNKSVDYQSVCEPC
 QY 901 GAGHSAYVPSVADILQIGWATAAAMSILQQLLSLTPRLLLEAVEMEDDDFTI
 Db 889 GAGHSAYVPSVADILQIGWATAAAMSILQQLLSLTPRLLLEAVEMEDDDFTI
 QY 961 SCITEQTYFFDNDKSGSVGLDCGNCRIHFHGEKLMNTNLIETMVSCKGTCPCI
 Db 949 SCITEQTYFFDNDKSGSVGLDCGNCRIHFHGEKLMNTNLIETMVSCKGTCPCI
 QY 1021 QAEQTSQDPNCDMVK 1036
 Db 1009 QAEQTSQDPNCDMVK 1024
 RESULT 7
 QY Q9UDQ3 PRELIMINARY; PRT; 745 AA.
 ID Q9UDQ3;
 AC 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 23, Last annotation update)
 DE WUGSC:H DJ0560014.1 protein (fragment).
 GN WUGSC:H DJ0560014.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063792; PubMed=9847074;
 RA Sulston J.E., Waterston K.;
 RT "Toward a complete human genome sequence.";
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Mead K., Bauer C.;
 RT "The sequence of Homo sapiens PAC clone RP4-560014.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston K.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006145; AAD20938.1; -.
 DR InterPro; IPR004010; Cache.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF02743; Cache; 1.
 DR Pfam; PF00092; vwa; 1.
 DR PROSITE; PS0234; VWF_A; 1.
 FT NON TER 1
 SQ SEQUENCE 745 AA; 84396 MW; BC07B53484B71EA4 CRC64;
 Query Match 67.4%; Score 3667; DB 4; Length 745;
 Best Local Similarity 99.7%; Pred. No. 2.1e-221;
 Matches 688; Conservative 1; Mismatches 1; Indels 0;
 QY 347 YNVSRANCNKIIMLFTDGGERAQEIIFKNYKDKKRVFRPSVQGHNYERGI

```
PRELIMINARY;          PRG;    1150 AA.

(TtEMBLrel. 15, Created)
(TtEMBLrel. 15, Last sequence update)
(TtEMBLrel. 23, Last annotation update)
nel, alpha 2/delta subunit 2.

; (Human).
; Craniata; Vertebrata; Ruteleostomi;
; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;
; Echinodermata; Cephalochordata; Hominidae; Homo.
);606;

OM N.A.
cid;

..
DEC-1999) to the EMEL/GenBank/DBJ databases.

OM N.A.
oid;
ai S., Marais E., Lacinova L.;
distribution and functional characterization of the calcium
hadelta-2 subunit."
http://www.genbank/dbj databases.
```


519 KKNQILGVGIDVALNDIKRLTPNYTLGANGYVFAIDLNGVLLHPNLKPIITIN
539 TLDFLDAELNDIKVEIRKMDIGSEGEKFTFLVKSDODERYIDKGNRTYTWTPVN
579 TLDFLDAELENDENKEETIRSMIDGKHQIIRTLVKSIDERYIDEVIRNYTWVPIR
599 SIALVLPYSPYTIKAEETITQARSKKGKMKDSITLKPDPFESGVTFTAPRDY
639 SUGLVLPYSPYTIQANLSQIILQVKLPISKLDPEFLLPSSFESEGHVFTAPREY
659 KISDNNTTEFLANFNEFIDRKTTPNNPSCNADLINRVLLDAGFTNELVONVWSKQ-N
699 NASDNNTTEFLKNFTIELMEKVTDPDSKQCNFLHLNLTLDGTITQOLVERVWRDQDLA
718 KARFVVTGGITRVVYPKEAGENQENPETYEDSFYKRSILDNDNTYFTAPYFNK-SC
759 LAVFAATDGGITRVFPNKAEDWTENPEPFAFYRSILDNRGYIYPKPPHQDSLFL
777 ES---GIMVSKAVEIYIQGLLKPAVVGIKIDVNSWIENF-----TKTSIROP---
819 ENDTVGVLVSTAVELSLGRTRLREAVVGVKLDLEAWAEKPKVLASNRTHODQPOKIK
826 ----VCDKRGNSDVMDCVILDDGGFLLMAHDDYTQIGRFFCEIDPDSLMRHLVN.
878 SSHCEMDCENVNEDLLCVLIDDGGFVLNSQNHQDQVGRFFSEVDANLMLALYNI
882 FNKSYDYQSVCEPGRAPKQAGHRSAYVPSVADILQIGMWATAAANSILQQFLLS:
938 RKESYDYQACAPQPPGNLGAAPRGVFTIADFLNLAWTTSAAANSILFQQLLYG
942 LLBAVEMEDDDFTASLSKOSCTITOTYFFNDSDKSPSGVLDCGNCSEIPIHGEKL
998 WFQADPAEAG-SPEPRESSCMVKQTYFYFSGVSNAYNAIIDCGNCSRLFHAQRL
1002 IFIMWSKGTCPDYTLILQASQ---TSDGPNPCDMVK 1036
1057 LFVVAEPLCSOCEVGRLLQKETHCPADGPEQCELVQ 1093

RESULT 10
Q9NY48 PRELIMINARY; PRT; 1143 AA.
AC Q9NY48
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium channel, alpha 2/delta subunit 2.
GN CACNA2D2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Klugbauer N.;
EL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the c
RL submitted alpha2delta2 subunit.";
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251367; CAB86192.1; --
DR InterPro; IPR004010; Cache.
DR pfam; PF02743; Cache; 1.
DR pfam; PF00092; vwa; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; WFER; 1.
SQ SEQUENCE 1143 AA; 129085 MW; 492556C9919A0CES CRC64;

:56:54 2004

53.7%; Score 2920.5; DB 4; Length 1143;
ity 54.3%; Pred. No. 2.6e-174;
servative 166; Mismatches 278; Indels 37; Gaps 14;

LFQSLIIPSSSEPPSAVITKSWDKQEDLVTLAKTAGVNLVDIYKYQD 66
LLPLAAPGASVSPFOHTMQHARRELOEVDGVMRIFGVQQLRIYKDNRN 103
ANARQVLEIARDIEKILSNESKALVSLAEAEKVQAHAHQWREDFASNEVYVN 126
NEPQKLVKAVAGDIESLDKVKQALKRLADAENFQKARWQDNKEEDIVYD 163
---DPKNDSEPGSQ--RIKPVIEDANFGRIQSIOHAAVHIPTDIYESTVLN 181
ELDDPSESDVERGSKASTLELDIEDPNFKQKVNYSYAAVQIPTDIYKSTVLN 223
3ALDEVFKKREEDPSLLMQVFGSATGLARYYPASVWDSNRTPNKIDLYDVER 241
3ALENFMENRRQDPTLLMQVFGSATGVTRYYPATPW----RAPKKIDLYDVER 279
3AASPDKMLILVDVSGVSGTLKLRISVSEMLETLSDDDFNVVASFNNAQDV 301
GASSPKDMVIIVDVSGVSGTLKLRISVSEMLETLSDDDFNVVASFNNAQDV 339
LVQANRNKVKLVDAVNNITAKGIDTYKGFSPAFQEQLLNYSVSRANCKIMLF 361
LVQANRNKVKLVDAVNNITAKGIDTYKGFSPAFQEQLLNYSVSRANCKIMLF 399
LVQANRNKVKLVDAVNNITAKGIDTYKGFSPAFQEQLLNYSVSRANCKIMLF 420
ERAQIEFNKYN-KDKKVVFRFSGVQOHYERGPLOMACENKGVYIPLSGAIR 459
DRVQDVFEKYNWNRTRVFTVFTSVGOHNYDVTPLQMACANKGVYIPLSGAIR 480
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 517
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 540
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 577
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 600
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 637
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 660
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 690
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 719
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 750
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 778
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 810
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 825
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 859
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 884
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 929
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YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 989
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 1004
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 1048
YLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGFENKTNLK 1084

DB 1049 VAEKPLCSOCEAGRLLOKETHSDGPEQCELVQ 1080

RESULT 11

Q9EQG2 PRELIMINARY; PRT; 1156 AA.

ID Q9EQG2

AC Q9EQG2; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE Voltage-dependent calcium channel alpha-2-delta-2 subunit.

GN CACNA2D2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=TKDU;

RC MEDLINE=21015416; PubMed=11130987;

RX Barclay J., Rees M.;

RA "Genomic organization of the mouse and human alpha2delta2 voltage-

RT dependent calcium channel subunit genes.";

RL Mamm. Genome 11:1142-1144 (2000).

DR EMBL; AF247139; AAG47846.1; --

DR MGD; MGI:1929813; CACNA2D2.

DR InterPro; IPR004010; Cache.

DR InterPro; IPR002035; VWF_A.

DR Pfam; PF02743; Cache; 1.

DR Pfam; PF00092; vwa; 1.

DR SMART; SM00327; VWA; 1.

DR PROSITE; PS0234; VWF_A; 1.

DR PROSITE; PS0234; VWF_A; 1.

SQ SEQUENCE 1156 AA; 130611 MW; A732545A2B302A52 CRC64;

Query Match 53.6%; Score 2918.5; DB 11; Length 1156;
Best Local Similarity 53.8%; Pred. No. 3.6e-174; Indels 33; G
Matches 568; Conservative 173; Mismatches 282;

QY 6 LLALTTLFOSLLIGP-SSEPPPSAVITKSWDKQEDLVTLAKTAGVNLVDI
45 LLLPPELPLLLPTAPGASVSPFOHTMQHARRELOEVDGVMRIFGVQQLREI
65 QDLTVFPNARQVLEIARDIEKILSNESKALVSLAEAEKVQAHAHQWREDFASN
105 RNLFEVQENEPQKLVKAVAGDIESLDKVKQALKRLADAENFQKARWQDNKEE
125 YNAKDDL---DPEKNDSEPGSQ--RIKPVIEDANFGRIQSIOHAAVHIPTDIYK
165 YDAKADAELDDPESEDMERGSKTSALRLDFIEDPNFKQKVNYSYAAVQIPTDIYK
180 LNELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASVWDSNRTPNKIDI
225 LNELNWTSALEDEVFKKREEDPSLLMQVFGSATGLARYYPASVWDSNRTPNKIDI
240 RRPWTIOGASPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDFNVVASF
281 RRPWTIOGASSPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDFNVVASF
300 DYSCFOHLQVANNRNKVKLVDAVNNITAKGIDTYKGFSPAFQEQLLNYSVSRAN
341 PVSCFTHLQVANNRNKVKLVDAVNNITAKGIDTYKGFSPAFQEQLLNYSVSRAN
360 LFTDGGEEARQELFNKCN-KDKKVVFRFSGVQOHYERGPLOMACENKGVYIY
401 MFTDGGEDRQVDFEYKYNWNRTRVFTVFTSVGOHNYDVTPLQMACANKGVYI
419 IRINTQYLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGF
461 IRINTQYLDVLRPWLKAGKAKQVQWNTVYLDALGLVITGLTPVNFITQGF
479 LKNQLILGWVGVDVSLSDIKELTFRFLCPNGYYPATDPNGYVLLHRNLOPKNFI

7:56:54 2004

105 RNLFEVQENEPQKLVEKVGADIESLLDRKVOALKRLADAAENFQKAHRWQDNKEED:
 125 YNAKDL--DKKNDSEPGSQ--RIKPVFIEDANFRQISYQAAVHIPDIIYEGS'
 165 YDAKADAEALDDPESEDMERGSKTSALRLDFTEDPNFKKNYSYTAQVPIPTIYKGS
 180 LNELNWTSALEDEVFKKREEDPSLLWQVFGSATGLARYVPASPMWDSRTPNKIDLY
 225 LNELNWTSALEDEVFKKREEDPSLLWQVFGSATGLARYVPASPMWDSRTPNKIDLY
 240 RRPWYIQAASPKDMLILVDYSGSYGLTLKIRTSVSEMLETSLDSDDDPVNVASFS
 281 RRPWYIQAASPKDMLILVDYSGSYGLTLKIRTSVSEMLETSLDSDDDPVNVASFS
 300 DVSCHLVOANVRNKKVLKDAVNITAKGITYKKGFSFAFEOLLNYSRANCN
 341 PVSCTHLVQANVRNKKVKEAVQGMVAGTGYKAGFEYAFDQNSNITRANCN
 360 LFTDGGEEARAEIENKYN-KDKKVRFRSVGOHNYERGPIONMACENKGYVEIP:
 401 MFTDGGEDRVQDVFEKYNWPNRTVRVTFVSGQHNVDVTPLOWNACTNKGYVEIP:
 419 IRTNQBYLDVLRGPMVLADKAKQVQWTVNVDLDALEGLVITGTLPVFNITQGE
 461 IRTNQBYLDVLRGPMVLADKAKQVQWTVNVDLDALEGLVITGTLPVFNITQ--D
 479 LKNOLILGVMGVDSLEDIKELTPRFTLCPNGYVFAIDPNGYVLLHNPLOKPKS
 519 KKNOLILGVMGVDSLEDIKELTPRFTLCPNGYVFAIDPNGYVLLHNPLOKPKS
 539 TLDLDALENDIKVIRNKMIDGESKERTLVKSODERYIDKGNRTYTTPV
 579 TLDLDALENDIKVIRNKMIDGESKERTLVKSODERYIDKGNRTYTTPV
 599 SLALVLPYFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRD:
 639 SLGLVLPYFYIYKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRD:
 659 KTDANNTREFLNFBFIDRKTNNPNSCNADLNRLVLDAGFTNELVONTWSKQK-
 692 NASDNNTEFLKPIELMEKVTDPDSKQNNFLNLILDTGITQOLVERVRQDL
 718 KARFVVTGGITRVYPKEAGENWQENPETEYEDSFYKRSNDNDNYVFTAPYFNK-S
 752 LAVFAATDGGITRVFPNKAADWTEPENPFNASFYRSLDNHGYIFKPPHODSLL
 777 ES---GIMVSKAYEIVIOGLKAPVAVGVIKIDVNSWIENF-----TKTSIRDP--
 812 ENDTVGLVSTAVELSIGRTLRPAVVGKLDLEAWAEKPKVLASNRTHODQPOF
 826 ----VCDCKRNSDVMDCVILDDGGLFMANHDDYTNOIGRFFGIDPSPMRHLV
 871 SSHCEMDCEVNNEDLLCVLIDGGLFVLSNQNHQWQVGRFFSEVDANLMLALV
 882 FNKSYDYOSVCEPGAAPKQAGHRSAYVPSVADILQIGMWATAAASWILQOFLIL
 931 RKEVDYIOACAPOPPGNLGAAPRGVFTIADFLNLAWMTSAAASWILQOFLIL
 942 LLEAVEMEDDDFTASLSKOSICITEQYFFDNDSKSGVGLDCGNCRSIFHEK
 991 WFOADPAEARG-SPETRESSCVMKQTYFYFGSVNAYNAILDCGNCRSLEHAQR
 1002 IFIMVESKGTCPDTRLLIQABOTSQDGNPCDMVK 1036
 1050 LFFVAEKLCSQCEAGRLLOKETHSDGPEQCELVQ 1084

RESULT 13

Q9Y268 PRELIMINARY; PRT; 1145 AA.
 ID Q9Y268
 AC Q9Y268;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)

116 LGMGIDVALNDIKELTPNYTLGANGYVFAIDNGYVLLHNPLOKQTNFREP 578
 125 JAELENDIKVEIRNKMIDGESKERTLVKSODERYIDKGNRTYTTPVNGTGY 598
 165 DAELENDIKVEIRNKMIDGESKERTLVKSODERYIDKGNRTYTTPVNGTGY 638
 180 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 658
 225 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 698
 240 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 717
 281 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 758
 300 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 776
 341 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 818
 360 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 825
 401 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 877
 419 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 882
 461 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 937
 479 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 942
 519 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 997
 539 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 1002
 579 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL 1056
 599 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
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 692 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 718 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 752 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 777 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 812 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 826 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 871 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 882 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
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 991 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 1002 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL
 1050 LPTSIFYIKAKLEETITQARSKKGMKDSSETLKPDPNFESGTYFAPRYCNDL

PRELIMINARY; PRT; 1148 AA.

(Tremblrel. 23, Created)
 (Tremblrel. 23, Last sequence update)
 (Tremblrel. 23, Last annotation update)

nel.

(Mouse).

Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

0090;

M N A.

J/67; TISSUE-Retina;

54683; PubMed:12466851;

Consortium.

genome Exploration Research Group Phase I & II Team;

f the mouse transcriptome based on functional annotation of

-length cDNAs.

563-573(2002).

603; BAC31998.1; --

1148 AA; 129780 MW; 9B49FF0547F82851 CRC64;

53.68; Score 2916.5; DB 11; Length 1148;

ilarity 53.94; Pred. No. 4.7e-174;

Conservative 169; Mismatches 278; Indels 39; Gaps 15;

ALTLTFLQSLIGP-SSEBPPFSAYTIKSWDKMQEDLVTLAKTASGVNQLVDIYEKY 64

LLPPLLLLPLTAPGASAYFFQOHTMQHWRRLQEIDGVMRIFGGVQQLREIYKDN 104

DLVTFEPNNAQVETAAARDIEKLLNRSKALVSLALEAEKVAQAQHWREDFASRVY 124

23 react annotation update)

protein KIAA0558.

man).
zoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cataxhini; Hominidae; Homo.

.A.
Parif E., Ding J., Lin J., Mathis M.,
E-M

candidate human tumor suppressor gene located in the
all lung cancer homozygous deletion region homologous to
calcium channel alpha 2/ delta subunit.";
calcium channel alpha 2/ delta subunit.";

I.A. Kashuba V.I.

f F., Duh F.-M., Adreazzoli-Angerona E., Johnson B., Lerman M.I.; delta subunit of the L-type voltage gated calcium channels in the lung cancer critical region on 3p21.3.";

V.A.

45; PubMed=9628581; Tanaka A., Kotani H., Nomura N.,

Okawa K., Miyajima N., and Tanabe T. (1990) the coding sequences of unidentified human genes. IX. sequences of 100 new cDNA clones from brain which can encode proteins *in vitro*."

39(1998).

; AAC70914.1;

1: AAB96913.1;
1: PAB25484.1;

CACNA2D2.

004010; Cache.

002035; VWF_A.
Cabo. 1

- wwa: 1.

7; VWA; 1.

234; VWFA; 1.

protein. 129268

1-44-61

53.48

conservative

4. 7. 2009

LTLEQSLIGPSS:

IPI.T.PT.T.AAPCAS

2025 RELEASE UNDER E.O. 14176

TEPNNARQLVEIAA

ОБЩЕСТВО С ОГРАНИЧЕННОЙ ОТВЕТСТВЕННОСТЬЮ

GENERAL ENQUIRY

DL---DPEKNDSEP

|||

DAEJONG

WTSALDEVFKKNRE

||| : ||| :

ATEALENVFMENT

IOGAASPKDMLIL

Figure 1

IQGASSPKDMVII

HOHLVOANVRNKKV

11-11-11

THLVQANVRNKKV

[illegible]

RESULT 14

Q8CHE9	PRELIMINARY; PRT; 1098 AA.
ID	
AC	
Q8CHE9;	(T-REMBRel. 23, Created)
DT	01-MAR-2003 (T-REMBRel. 23, Last sequence update)
DD	01-MAR-2003 (T-REMBRel. 23, Last annotation update)
DE	KTIAA0558 protein (Fragment).
DE	KTIAA0558.
CN	Mus musculus (Mouse).
OS	Mus musculorum (Musculi); Vertebrata; Euteleostomi
OC	Eukaryota; Metazoa; Chordata; Rodentia; Muridae; Murinae; Mu
OC	mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RA	Oikarinen M., Kinnunen R., Ohara Y., Nagase T.,
RA	Oikarinen M., Kinnunen R., Ohara Y., Nagase T.,
RA	"Prediction of the coding sequences of mouse homologues of KIAA
RT	I. The complete nucleotide sequences of 100 mouse KIAA-homologous
RT	cDNAs identified by screening of terminal sequences of cDNA clon-
RL	randomly sampled from size-fractionated libraries.";
RL	Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.

[illegible]

:56:54 2004

February 20, 2004, 16:58:11
secs

[illegible]

February 20, 2004, 16:58:11
secs

us-10-090-827-14.rapb

7:56:53 2004

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

1 search, using sw model

uary 20, 2004, 16:58:20 ; Search time 30.9105 Seconds
(without alignments)
7017.684 Million cell updates/sec

10-090-827-14

3 RAGCLLALTLFQSLIG.....RLIIQAETSDGNPCDMVK 1036

SUM62

op 10.0 , Gapext 0.5

455 seqs, 209382283 residues

s satisfying chosen parameters: 801455

jth: 0

jth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications AA:
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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3 the number of results predicted by chance to have a
3r than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
00.0	1036	15	US-10-090-827-14	Sequence 14, Appl
00.0	1063	15	US-10-090-827-15	Sequence 15, Appl
00.0	1091	9	US-09-875-423-4	Sequence 4, Appl
00.0	1091	12	US-10-162-102-17	Sequence 17, Appl
00.0	1091	15	US-10-162-102-17	Sequence 17, Appl
00.0	1091	15	US-10-090-827-16	Sequence 16, Appl
99.3	1086	12	US-10-375-253-49	Sequence 49, Appl
99.0	1084	12	US-10-375-253-53	Sequence 53, Appl
98.8	1036	15	US-10-090-827-7	Sequence 7, Appl
98.8	1063	15	US-10-090-827-8	Sequence 8, Appl
98.8	1069	15	US-10-090-827-9	Sequence 9, Appl
98.8	1091	15	US-10-090-827-5	Sequence 5, Appl
98.6	1103	12	US-10-375-253-47	Sequence 47, Appl
98.2	1079	12	US-10-375-253-51	Sequence 51, Appl
98.2	1018	15	US-10-090-827-13	Sequence 13, Appl

16	5316	97.7	1091	12	US-10-375-253-20	Sequence 2
17	5288	97.2	1018	15	US-10-090-827-6	Sequence 6
18	2907.5	53.4	1145	15	US-10-116-949-2	Sequence 2
19	2907.5	53.4	1145	15	US-10-116-949-4	Sequence 4
20	2886.5	53.0	1076	15	US-10-116-949-6	Sequence 6
21	1085	19.9	1091	9	US-09-875-423-5	Sequence 5
22	1085	19.9	1091	12	US-10-162-102-18	Sequence 1
23	1085	19.9	1091	15	US-10-162-012-18	Sequence 2
24	1084	19.9	1091	9	US-09-875-423-2	Sequence 1
25	1084	19.9	1091	12	US-10-162-102-15	Sequence 1
26	1084	19.9	1091	15	US-10-162-012-15	Sequence 1
27	1051	19.3	1090	12	US-09-833-222A-10	Sequence 1
28	1051	19.3	1090	12	US-10-119-624-10	Sequence 2
29	365.5	6.7	223	14	US-10-005-168-2	Sequence 2
30	343.5	6.3	1223	11	US-09-964-256A-2	Sequence 4
31	343.5	6.3	1223	12	US-10-146-733-44	Sequence 3
32	286	5.3	75	12	US-10-264-049-3575	Sequence 4
33	272	5.0	51	9	US-09-864-761-44281	Sequence 3
34	272	5.0	53	9	US-09-864-761-38267	Sequence 3
35	190	3.5	35	9	US-09-864-761-38318	Sequence 3
36	187	3.4	74	12	US-10-029-386-28507	Sequence 3
37	185	3.4	35	9	US-09-864-761-36461	Sequence 5
38	182	3.3	885	9	US-09-828-423-5	Sequence 1
39	169	3.1	497	12	US-10-334-143-23	Sequence 1
40	167	3.1	796	12	US-10-369-493-18214	Sequence 1
41	161	3.0	1829	12	US-10-435-766-13	Sequence 1
42	159.5	2.9	173	11	US-09-992-600A-100	Sequence 1
43	159.5	2.9	173	11	US-09-924-340-100	Sequence 1
44	159.5	2.9	173	12	US-09-992-095B-100	Sequence 1
45	159.5	2.9	173	12	US-10-154-678-100	Sequence 1

ALIGNMENTS

RESULT 1
US-10-090-827-14
; Sequence 14, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sul
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-14

Query Match 100.0%; Score 5443; DB 15; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0;
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Db 1 MAAGCLLALTLFQSLIGPSSEPPPSAVTIKSWDKMQEDLVTLAKTASGV
Qy 61 YEKQDLYTVEPNARQLVEIAARDIEKLNSRKALVSLAEKQVAAHWR
Db 61 YEKQDLYTVEPNARQLVEIAARDIEKLNSRKALVSLAEKQVAAHWR
Qy 121 EWYVYNAKDDLDPKNDSEPGSQRIKVFIEDANFGRIQISYQHAHVHPTDIYEK
Db 121 EWYVYNAKDDLDPKNDSEPGSQRIKVFIEDANFGRIQISYQHAHVHPTDIYEK
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 1021 QABQTSQDGNPCDMVK 1036
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RESULT 4
 US-10-162-102-17
 Sequence 17, Application US/10162102
 Publication No. US20030232336A1
 GENERAL INFORMATION:
 APPLICANT: Curtiss, Rory A.J.
 APPLICANT: Silos-Santiago, Immaculada
 APPLICANT: Gu, Wei
 TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY
 FILE REFERENCE: 10448-190001
 CURRENT APPLICATION NUMBER: US/10162,102
 CURRENT FILING DATE: 2003-04-04
 PRIOR APPLICATION NUMBER: US 60/209,845
 PRIOR FILING DATE: 2000-06-06
 PRIOR APPLICATION NUMBER: US 09/875,321
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: PCT/US01/18340
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/209,257
 PRIOR FILING DATE: 2000-06-05
 PRIOR APPLICATION NUMBER: US 09/875,423
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: PCT/US01/18398
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/209,238
 PRIOR FILING DATE: 2000-06-05
 PRIOR APPLICATION NUMBER: US 09/875,363
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: PCT/US01/18247
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/227,068
 PRIOR FILING DATE: 2000-08-22
 Remaining prior application data removed - See File Wrapper or PAL
 NUMBER OF SEQ ID NOS: 48
 SOFTWARE: Fast-Seq for Windows Version 4.0
 SEQ ID NO 17

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 DGNPCDMVK 1036
 DGNPCDMVK 1036
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 081657A1
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 1, RORY A.J.
 N: 21784, A NOVEL HUMAN CALCIUM CHANNEL
 N: FAMILY MEMBER AND USES THEREOF
 0448-059001
 ON NUMBER: US/09/875,423
 ATE: 2001-06-05
 I NUMBER: US 60/209,257
 3: 2000-06-05
 NOS: 6
 2 for Windows Version 4.0
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 100.0%; Score 5443; DB 9; Length 1091;
 rity 100.0%; Pred. No. 0;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 6
US-10-090-827-16
; Sequence 16, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subunit
; FILE REFERENCE: 179
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-090-827-16
Query Match 100.0%; Score 5443; DB 15; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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DB 61 YEKYQDLVTVBNARQVIAARDIEKLISNRSKALVSLALEAEKVAQAHOHWRDE
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DB 121 EYVYVNAKDDLPKNDSEPGSQRKIPVFIEDANFGRQISYQHAHVHIPTDIYEGST
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DB 241 RPYVIOGAASPKOMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVSFNS
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DB 361 FTDCGGERAQEIFNKYNKDKKVRFRFVSQGHNYERGPIONMACENKGYVYIEIPSI
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DB 421 INTQEXLDVLGRPMVLGAKAKQVQWNTVYLDLAEGLVITGTLPVFNITGQFEN
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DB 481 NQLILGVMGVDVSLIEDIKRLTPTFTLCPNGYYPFADIPNGYVLLHPLNLPKNPKSQ
QY 541 DPLDAELNDIKVEIRNKMIDGSGSKTFTLTKSODERYIDKGNRTYTPVNG
DB 541 DPLDAELNDIKVEIRNKMIDGSGSKTFTLTKSODERYIDKGNRTYTPVNG
QY 601 ALVLTYSFYIYKAKLETTIQAARKKGMKDSSTLAPDNFESGYTFIAPRDYCI
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QY 661 SDNNTTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK
DB 661 SDNNTTEFLNFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQYWSKQKNIK

7:56:53 2004

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JS20040018510A1
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ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ION: METHODS
SD9813DA
TION NUMBER: US/10/375,253
DATE: 2003-02-27
ON NUMBER: 08/450,273
TE: 1995-05-25
ON NUMBER: 08/404,354
TE: 1995-02-15
ON NUMBER: 07/914,231
TE: 1992-07-13
ON NUMBER: 08/314,083
TE: 1994-09-28
ON NUMBER: 07/914,231
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TE: 1993-11-05
ON NUMBER: 08/105,536
TE: 1993-08-11
ON NUMBER: 08/149,097
TE: 1993-11-05
Application data removed - See File Wrapper or PALM.
ID NOS: 65
SEQ for Windows Version 4.0

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Conservative 99.5%; Pred. No. 0; Mismatches 0; Indels 5; Gaps 1;
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RESULT 8
US-10-375-253-53
; Sequence 53, Application US/10375253
; Publication No. US20040018510A1

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VA	KDDLDP	PKNDSE	PGSQR	IKPV	IEDAN	FGROI	SYQHA	VHLP	TDI	YEG	STIVL	180																																							
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YL	D	V	L	G	R	P	M	L	A	G	K	A	Q	O	V	N	T	N	V	L	D	A	E	L	G	V	I	T	G	L	T	P	V	N	I	T	O	Q	E	N	T	N	L	K 480							
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LG	W	M	V	G	D	V	S	L	E	D	I	K	R	L	T	P	R	T	L	C	P	N	G	Y	F	A	I	D	P	N	G	V	L	L	H	P	N	I	O	P	N	K	S	Q	E	P	V	T	L 540		
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AE	L	E	N	D	I	K	V	E	I	R	N	K	M	I	D	G	S	E	G	E	T	F	R	T	L	V	K	S	O	B	E	R	Y	I	D	K	G	N	R	Y	T	T	P	V	N	G	T	D	Y	S	L 600
AE	L	E	N	D	I	K	V	E	I	R	N	K	M	I	D	G	S	E	G	E	T	F	R	T	L	V	K	S	O	B	E	R	Y	I	D	K	G	N	R	Y	T	T	P	V	N	G	T	D	Y	S	L 600
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TE	F	L	L	N	F	E	I	D	R	T	P	N	N	S	C	N	A	D	L	I	N	R	V	L	L	D	A	G	F	T	N	E	L	V	O	N	Y	W	S	K	O	K	N	I	G	V	K	A			

Publication US/10090827
 . US20030073132A1
 ATION:
 mer-Lambert
 ATION: Method for the screening of alpha 2 delta-1 subunit
 ATION: binding ligands

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FILE REFERENCE: 179
CURRENT APPLICATION NUMBER: US/10/090,827
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: US/09/397,549
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 1063
TYPE: PRT
ORGANISM: Sus scrofa
US-10-090-827-8

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Query Match	98.8%;	Score 5380;	DB 15;	Length 1063;
Best Local Similarity	98.7%;	Prod. No. 0;		
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DB	1	MAAGCLLALTLFQSLILGPSSQEPFPSSATYIKSWDKMQEDLVTLAKTASGVNQI		
QY	61	YEKQDLYTYVEPNNAQLVEIARIDIEKLLSNRKSALVSLALEAEKVQAAAHQWRED		
DB	61	YEKQDLYTYVEPNNAQLVEIARIDIEKLLSNRKSALVRLALEAEKVQAAAHQWRED		
QY	121	EVVYTNAKDLDLPEKNDSEPGSQRIKPVFIEDANFGROI SYQHAAVHIPTDIYEGS		
DB	121	EVVYTNAKDLDLPEKNDSEPGSQRIKPVFIDIDANFGROI SYQHAAVHIPTDIYEGS		
QY	181	NELNWTSAIDVFFKKNREEDPSLLWQVFGSAGTLARYYPASPWDNSRTPNKIDLY		
DB	181	NELNWTSAIDVFFKKNREEDPSLLWQVFGSAGTLARYYPASPWDNSRTPNKIDLY		
QY	241	RPWYTOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDPWNVASFNS		
DB	241	RPWYTOGAASPKDMLILVDVSGVSGITLKLIRTSVSEMLETLSDDDPWNVASFNE		
QY	301	VSCFQHLVQAVNRKVKVLKQAVNNI TAKGITDYKKGFSFAPEQLIANYNSRANCW		
DB	301	VSCFQHLVQAVNRKVKVLKQAVNNI TAKGITDYKKGFSFAPEQLIANYNSRANCW		
QY	361	FTDGGERAQEIFNKYNKKVRVFRPSVGOHNVERGPIQWMAACENKGYIYEIIPS		
DB	361	FTDGGERAQEIFAKYNKKVRVFTFSVGOHNYDRGPIQWMAACENKGYIYEIIPS		
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DB	481	NQLILGVMGVDVLSLEDI KRLTPRFTLCPNGYTFPAIDPNGVYLLHPLNQENPKSQ		
QY	541	DFDLAELENDIKVETRNKMDIGESGEKTRFLVKSQDERYIDKGNRTYTWTPVNG		
DB	541	DFDLAELENDIKVETRNKMDIGESGEKTRFLVKSQDERYIDKGNRTYTWTPVNG		
QY	601	ALVLPYTSFYVIKALEETITQARSKGKMKDSTLKPDPNFSSGTYTFIAPRDYC		
DB	601	ALVLPYTSFYIIVKALEETITQARSKGKMKDSTLKPDPNFSSGTYTFIAPRDYC		
QY	661	SDNNTEFLANFNBFIDRKTPNPNPSCNADLINRVLLDAGFTNELVQNTWSKQNIK		
DB	661	SDNNTEFLANFNBFIDRKTPNPNPSCNTDLINRVLLDAGFTNELVQNTWSKQNIK		
QY	721	PVVTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNTVFTAPYFNKSGPGF		
DB	721	PVVTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNTVFTAPYFNKSGPGF		
QY	781	MYSKAVEIYIOGKLLKPAVVGIKIDVNSNIENFTKTSIRDPACGVPDCCKRSDI		
DB	781	MYSKAVEIYIOGKLLKPAVVGIKIDVNSNIENFTKTSIRDPACGVPDCCKRSDI		

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SDGNPCDMVK 1036
c cation US/10090827
IS20030073132A1
ON:
r-Lambert
ON: Method for the screening of alpha 2 delta-1 subunit
ON: binding ligands
179
TION NUMBER: US/10/090,827
DATE: 2002-03-06
ON NUMBER: US/09/397,549
TE: 1999-09-16
NOS: 21
In Ver. 2.1
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arity 98.8%; Score 5380; DB 15; Length 1069;
onservative 6; Mismatches 7; Indels 0; Gaps 0;
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CLLALTTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDI 60
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Db 481 NQLILGVMGVDVSLIEDIKRLTPRTILCPNGYFFAIDPNGYVLLHPNLOPKPKSQEP
QY 541 DFLDAELENDIKVELIRNKWIDGESGEKTRTLVKSQDSERYIDKGNRTYTTWTVPVNGTL
Db 541 DFLDAELENDIKVELIRNKWIDGESGEKTRTLVKSQDSERYIDKGNRTYTTWTVPVNGTL
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Db 601 ALVLPTYSFYIKAKLEETITQARSKKGMKDSSETLKPDNPFESGYTIFAPRDYCNM
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Db 721 FVVTGGITRVYPKBAGENQWENPEYEDSFYKRSILDNDNYFTAPYFNKSGPGAYI
QY 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPYCDCKRNSDVM
Db 781 MYSKAVEIYIOGKLLKPAVVGKIDVNSWIEFTKTSIRDPKAGPYCDCKRNSDVM
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Db 841 LDDGGFILMANHDDVTNOIGRFFGIBDPSLMRHLVNIISVYAFNKSVDYOSVCEPAA
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Db 901 GAGHRSAYVPSVADILQICGWATAAASWTLQOFLLSLTPRLLLEAVEMEDDDFTAS
QY 961 SCITEQTYFFDNDKSKFSVGLDCGNCSPRIFHGEKLMNTNLIIFIMVESKGTGTCPT
Db 961 SCITEQTYFFDNDKSKFSVGLDCGNCSPRIFHGEKLMNTNLIIFIMVESKGTGTCPT
QY 1021 QAEQTSDDGNPCDMVK 1036
Db 1021 QAEQTSDDGNPCDMVK 1036

RESULT 12
US-10-090-827-5
; Sequence 5, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sul
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-5
Query Match 98.8%; Score 5380; DB 15; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0;

QY 1 MAAGCLLALTTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN
Db 1 MAAGCLLALTTLFQSLIGPSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVN
QY 61 YEKQDLYTVENNAQVIEIARDEIKLLSNRSLVLALEAEKVQAAHQWRE

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TITLE OF INVENTION: METHODS									
FILE REFERENCE: SD9813DA									
CURRENT APPLICATION NUMBER: US/10/375,253									
CURRENT FILING DATE: 2003-02-27									
PRIOR APPLICATION NUMBER: 08/450,273									
PRIOR FILING DATE: 1995-05-25									
PRIOR APPLICATION NUMBER: 08/404,354									
PRIOR FILING DATE: 1995-02-15									
PRIOR APPLICATION NUMBER: 07/914,231									
PRIOR FILING DATE: 1992-07-13									
PRIOR APPLICATION NUMBER: 08/314,083									
PRIOR FILING DATE: 1994-09-28									
PRIOR APPLICATION NUMBER: 07/914,231									
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PRIOR FILING DATE: 1994-08-11									
PRIOR APPLICATION NUMBER: 08/149,097									
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PRIOR APPLICATION NUMBER: 08/105,536									
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7:56:53 2004

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; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Human
US-10-375-253-51

Query Match
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Matches 1023; Conservative 0; Mismatches 1; Indels 12; Gaps
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ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ION: METHODS
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DATE: 2003-02-27
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7:56:53 2004

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ION:
r-Lambert
ION: Method for the screening of alpha 2 delta-1 subunit
ION: binding ligands
179
TION NUMBER: US/10/090.827
DATE: 2002-03-06
ON NUMBER: US/09/397,549
FE: 1999-09-16
D NOS: 21
cin Ver. 2.1

sapiens

98.2%; Score 5346; DB 15; Length 1018;
arity 100.0%; Pred. No. 0;
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GenCore version 5.1.6
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in search, using sw model

bruary 20, 2004, 16:48:25 ; Search time 11.3006 Seconds
(without alignments)
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-10-090-827-14

43 MAAGLLALTLTFLQSLIG.....RLLIQAEQTSQGNPCDMVK 1036

OSUM62

pop 10.0 , Gapext 0.5

7863 seqs, 47026705 residues

ts satisfying chosen parameters: 127863

gth: 0

gth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

WiseProt_41.*

; the number of results predicted by chance to have a
; r than or equal to the score of the result being printed,
; ed by analysis of the total score distribution.

SUMMARIES

Arch	Length	DB	ID	Description
10.0	1091	1	CIC2 HUMAN	P54289 homo sapien
96.2	1091	1	CIC2 RAT	P54290 rattus norv
96.0	1106	1	CIC2 RABIT	P13806 oryctolagus
13.1	1249	1	UN36 CAPEL	P34374 caenorhabdi
3.6	886	1	ITH3 MOUSE	Q61704 mus musculu
3.3	885	1	ITH3 HUMAN	Q06033 homo sapien
3.3	887	1	ITH3 RAT	Q63416 rattus norv
3.0	886	1	ITH3 MESAU	P97280 mesocricetu
3.0	1829	1	DPOL_THREST	C13845 thermococcu
2.9	1956	1	ATX1 PLAPA	Q04956 plasmodium
2.9	575	1	YFBK ECOLI	P76481 escherichia
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2.8	921	1	ITH4 PIG	P79263 sus scrofa
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2.7	930	1	ITH4 HUMAN	Q14624 h inter-alp
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ALIGNMENTS

RESULT 1
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ID -CIC2 HUMAN STANDARD; PRT; 1091 AA.
AC P54289;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.
GN CACNA2D1 OR CACNL2A OR CCHL2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92110010; PubMed=1309651;
RA Williams M.E., Feldman D.H., McCue A.P., Brenner R.,
RA Velicelebi G., Ellis S.B., Harpold M.M.;
RT "Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype";
RL Neuron 8:71-84(1992)
CC -FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT R
CC -FUNCTION: CONTRACTION COUPLING.
CC -SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBU
CC ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
CC HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
CC -SUBCELLULAR LOCATION: Integral membrane protein.
CC -TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE
CC AORTA TISSUES
CC -PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE
CC A PRECURSOR FORM (BY SIMILARITY).
CC -SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
CC -SIMILARITY: Contains 1 VMFA domain.

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the European Bioinformatics Institute. There are no restrictic
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or send an email to license@isb-sib.ch).

CC EMBL; M76559; AAAS1903.1; --
CC PIR; JH0565; JH0565.
CC Genew; HGNC:1399; CACNA2D1.
CC MIM; 114204; --
CC GO; GO:0005891; C: voltage-gated calcium channel complex; TAS.
CC GO; GO:0015270; F: dihydropyridine-sensitive calcium channel a..
CC GO; GO:0006832; P: small molecule transport; TAS.
CC InterPro; IPR004010; Cache.
CC InterPro; IPR002035; VNF_A.
CC Pfam; PF02743; Cache; 1.
CC Pfam; PF00092; vwa; 1.
CC SMART; SM00327; VWA; 1.
CC PROSITE; PS50234; VMFA; 1.

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 (Rel. 36, Created)
 (Rel. 36, Last sequence update)
 (Rel. 41, Last annotation update)
 trypsin inhibitor heavy chain H3 precursor (ITI heavy
 ater-alpha-inhibitor heavy chain 3).
 (Mouse).
 etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 0090;
 M N A.
 /6N; TISSUE=Liver;
 4326; PubMed=7534067;
 ler J.-L., Raguez G., Salier J.-P.;
 eavy-chain precursors for the inter-alpha-inhibitor
 use: new members of the multicopper oxidase protein group
 ntial transcription in liver and brain.";
 306:505-512(1995).
 I: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 IG THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 ATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 AL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 ITY).
 : I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 . INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 JNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 , AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.
 SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
 AVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 TE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 ITY).

CC -!- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -!- SIMILARITY: Contains 1 WFPA domain.
 CC This SWISS-PROT entry is copyright. It is produced through a colla
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 CC -----
 CC EMBL: X70393; CAA49843.1; -;
 DR PIR: S54355; S54355.
 DR MGI: 96620; Itih3.
 DR InterPro: IPR006587; VIT.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00609; VIT; 1.
 DR SMART: SM00327; VWA; 1.
 DR PROSITE: PS0234; VWEA; 1.
 DR Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 30
 FT CHAIN 31 646
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 FT PROPEP 647 886
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 FT SEQUENCE 886 AA; 98977 MW; 15955308CF5030A CRC64;
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 Db 154 EELL-KRNGKVEMLKVQPKQLVRHFEID-----AHIFEP-
 QY 147 PVFIEDANFGRQISYOHAAVHIPTDIYEGSTIVLNLNWTSLALDEVFKKRBEDP
 Db 190 GISMLDAE-----ASPTINDL-LGSALTQSF-----
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MEDLINE=91093267; PubMed=1898736;
Englind J.J., Salvesen G., Hefta S.A., Thøgersen I.B.,
Rutherford S., Pizzo S.V.,
"Chondroitin 4-sulfate covalently cross-links the chains of the
human blood protein pre-alpha-inhibitor";
J. Biol. Chem. 266:747-751(1991).
-I- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
-I- SUBUNIT: 1-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (1-ALPHA-I) IS COMPOSED OF H1,
AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (1-ALPHA-LI) OF H2 AND
BIKUNIN. AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN
-I- PTM; HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.
-I- SIMILARITY: BELONGS TO THE ITIH FAMILY.
-I- SIMILARITY: CONTAINS 1 VWFA DOMAIN.

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modified and this statement is not removed. Usage by and for com-
mercial entities requires a license agreement (See <http://www.isb-sib.ch/itih/>).
Contact: info@isb-sib.ch

```

MM; 146650; . P:plasma glycoprotein; TAS.
DR GO; GO:0005211; F:plasma protein; TAS.
DR GO; GO:0005209; F:plasma protein; TAS.
DR InterPro; IPR006587; VIT.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00609; VIT; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Serine protease inhibitor; Repeat; Signal; Multigene family;
XW Glycoprotein. 1 17
FT SIGNAL 18 30
FT PROPEP 31 647
FT CHAIN H3.
FT FT
FT FT
FT PROPEP 648 885
FT DOMA1X 278 438
FT CARBOHYD 87 87
FT CARBOHYD 576 576
FT BINDING 647 647
FT CONFLICT 344 344
FT CONFLICT 357 357
FT CONFLICT 846 846
FT CONFLICT 885 AA; 99121 MW; BC63856F8F5EA1B CRC64;
SQ SEQUENCE 3.3%; Score 182; DB 1; Length 885;

Query Match 3.3%; Score 182; DB 1; Length 885;
Best Local Similarity 20.2%; Pred. No. 0.003;
Matches 132; Conservative 107; Mismatches 243; Indels 170; (

27 FPSAVTIKSWDKQEDLVTLATASGVLVDIYEKYQDLVTEPPNNAQLVEL
: : : : : |||
: : : : : |||
97 YPGNVKEKEVAKKQYKAVSQGKTAG-----LTKA
: : : : : |||
: : : : : |||
87 EKLNSRKAL---VSLALEAKVKQAQHWRDPASNEVVYTNAXODLDPEKND
: : : : : |
: : : : : |
132 EKTVTSVNVAAGSKVTPELTYTELLKKHKG-----YEWYLKVQPK-
: : : : : |
144 RIKPVFIEDANFGRIQSVOHAAVHIPTDIYEGSTVIINELNWTLSALDEVFKNRE
: : : : : |
: : : : : |
174 LVGFIFET-----VDIFEPOGISMLDAEASFITDDL-

```

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modified and this statement is not removed. Usage by and for co
entitled requires a license agreement (see http://www.isb-sib.ch/a
or send an email to license@isb-sib.ch).

EMBL; D89287; BAA13940.1; -
InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF_A.
PFam; PF00092; vwa; 1.
SMART; SM00609; VIT; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS0234; VWF; 1.
Serine protease inhibitor; Repeat; Signal; Multigene family;
Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 30
FT CHAIN 31 646
BY SIMILARITY.
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY C
H3.
BY SIMILARITY.
FT PROPEP 647 886
FT DOMAIN 279 439
FT CARBOHYD 88 88
FT CARBOHYD 577 577
FT BINDING 646 646
(BY SIMILARITY).
FT CHAIN 646 646
SEQUENCE 886 AA; 99018 MW; AC0594C6852576B8 CRC64;

Query Match 3.0%; Score 164.5; DB 1; Length 886;
Best Local Similarity 23.2%; Pred. No. 0.034;
Matches 56; Conservative 56; Mismatches 112; Indels 51; G

202 SLIMVFGSATGLARYPPASPDVNSRT-PNKID-----LYDVRER-PWYIQ
208 SALTSPGSGKGVSPKPS---LDQORSCPTCTDSLLNGDFTIVDVNRESPGVQ
249 -----ASPKDMLIVDVSGVSGTLKLTISVSEMLTSDDDFNVA
265 YVHFPAQGLFVVPKIVFVIDISGSMAGKIQOTRVALLKILDDMKDDYLNFI
297 NAQDVSCFOHLVQANVRNKKVLKADANNITAKGITDYKGFSPAFEOLLN----YN
325 GV--TTWKDSIVQATPANLEARTFVASISDQGTININDGLLRIGRLMTDREOHT
353 NCKNIMLFTDG-----GHERAQEIPFNKYNKKVRFVRSVVG-QHNYERGPQWMP
383 STSIIML-TDGDANTGESPEKIOENVRKAIERGFPLNYLGFGNLNYNLETW
408 GYVEIPSGAIRINTQBYLDVLRPMVLADGKAKQVMTNYLD 452
442 GVARIYEDSDANLQLOGFYEIVANPLL-----TNVEVE 475

RESULT 9
DPOL THEST STANDARD; PRT; 1829 AA.
ID DPOL THEST
AC O33845;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
GN FOL.
OS Thermococcus sp. (strain TY).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococca
OC Thermococcus.
OX NCBI_TaxID=110163;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98094267; PubMed=9434178;
RA Niehaus F., Frey B., Antranikian G.;
RT "Cloning and characterization of a thermostable alpha-DNA polyme
from the hyperthermophilic archaeon Thermococcus sp. TY.";
RL Gene 204:153-158(1997).

FEESGYTPIAPRDYCNLDIKISDNNTEFLNF---NEFIDRKTNNPSCNADLIN 691
SSHSPIYV-----DGDPHFIQVPGKNDTICFNIDKPGTVLSLIQ 677
IGFTNELQVWSKQKNIQVKARFVVTGDIRVYPKEAGENWQENPETYEDSF 751
[AVTGQII-----GEKNNASRTGKT----- 704
NDNNYFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLKPAVVGKIDVNSWIE 811
-----YFGKLGIANWMDFRIVTTEKILGN-----GDALSTFSLD 742
SIRDPACAGVCDCKRSDVMDCVILDDG-GFLMAN-----HDDYTNQIGRF 862
Q-----TGLSVTINRKNMV--VSFEDGISFVILHQQWKKHPVHQDFLG----- 790
PSLMRHLVNVSVAFNKSVDYQSV-CRPGAAP 898
SHRMSAQTHGLLGQFFQPFDFKVFDPVPGSDP 827

STANDARD; PRT; 886 AA.

el. 36, Created)
el. 36, Last sequence update)
el. 41, Last annotation update)
ypsin inhibitor heavy chain H3 precursor (ITI heavy
er-alpha-inhibitor heavy chain 3) (HC3).

uratus (Golden hamster).
azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Rodentia; Sciurognathi; Muridae; Cricetinae;
336;
N.A.

688; PubMed=9276673;
Suzuki Y., Yamamoto T., Sinohara H.;
oning and sequencing of cDNAs encoding three heavy-chain
the inter-alpha-trypsin inhibitor in Syrian hamster;
for the evolution of the inter-alpha-trypsin inhibitor
amily";
22:71-82(1997).

1-50; 446-472 AND 504-523, AND SUBUNITS.
241; PubMed=8864857;
Yamamoto K., Sinohara H.;
trypsin inhibitor and its related proteins in Syrian
and plasma";
20:145-152(1996).

MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
TION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
TY).

I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
HO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, H2
INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
NIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.
VY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
E BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
TY).
TY: BELONGS TO THE ITIH FAMILY.
TY: Contains 1 VWF A domain.

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ACTIVITY: N deoxynucleoside triphosphate = N diphosphate

PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
NSLATIONAL EXCISION OF THE THREE INTERVENING REGION
FOLLOWED BY PEPTIDE LIGATION.

: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.

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il to license@sib-sib.ch).

CAA73475.1; -

ITGO.

006172; DNA_pol_B.

006134; DNA_pol_B_dom.

006133; DNA_pol_B_exo.

003586; Hedgehog_hintC.

003587; Hedgehog_hintN.

006141; Intein.

006142; Intein.

004042; Intein_endonuc.

004578; Pol2.

; DNA_pol_B; 4.

; DNA_pol_B_exo; 1.

79; Intein.

5; HintC; 3.

6; HintN; 3.

6; POLBC; 1.

R01443; Intein_Cterm; 3.

R01445; Intein_Nterm; 3.

R00592; pol2; 2.

116; DNA POLYMERASE B; FALSE_NEG.

1818; Intein_C TER; 3.

1819; Intein_ENDONUCLEASE; 2.

1817; Intein_N TER; 3.

DNA-directed DNA polymerase; DNA replication;
Hydrolase; Endonuclease; Autocatalytic cleavage;

ing.

1 409 DNA POLYMERASE, 1ST PART (POTENTIAL).

410 769 Intein I.

770 855 DNA POLYMERASE, 2ND PART (POTENTIAL).

856 1392 Intein II.

393 1441 DNA POLYMERASE, 3RD PART (POTENTIAL).

442 1598 Intein III.

599 1829 DNA POLYMERASE, 4TH PART (POTENTIAL).

829 AA; 211875 MW; A113ABBC57EB9CB3 CRC64;

larity 3.0%; Score 161; DB 1; Length 1829;

Conservative 101; Mismatches 301; Indels 282; Gaps 39;

IGPSEPPFPs-----AVTKSWV-----DKMQSDLVTLA 48

LGDRKEHPKPHRGDSFAVEIKGRIFDFLPVVRRTINLPITYLEAVEVLGKT 288

SGVNLVDIYEKYODL-----YTVFPNNARQLVEIAARDIEKLLSNRSKALVSLALE 103

LGAEIAIAWETESMKLAQYSME--DARATYEL-----GKEFFPMEAE 334

QVAAHQWEDFAS--NEVVY-----NAKDDLDPEKNDSEPCSORIKPVFI----- 150

CLIGQSVWDVSRSTGNLVEWYLLRVAYERNAPKNPDEEYRRRLRTYLGYYKE 394

INFGROIYQHAHVHPTD---IYEGSTIV---LNLNWTSLADSVFKNREEDPSL 203

RGLWENIAYLDFFCH-PADTKVIVKGGIWNISDVKEGDIILGDG----- 441

QVFGSGLARYYPASPDVNSR---TPN-KIDLVDVRRRPWTYIQGAASPKMILVD 259

Db 442 *WQ---RVKKWKVHYEGKLININGLKCTPNHKVPVVTENDRQTRI-----RDSLF

QY 260 VSGSVSGLTLKIRTSVSEMLETLSDDDFVNVSFNSN-----

Db 492 LSGKVGK---KIITTKL-----FEKIAEFKNKPSSEELKGLSGILLAI

QY 298 -AQDVSCF-----QHLVQANV-RNKKVLDAV-----NNITAKG-

Db 538 LRKDIEYFSSRGKKRISHQYRVEITIGENEKELLERILYIPDKLFGIRSPVKKGI

QY 330 --ITDYKGFSAFEQLNLYNVSANCNKIIMLFTDGGGERAQEIYFNKYKOKKVR

Db 598 LKITTAKKAVYLQIEELLK-NIESLYAPAVLRGF-----FERDATVNI

QY 388 SV---GQHYERGPOMWACENKGY---YYEIPSGAIRINTQEVLDVLRPMVL

Db 643 TIVVTQGTNNKWKIDIVAKLLDSLGIPSYRYEYKYLENGKELTKHILEITGRD-

QY 441 AKQVQNTNVYLDALGLVITGLPVFNITQFE-----NKTNLKQLILGV

Db 696 -----GLILFQTLVGFISSEKNEALEKAIEVREMNLKNSFYNL

QY 492 VSGEDIKRLTPRFTLCPNGYFAIDPNGYVLLHPNLOPKPKSQEPVTLDFDAEL

Db 740 VSSEYKGEVVDLTLEGNPYFA---NG-ILTHNSLYPSIIVTHN-VSPDTLRE-

QY 552 KVEIRNMIDGESGEKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDYSLALVLPY

Db 790 -----GCKNYDVAPIVG--YKFCXDFPG-

QY 612 IKAKLEETITQARSKGKMKDSETLKPNPFESGY-----TFTAPRYCNDI

Db 812 IPSILGELLITMRQEIKKQWK--ATIDPIEKMDYRQRAVKLLANSILPNSEW---I

QY 663 NNTPELFNFPIDRKTPNPNFNSCHADLINRVLLDAGFTNELVQVYWSKQNKIKVI

Db 867 NGEVFKVAKIGFIDRYMBEOKDKVTVNDNTVEVLDNIFAFSLNKESSKSELKVI

QY 723 VTDGQITRVYKPEAGE 738

Db 925 -----IRHKYGEAYE 935

RESULT 10

ATX1_PLAFA STANDARD; PRT; 1956 AA.

ID ATX1_PLAFA

AC Q04956;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=5833;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=T9/96;

RX MEDLINE=93132070; PubMed=8421054;

RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,

RA Robson K.J.

RT "A family of cation ATPase-like molecules from Plasmodium falciparum";

RL J. Cell Biol. 120:385-398(1993).

CC -- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

CC -- SUBCELLULAR LOCATION: Integral membrane protein.

CC -- SIMILARITY: Belongs to the cation transport ATPases family (ATPases). Subfamily V.

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RESULT 11
YFBK_ECOLI STANDARD; PRT; 575 AA.
ID YFBK_ECOLI
AC P76481;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Hypothetical protein yfbK.
DE YFEK OR B2270.
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RX Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland I.
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RT Science 277:1453-1474 (1997).
RL -I- SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLL0103.
CC -I- SIMILARITY: Contains 1 VFMA domain.
CC -----
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CC the European Bioinformatics Institute. There are no restriction-
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; AAC75330.1; --
64998.
95; yfBK.
02035; WVF_A.
VWA; 1.
34; WFA; 1.
rotein; Complete proteome.
6 394 WFA.
; AA; 63634 MW; 7BB6ALA7A2BE111 CRC64;
2.94; Score 157.5; DB 1; Length 575;
urity 21.6%; Pred.No. 0.047; Indels 105; Gaps 25;
nservative 93; Mismatches 206; Indels 105; Gaps 25;
ARQLVRIADRIEKLNSRSKALVSLALEAEKVOAAHOMREDPASNEVYVYNKOD 130
CESQQQSPPTPEQVLLAAQRAIK---EAEQSA---AKALAQEQEVQYSDKQA 75
KND-----SEPGSORIKPVFIEDANFGRIQISYCHAA---VHIPTDI 172
LQEAPTFAAKAKATHIANPGTARYQOF---DDNPVKVAQNPLATFSLDVTGS 132
IIVUNE-----LNWTSALDEVPKKNREEDPSLLMQVFGSATGLARYY 218
RRFLNQGLPPPDARVVEIIVNYFPDWDI---KQKQIPASKPIPFAMRYELA--- 187
WVDSNRPNKIDLVDRRRPWYIQGAASPKDMLILVDVSGS-VSGLTCLKIRTSVS 277
W-NEQRTLLKVDILAKORKSEELPAS---NLVFLIDTSGSMISDERLPTQSSLK 241
TLSDDDDFNVASFSNAQVSCFOHLVQAVNRNKKVLKDAVNNITAKGIDYKKG 337
ELREQDNIAIVTYAGDSRIA-----LPSISGSHKAEINAAIDSLDAESTNGAGL 296
EQLLNNTVSRANCKNIIMFTDG-----GEARQEIFENKYNKDKKVRFPFVSQ 391
QOATK-GPIKGGINR-ILLATDGFNVGIDDPKSIEMVKKQRESGVTLSTFGVN 354
RGPIQWMAENKGYEYIPSGAIRINTQEVLDVLRPMVL--AGDKAKQVQ---- 445
TEAMVRIADVNGNYSYIDTLS-----EAQKVLNSENMQMLITVAKDVKAIEFNP 410
YLDALGLGVITGTLPVFENITQFENKTMKQLILGVGVD-VSLEDI---KRLT 501
3Y---RQIG-----YE-----KQRLRVEHFNNDVNDAGDIGAGKHIT 447
TLCNGYFFAIDPNGVYLLHPNLPQKPKSQE 536
ELTLNGQKASIDKLRYA--PDNKLAKSDKTK 480
STANDARD; PRT; 946 AA.
59; Q15484;
(Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 42, Last annotation update)
trypsin inhibitor heavy chain H2 precursor (ITI heavy
inter-alpha-inhibitor heavy chain 2) (inter-alpha-trypsin
complex component 1) (Serum-derived hyaluronan-associated
IAP).
IBP2.
(Human).
(etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
1606;
M N.A., AND PARTIAL SEQUENCE.
52237; PubMed=2450046;

RA Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;
RT "Complementary DNA and derived amino acid sequence of the precursor
of one of the three protein components of the inter-alpha-trypsin
inhibitor complex.";
RL FEBS Lett. 229:63-67(1988).
RN [2]
RX SEQUENCE OF 384-865 FROM N.A.
RP MEDLINE=89068576; PubMed=2446322;
RA Sallier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RA Benarous R., Okubo I., Kurachi K., Martin J.P.;
RT "Isolation and characterization of cDNAs encoding the heavy chain
human inter-alpha-trypsin inhibitor (I alpha TI): unambiguous
evidence for multipolypeptide chain structure of I alpha TI.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
RN [3]
RX SEQUENCE OF 384-766 FROM N.A.
RP MEDLINE=89076497; PubMed=2462430;
RA Sallier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
RA Martin J.P.;
RT "Human inter-alpha-trypsin inhibitor. Isolation and characterizat
of heavy (H) chain cDNA clones coding for a 383 amino-acid sequen
of the H chain.";
RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).
RN [4]
RX PARTIAL SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=88024442; PubMed=3663330;
RA Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
RA Gebhard W.;
RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses th
different proteins.";
RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).
RN [5]
RX SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
RP MEDLINE=89380192; PubMed=2476436;
RA Englund J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
polypeptide chain stoichiometry and assembly by glycan.";
RL J. Biol. Chem. 264:15975-15981(1989).
RN [6]
RX SEQUENCE OF 55-64.
RP TISSUE=Plasma;
RX MEDLINE=93039735; PubMed=1384548;
RA Malki N., Balduyck M., Maes P., Capon C., Mizon C., Han K.K.,
RA Tartar A., Fournet B., Mizon J.;
RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor:
isolation, their identification by electrophoresis and partial
sequencing. Differential reactivity with concanavalin A.";
RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
RN [7]
RX SEQUENCE OF 55-64 AND 681-702, CROSS-LINK STRUCTURE, AND
RP CARBOHYDRATE-LINKAGE SITES THR-691.
RX MEDLINE=93232026; PubMed=7682553;
RA Englund J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
RA Pizzo S.V., Hefta S.A.;
RT "Presence of the protein-glycosaminoglycan-protein covalent cross
in the inter-alpha-inhibitor-related proteinase inhibitor heavy
2/bikunin.";
RL J. Biol. Chem. 268:8711-8716(1993).
RN [8]
RX SEQUENCE OF 67-101, AND HYALURONAN BINDING.
RP TISSUE=Serum;
RX MEDLINE=94075371; PubMed=7504674;
RA Huang L., Yoneda M., Kimata K.;
RT "A serum-derived hyaluronan-associated protein (SHAP) is the hea
chain of the inter-alpha-trypsin inhibitor.";
RL J. Biol. Chem. 268:26725-26730(1993).
RN [9]
RX SEQUENCE OF 699-702, AND COVALENT LINKAGE WITH CHONDROITIN SULF
RP TISSUE=Plasma;
RX MEDLINE=94229087; PubMed=7513643;
RA Morelle W., Capon C., Balduyck M., Sautiere P., Kouach M.,

1:56:54 2004

MIC

ournet B., Mizon J.;
lphate covalently cross-links the three polypeptide
-alpha-trypsin inhibitor.";
. 221:881-888(1994).

NKAGE SITES, AND MASS SPECTROMETRY.

6; PubMed=9677337;
on C., Balduyck M., Ricart G., Sautiere P., Mizon J.;
pattern of human inter-alpha-inhibitor heavy chains.";
:749-756(1998).

NKAGE SITES, AND DISULFIDE BONDS.

10; PubMed=9425062;
ahbek-Nielsen H., Thøgersen I.B., Roepstorff P.,

mal modifications of human inter-alpha-inhibitor;
of glycans and disulfide bridges in heavy chains 1 and

1:408-416(1998).
WAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
JTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
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NTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
N, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
ND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
BRIDGE TO THE THEIR C-TERMINAL ASPARTATE.
ROMETRY: MW=76508; METHOD=MALDI; RANGE=55-702.
: BELONGS TO THE ITIH FAMILY.
: Contains 1 VWFA domain.

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ill to license@isb-sib.ch).

CAA30160.1; ALT_SEQ.

AAA60558.1; -

AAA59195.1; -

(VHU2

PI9823; -

[67; ITIH2.

1; F:plasma glycoprotein; TAS.

06587; VIT.

002035; VWF_A.

; vwa; 1.

9; VIT; 1.

7; VWFA; 1.

234; VWFA; 1.

se inhibitor; Repeat; Signal; Multigene family;

glutamic acid; Glycoprotein.

POTENTIAL.

1 18

19 54

55 702

H2.

03 946

08 468

.61 284

.50 651

.18 118

.66 666

.71 671

.73 673

INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN

H2.

VWFA.

N-LINKED (GLCNAC. . .) (COMPLEX).

/FTID-CAR 000140.

O-LINKED (GALNAC. . .) (PARTIAL).

/FTID-CAR 000214.

N-LINKED (GLCNAC. . .).

O-LINKED (GALNAC. . .).

FT CARBOHYD 675 675 /FTID-CAR 000215.
FT O-LINKED (GALNAC. . .).
FT /FTID-CAR 000216.
FT O-LINKED (GALNAC. . .).
FT /FTID-CAR 000217.
FT MOD_RES 282 282 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 283 283 CHONDROITIN 4-SULFATE, CROSS-LINK SITE
FT BINDING 702 702 K -> L (IN REF. 5).
FT CONFLICT 374 374 P -> A (IN REF. 2 AND 3).
FT CONFLICT 674 674 F -> S (IN REF. 2 AND 3).
FT CONFLICT 705 705 N -> D (IN REF. 2 AND 3).
FT CONFLICT 729 729 V -> A (IN REF. 2 AND 3).
FT CONFLICT 731 731
SQ SEQUENCE 946 AA; 106436 MW; 1478CF3E8F3BA776 CRC64;

Query Match 2.8%; Score 154.5; DB 1; Length 946;

Best Local Similarity 19.8%; Pred. No. 0.15;
Matches 133; Conservative 106; Mismatches 259; Indels 171; Ga

QY 33 IKSWVDKMQEDLVTLAKTAGVGNOLVDIYEKQDLYTVPEPNNARQOLVEIAADIEKL
Db 26 LSEFYD--YEDLVEL---APGKQLVAENRRYQRLSPGSEEMEEVDQVTLISYKV
QY 93 RSKALVSLAAEKVQAAHQWRE-----DFASN-----
Db 81 ITSRWATNIGSKVNNVSPQNVVDFVQIPKGAFIGSNFMSMTVDGKTFRSSIKEKTV
QY 123 VYNNAK-----DDLDEKNDSE-----PGSQRIKPFVIEDANFGROISYQH-
Db 141 LYAQAARAKGTAGLVRSALDMENFTEVNLPGAKVQFELHYQVYKMKLGSYEHF
QY 164 -----AAVHIPTDIYEGSTIVLNELNWTSLD-----EVFKKNRBE-----DPSLLY
Db 201 QPRLAKHLEVVDVWVIEPQGLRFLHVDFTFEGHDFGVFVSKGQKAKHVSFKPTVA(
QY 209 GSATGLARYTPASPWVDNSRTPNKIDLYDVRPP-----WTYQGAAS-----
Db 259 -----RCPSCR--ETAVDGLVLYDVKREKAGELEVNGYFVHFPAFNDLDI
QY 253 DMLILVDVSGSVGTLKLIKRTSVSEMLETLDSDDFVNVVASNSNAQDVSCFQHLV(
Db 310 NILFVIDVSGSMGVKMKQTVEAMKTILODLRAEDHPSVIDFNQINR--TWNDLLI
QY 313 RNKKVLKADVNNITAKGIDTYKGF---SFAPEQLNINVSANCKNIIMLFTDG-
Db 368 TVADAKRYIEKIQPSGGTNINEALLRAIFILNEANNLGLDPSVSLILLVSDGD
QY 366 EERAQELFNKYNKDKKVRVFRFSVGQ-----HNYERGPQMM-----A
Db 428 ELKSLKIQKVKENIQDNISLFLGMGFDYDYLKRLSNENHIGIAQRIYGNQDTS
QY 408 GYTYEI--PSIGAIRIN--TQEVLDVL-----GRPMVLAG--DKAKQVQWNTN
Db 488 KFTYQVSTPLLRNVQFNYPHTSVTDVTQNNFNHYFGGSEIVVAGKFDPAK-----
QY 453 ALEGLVITGTLPVFNITGQFNKTNLKNOLILGVMGVDVSLDI---KELTPRF
Db 540 QIE--SVITA-----TSANTQLVLETIAQMDLQDFLSKQKHPDF
QY 509 NGYFATDPNGYVLLHPNLQPKPKSQEPVTLDFDLAELENDIKVEIRNKGIDGES
Db 583 LWAYLTIN---QLLAERSLAP-TAAAKRITRSILOMSLDHHTVPLTSLVIENEF
QY 569 FRTLIVKSDQ 577
Db 639 MLADAPPD 647

RESULT 13

BXCL CLOBO

ID BXCL CLOBO STANDARD; PRT: 1290 AA.

AC P18640;

DT 01-NOV-1990 (Rel. 16, Created)

7:56:54 2004

al. 16, Last sequence update)
 al. 41, Last annotation update)
 toxin type C1 precursor (BC 3.4.24.69) (BONT/C1
 Cl).
 tulinum.
 icutes; Clostridia; Clostridiales; Clostridiaceae;

1;

N.A.
 87; PubMed:2204031;
 and M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
 off M.R.;
 sequence of Clostridium botulinum C1 neurotoxin.";
 Res. 18:4924-4924(1990).

N.A.
 Stockholm / C-ST;
 198; PubMed:2222445;
 li N., Tazuki K., Murakami T., Indoh T.,
 akeshi K., Syuto B., Oguma K.;
 nucleotide sequence of the gene coding for botulinum
 in the C-ST phage genome.";
 yst. Res. Commun. 17:1304-1311(1990).

-25.
 Stockholm / C-ST;
 072; PubMed:2450568;
 okosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
 t of a monoclonal antibody recognizing an antigenic site
 stridium botulinum type B, C1, D, and E toxins and
 .";
 . 56:898-902(1988).

N OF SUBSTRATE.
 966; PubMed:7901002;
 pman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
 urotoxin C1 blocks neurotransmitter release by means of
 1/syntaxin.";
 21-4828(1993)
 BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 ; BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

[DASE THAT CLEAVES SYNTAXIN.
 : ACTIVITY: Limited hydrolysis of proteins of the
 cytosol apparatus, synaptobrevins, SNAP25 or syntaxin. No
 action on small molecule substrates.
 : Binds 1 zinc ion per subunit (By similarity).
 DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A
 AIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,
 E-N AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL

N AND TOXIN BINDING, RESPECTIVELY.

LAR LOCATION: Secreted.

NEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF

M NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

NEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C

F CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE

PHAGE.

TY: BELONGS TO PEPTIDASE FAMILY M27.

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mail to license@isb-sib.ch.

3; CAA47060.1; -

3; CAA51313.1; -

DR EMBL; X53751; CAA37780.1; -;
 DR EMBL; D90210; BAA14235.1; -;
 DR EMBL; X62389; CAA44263.1; -;
 DR HSSP; P10845; 3BTA.
 DR MEROPS; M27.002; -;
 DR InterPro; IPR000395; Bontoxilysin.
 DR InterPro; IPR006025; Zn_MTPeptidse.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; Bontoxilysin.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 KW INIT MET 0
 FT CHAIN 1 448
 FT CHAIN 449 1290
 FT METAL 228 228
 FT ACT SITE 229 229
 FT METAL 232 232
 FT DISULFID 436 452
 FT CONFLICT 84 84
 FT SEQUENCE 1290 AA; 148734 MW; 71FB379F97129E8 CRC64;
 SQ
 Query Match 2.8%; Score 152; DB 1; Length 1290;
 Best Local Similarity 20.3%; Pred. No. 0.33;
 Matches 205; Conservative 125; Mismatches 346; Indels 334; G;
 QY 106 KVOAAHQWREDFASNVVYNAKDDLDPEKNDSEPGSQRIK---PVFIEDANFR-
 Db 138 KTRQGNWVKTGSINPSVIITG-----PRENIIDPETSTFKLTNNYFAOEGFGAL
 QY 158 -----QISYOHAAVHIPTDIYEGS-----TIVLMELNWTSAIDVEFK---
 Db 193 ISPRFMLTYSNAT-----NDVGEGRFSKSEFCMDPILIMHELN---HAMHNLGYIAI
 QY 199 EDPILLWQVFGSATGLARYYP-----ASPWVDNSRTNPKIDLDYVRRRPWYIOGAA
 Db 247 TISSVTNIFYSQVNVKLEYAEIYAFGGPTID--LIPKSAKRYFEKALDYRSIP
 QY 254 MLILVDVSG---SVSGLTKLIR-----TSVSEMLETLDSDDFVNVASFNSNAQI
 Db 305 SITTANPSSFNKYIGEYKQKILRYRFVSVESGEV--TVNRNKFVEL--YNELTQI
 QY 305 QHLVQANVKNKV-LKDAVNNTAK---GITDYKKGFSAPEQL-----LNVNVI
 Db 361 NYAKIYNQNRKIYLSNVYTPVTANILDDNVYDIQNGFNPKSNLNLVFMGQNLIS
 QY 352 --ANCKNIIMLFT-----DGGEERAQEIFNK-----YNKD-----KK
 Db 421 KVNPNEMLYLTKFKHKAIDG-----RSLYNTKLTDCRELLVKNYDLPPIGDISD
 QY 387 FSVGQHYRGPQIOWACENKGYIYELPSIGAIRI--NTOEY--LDVL-----
 Db 476 FLRKQDINBETEV-----YYPDNVSDVQVILSKNTSEHGQDLDPYSDISE
 QY 431 GRPMVLGAKAKOVQWTVN--VYLDALGLGLVITGLPLVFNITGQFENKTN-----
 Db 527 GENQVYDNRNTQNDVYNSYYLESQKL-----SDNVEDFTFRSIEALDNSAKV
 QY 479 -LKNQILITVYG-----VDVSLDEIKLTTPRTLCPNGYIEAIDPNGVILLHP
 Db 583 TLANKVNAVQGGFLMWANDVVEFTNIRKDTLDKISDVSAIIP-----YIGE
 QY 531 NPKSQEPVTLDF-----LDAELENDI-----KVEIRNKMIDGESGEF
 Db 639 NSVRRCNFTFAFVAVGTVILLPEPPTIPALGAFVYISKVQERNEII-----K
 QY 573 VKSQDERYIDKGRNTYTW-----TFVNGTDYSLALVLPYTSFYIYAKLIE
 Db 693 LEORIKKWKD-----SYEMWMTLSRLITQFNNTISYQMYDSL-NYQAGAKAKII
 QY 623 ARSKKGRMKDSETLKP--DNPEBSGYTFIAPRDYCNLDKISDNNTEFLLNFNEF
 Db 743 LEYKYSKSSDKENIKSVOENLKN-----LDVKIS-----EAMNNINKE.

```

-----DRKTPNPSCADLINRVLLDA----- 697
||| ||| ||| ||| |||
MLPKVIDELNEFRDNT-----KAKLIN--LTDSHNIIIVGEVDKIKAVNNVF 839
-----GFTN-----
||| ||| ||| ||| |||
NIFSNTNSSLKDIINEFNNINDSKILQNRKTLVDTS-----YNAEVS 894
INPETYEDSPYKSLDNDNYFTAPYFNKSGPGAYESGMVSKAVEIYQGLLK 796
||| ||| ||| ||| |||
INP-----IF--PPDFKLGSSGEDRGKVVIVTQENINIVNYSME 935
[KIDVSWINFTKTSIRDCAGVCDCKNSVDMCDVILDDGGFLLMNHED--- 853
||| ||| ||| ||| |||
FIRINKWVSNLPGYTIID-----SVKNKSGWISGIIISNFIIVFTLKQNHEDSEQ 988
-DYTNQIGR-----FFGIDPSLMHNLVNSIVAFNKSVDYQSVCE 893
||| ||| ||| ||| |||
YDISNAPGNKYNKFFVTVTNMMG---NMKIYNGKLIDITIKVE 1035
STANDARD; PRT; 420 AA.
el. 35, Created)
el. 35, Last sequence update)
el. 41, Last annotation update)
protein all0103.
sp. (strain PCC 6803).
obacteria; Chroococcales; Synechocystis.
8;
N.A.
29; PubMed=8590279;
aka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
bata S.;
ysis of the genome of the unicellular cyanobacterium
sp. strain PCC6803. I. Sequence features in the 1 Mb
up positions 64% to 92% of the genome.";
1-166(1995).
/: TO E.COLI YFBK.
/: Contains 1 VFMA domain.
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BAA10635.1; -.
S76691.
002035; VFMA.
; vwa; 1.
7; VWA; 1.
234; VFMA; 1.
protein; Complete proteome.
43 215
0 AA; 45849 MW; E7111B51478E74F3 CRC64;
2.8%; Score 151.5; DB 1; Length 420;
arity 20.8%; Pred. No. 0.067;
onservative 85; Mismatches 183; Indels 55; Gaps 16;
ILILDVSGSVGLTKLIRTSVSEMLETISDDDFNVASFNQAQVSCFOHLVQA 310
||| ||| ||| ||| |||
CLVLDHSGSGMDQPLETVKSAALGLIDRLBEDRLSVIAFOHRAKIV-----INQ 95
IKKVLKDAVNNITAKGITYKGFSPAFQLNLYNVSRANCKNIIMLFTDGGGEAAQ 370

```

```

||| ||| ||| ||| |||
96 QVNGRAIAIAIRLKAEGGTADDEGLKLGIOEAAKGEDRVS---HIFLLTDGENE
371 E-----IFNKYNKDKKVRVFRFSVQHNHYERGPIQWMACENKG---YYEIPISGAIIRI
||| ||| ||| ||| |||
153 NDRCLKGTGTVASDVKLIVHTLGFGDH--WQDVLEAIAASAGSLSYIENPS-EALHT
425 EYLDVLRPMVLADGKAKQVQMTNVYLDALGLG-----LVITGTLPVFNITQGFENKI
||| ||| ||| ||| |||
211 LF-----QRMNSVGLTNAHL--LLELAPQAHAI--VKEVAQVSPETMDLT
481 NQLILGVMGVDVSLIEDIKLTPRTFLCPNGYFALDPNGYVLLHPLNLPQKPKSOE-
||| ||| ||| ||| |||
255 NQGAIEEVRLLGDLMTQDERV-----LLNLKLDQLLPQHVIGQVIRYDDPASQT
537 ----PVLIDFDLDAELENDIKVEIRNKMIDSGSEKRT--FRTLVSQDERYIDKGNRT
||| ||| ||| ||| |||
310 SDPLPLTIQ-VQTQYQPTDVQVQESILTLAKYRQTQIAETKLGADRGGAATMLQT
591 TPVNGTDSYSLALVLPYSFYIKAKLETITQARSKGKMKDSETLKP 638
||| ||| ||| ||| |||
369 TALQMGDKNGATILQTNA---TRLQSGEDLSEGDGRKTRMVSNTTLQP 413

```

RESULT 15

```

ITH4 PIG
ID ITH4 PIG STANDARD; PRT; 921 AA.
AC P79263;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H4 precursor (ITI heavy
chain H4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-tryp-
sin inhibitor family heavy chain-related protein) (IHRP) (Major acute
phase protein) (MAP).
DE ITIH4 OR IHRP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-36; 695-703 AND 710-722.
RC TISSUE=Liver;
RX MEDLINE=96271024; PubMed=8930057;
RA Hashimoto K., Tobe T., Sumiya J.-I., Sano Y., Choi-Miura N.-H.,
RA Ozawa A., Yasue H., Tomita M.;
RT "Primary structure of the pig homologue of human IHRP: inter-alpha-
trypsin inhibitor family heavy chain-related protein.";
RL J. Biochem. 119:577-584(1996).
[2]
RN PRELIMINARY SEQUENCE OF 267-556 FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=90371455; PubMed=1697703;
RA Buchman T.G., Cabin D.E., Vickers S., Deutschman C.S., Delgado E.
RA Suesman M.M., Bulkley G.B.;
RT "Molecular biology of circulatory shock. Part II. Expression of f
groups of hepatic genes is enhanced after resuscitation from
cardiogenic shock.";
RL Surgery 108:559-566(1990).
[3]
RN SEQUENCE OF 28-54 AND 223-240.
RP TISSUE=Serum;
RX MEDLINE=96013138; PubMed=7556597;
RA Gonzalez-Ramon N., Alava M.A., Sarsa J.A., Pineiro M., Escartin A
RA Garcia-Gil A., Lampreave F., Pineiro A.;
RT "The major acute phase serum protein in pigs is homologous to hum
plasma kallikrein sensitive PK-120.";
RL FEBS Lett. 371:227-230(1995).
CC -!- FUNCTION: MAY BE INVOLVED IN ACUTE PHASE REACTIONS.
CC -!- TISSUE SPECIFICITY: Liver-specific.
CC -!- INDUCTION: LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC
SHOCK.
CC -!- PTM: APPEARS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY)

```

SD BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA

: BELONGS TO THE ITTH FAMILY.
: Contains 1 VWFA domain.
EF 2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER
ERRORS.

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il to license@isb-sib.ch).

AAD00024.1; -
AAB46821.1; -
-; NOT_ANNOTATED_CDS.
(C4625. VIT.
06587; VIT.
02035; VWF_A.
; vwa; 1.
; vit; 1.
; vwa; 1.
; vwa; 1.
234; VWFA; 1.
se inhibitor; Repeat; Signal; Multigene family;

1 27
28 921
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN
H4.
VWFA.
70 428
30 80
05 205
42 242
13 513
77 577
49 50
03 703
1 AA; 102146 MW; E2BF9525DE8D07C CRC64;
2.8%; Score 150.5; DB 1; Length 921;
arity 19.9%; Pred. No. 0.25;
onservative 100; Mismatches 264; Indels 265; Gaps 36;
ALTUTL-----FQSLIGSSSEPPPSAVTIKSWDK--MOED--- 43
VLELLAVLQSTTAHKNDINIYSLTVDSKVSREFAHTVTVSRVKNKGSAGVQEAFTQ 69
-----LVTLAKTASGVNQLDIVEK--YQDLYT-VEPNNAQLVEIAARDIEKL--- 89
'KKAFTNFMIIDGVTPGNIKEKAAQEQYSAVARGESAGLVRAIGRKRTEQFOVA 129
'SKALVSLALEAEKQVAAHQWREDPASNEVVVYNAKDDLDPEKNDSEPGSQRKVPF 149
'APAAKVTVELVEELLARH-----LGVYELLKTKPQ-----QLVKHLQ 171
ANFGRO-ISKY-QHAAVHIPTDIYEGSTIVNE---LWNTSALDEVFKKNREEDPSL 203
HFEFGQISFLETESTFMTNELAELTISQNKTKAMIRFPKPTLSQO-QKSPEQOEV 230
-----WQVFGSATG-----LARYYPASPWVDSNRTPNKIDLYDVRPPWYIQG 247
NFIVRYDVNRVTVGGSIQIENGYPVHYFAPEVW----- 266
PKDMLILVDVSGVSGLTSLKIRTSVSEMLETSLDDDFVNVASPNASNAQDVSCFQHL 307
PKNVIFVIDISGSGRGRKIQTREALIKILGLGRDQFNLSVSGEAPR-----RRA 322
NVRNKKVLKDAANNITAKGTDYKGFSPAFEQLLNYSRANCNKI-----IM 359
SAENVEBAKSYAAETHAQGGTNINDAMLMVQLL-----ERANREELLPARSVTFII 377
DG-----GEERAQELFNKYNKDKKVRV-----FRFSVGQHNYERGPIQWMA 403

Db 378 LLTGDPTVGETNFSKI-----QKNVREADGQHSFLCIGFGFDVVPYAFLEK-----
QY 404 CENKG-----YY-----YBPSIGAIRINTOEYLDVL-
Db 427 LENGGLARRIYEDSDALQLEDFYQEVANPLRLVAFEYPS-NAVEEVTQDNFRLEFF
QY 433 PMVLAG---DKAKQVQWNTNVYLDLELGLVITGLTPVENITGQFENKTNLKNQLILG
Db 486 ELVWAGKLRDQSPDV-----LSAKVRGQLHMENTVTFMESRVAEQEAEPLE
QY 487 -----VMGVDSLEDI--KELTPRFTLCPNGYFAIDPNGYVLLF
Db 535 IFHSFMRERLWAVLTQQLLAQTVSADAEKKALEARALSLSLNYSEVTPLTLSNVIT
QY 528 QPKNPKSQPFVTLDFDAELENDIKVEIRNKMIDGESGKTFRTLKVSQDERYDK
Db 595 QBSQVAKRP-----VENGROQNTSHGHSF-----QFHSVK
QY 588 YTWTPVNGTDYSLALVLPYTFYIKAKLEETITQARSKKGMKDSKSETLKPDPNFEE
Db 631 SRLTGGSSVD-----PVFS-----HRRGKGOAQ-----GFEEK
QY 648 FIAPR 652
Db 662 -LPPR 665

Search completed: February 20, 2004, 16:56:12
Job time : 15.3006 secs

GenCore version 5.1.6
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n search, using sw model

uary 20, 2004, 16:52:19 ; Search time 18.2804 Seconds
(without alignments)
5450.141 Million cell updates/sec

-10-090-827-14

13 MAAGCLLALTTLFQSLIG.....RLLIQAEQTSDEGNPCDMVK 1036

SUM62

op 10.0 , Gapext 0.5

1308 seqs, 96168682 residues

is satisfying chosen parameters: 283308

th: 0
th: 2000000000

imum Match 0%
ximum Match 100%
isting first 45 summaries

IR 76.*

Pir1.*

Pir2.*

Pir3.*

Pir4.*

the number of results predicted by chance to have a
r than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

ery	ch	Length	DB	ID	Description
0.0	1091	2	JH0565		calcium channel al
6.2	1091	2	A44147		calcium channel pr
6.0	1106	1	CHBA2		calcium channel al
9.9	1091	2	T30256		C50C3.11 protein -
1.2	734	2	S44617		probable calcium c
0.5	1148	2	T18770		hypothetical prote
3.6	1450	2	C86880		inter-alpha-trypsi
3.6	886	2	S54355		inter-alpha-trypsi
3.4	885	2	S30350		uncharacterized pr
3.2	1819	2	D97033		inter-alpha-trypsi
3.0	889	2	JCS576		variant-specific s
3.0	2706	2	T28155		p-type cation tran
2.9	1984	2	A44396		hypothetical prote
2.9	575	2	D64998		lipoprotein (impor
2.9	918	2	E90542		membrane associate
2.9	680	2	A97331		RAD2 endonuclease
2.8	1516	2	E71619		cytotoxin I - Clo
2.8	2364	2	I40884		inter-alpha-trypsi
2.8	946	1	IYH02		fibrinogen-binding
2.8	1315	2	T28679		inter-alpha-inhibi
2.8	932	2	JCS953		botulinum neurotox
2.8	1291	2	S46431		botulinum neurotox
2.8	1291	2	A49777		hypothetical prote
2.8	420	2	S76691		hypothetical prote
2.8	1426	2	A99580		inter-alpha-trypsi
2.8	921	2	JC4625		hypothetical prote
2.8	1385	2	D89824		methyl-accepting c
2.8	654	2	A69656		atp-binding protei
2.8	1027	2	B90527		

proteinase
inter-alpha-
rho-try prot
DNA-directec
hypothetica
methyl-accet
hypothetica
hypothetica
hypothetica
probable rei
inter-alin l
probable pei
hypothetica
hypothetica
cellulose 1
fibronectin-1
ATP-depende

ALIGNMENTS

RESULT 1

JH0565
calcium channel alpha-2b chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug
C:Accession: JH0565
P:Williams, W.E.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi,
Neuron 8, 71-84, 1992
A:Title: Structure and functional expression of alpha1, alpha2, and beta
A:Reference number: JH0564; MUID:92110010; PMID:1309651
A:Accession: JH0565
A:Molecule type: mRNA
A:Residues: 1-1091 <WIL>
A:Cross-references: GB:M76559; NID:G179761; PIDN:AAA51903.1; PID:G1797
A:Experimental source: basal ganglia
A:Note: Several conflicts are found between GenBank submission, author
C:Comment: This protein is a subunit of the voltage dependent calcium
C:Superfamily: calcium channel alpha-2 chain
C:Keywords: glycoprotein; phosphoprotein
P:1-24/Domain: signal sequence #status predicted <SIG>
F:1-1067/Product: calcium channel alpha-2b chain #status predicted <C
F:32,262,326,539,635,1087/Binding site: phosphate (Thr) (covalent) (by
F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by prot
F:92,136,184,324,348,468,475,585,594,663,682,769,812,876,883,973,986/E
F:501/Binding site: phosphate (Thr) (covalent) #status predicted
F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase

Query Match	100.0%	Score	5443;	DB	2;	Length	1091;
Best Local Similarity	100.0%	Pred. No.	0;				
Matches	1036;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MAAGCLLALTTLFQSLIGSSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNM					
DB	1	MAAGCLLALTTLFQSLIGSSSEPPSPSAVTIKSWDKMQEDLVTLAKTAGVNM					
QY	61	YEKQDLYTFEPNNARQLVEIAARDIEKLLNRSKALVSLAEAEKVQAQAAHQWREI					
DB	61	YEKQDLYTFEPNNARQLVEIAARDIEKLLNRSKALVSLAEAEKVQAQAAHQWREI					
QY	121	EVVYNKADLDPEKNDSEPGSQRIKPVFIEDANFGROIISYQHAHVHPTDIYEG					
DB	121	EVVYNKADLDPEKNDSEPGSQRIKPVFIEDANFGROIISYQHAHVHPTDIYEG					
QY	161	NEIWNKTSALDEVFKKRNREDPSLLMQVFGSATGLARYYPASFPWVNSRTPNKIDIL					
DB	161	NEIWNKTSALDEVFKKRNREDPSLLMQVFGSATGLARYYPASFPWVNSRTPNKIDIL					
QY	241	RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLSDDDDFVNVASFN					
DB	241	RPWYIQGAASPKDMLILVDVSGVSGSLTKLIRTSVSEMLETLSDDDDFVNVASFN					
QY	301	VSCFQHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSFAPEQLLNVNVRANCN					

```

|||||
HLVQANVRNKKVLDKDAVNNITAKGIDYKGFSAFEPQLLNNVSRANCKIML 360
EERAEQEIFNKYNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSIGAIR 420
EERAEQEIFNKYNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSIGAIR 420
YLDVLGRPMVLADGAKAKQVQNTNVLDALELGLVITGTLVPFNITGQENKTNLK 480
YLDVLGRPMVLADGAKAKQVQNTNVLDALELGLVITGTLVPFNITGQENKTNLK 480
GVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPENGIVLLHPNLQPNPKSQBPVTL 540
GVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPENGIVLLHPNLQPNPKSQBPVTL 540
AELENDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
AELENDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
PTYSFYIYKAKLBETITQARSKKGMKDSITLKPDMFEESGYTFIAPRDYCNLDKI 660
PTYSFYIYKAKLBETITQARSKKGMKDSITLKPDMFEESGYTFIAPRDYCNLDKI 660
TEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNIKGVKAR 720
TEFLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNIKGVKAR 720
DGGITRYYPKEAGENWOENPETYEDSFYKSLDNDNTVFTAPFNKSGPGAYESGI 780
DGGITRYYPKEAGENWOENPETYEDSFYKSLDNDNTVFTAPFNKSGPGAYESGI 780
AVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCCKNSDVMDCVI 840
AVEIYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCCKNSDVMDCVI 840
GFLLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900
GFLLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSIDYQSVCEPGAAPKQ 900
RSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
RSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
TQTOYFFNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCPDTRLLI 1020
TQTOYFFNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCPDTRLLI 1020
YSDGNPCDMVK 1036
YSDGNPCDMVK 1036

rotein alpha-2 chain precursor - rat
: dihydropyridine-sensitive L-type
im channel alpha-2 chain
norvegicus (Norway rat)
94 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
17
H.; Lee, P.; King, R.G.; Chin, H.
Sci. U.S.A. 89, 3251-3255, 1992
n expresses an alternatively spliced form of the dihydropyridine-sensit
r: A44147; MUID:92228762; PMID:1314383
47
nary
mRNA
1 <KIM>
s: GB:M6621; NID:g203954; PIDN:AAA41088.1; PID:g203955
licium channel alpha-2 chain
um; glycoprotein; ion channel; transmembrane protein

96.2%; Score 5234; DB 2; Length 1091;

```

```

Best Local Similarity 95.7%; Pred. No. 2.7e-307;
Matches 992; Conservative 24; Mismatches 19; Indels 2; Gs

QY 1 MAAGCLLALTTLFQSLIGPSSEBPPFSAVTIKSWVDKQBEDLVTLAKTAGVNOI
DB 1 MAAGCLLALTTLFQSLIGPSSEBPPFSAVTIKSWVDKQBEDLVTLAKTAGVNOI
QY 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSLVSLAEAEKVQAAHQRREDI
DB 61 YEKYQDLYTVENPNARQLVEIAARDIEKLLSNRSLVSLAEAEKVQAAHQRREDI
QY 121 EYVYNAKDDLPENKDSBPGRQIKPVFIEDANFCRQISYQHAHVHPTDIYEGS'
DB 121 EYVYNAKDDLPENKDSBPGRQIKPVFIEDANFCRQISYQHAHVHPTDIYEGS'
QY 181 NELNWTSALEDEVFKNREEDPSLLVQVGSATGLARYYPASPWVDSRTPNKIDLYI
DB 181 NELNWTSALEDEVFKNREEDPSLLVQVGSATGLARYYPASPWVDSRTPNKIDLYI
QY 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETLDSDDFVNVASFNSI
DB 241 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETLDSDDFVNVASFNSI
QY 240 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETLDSDDFVNVASFNSI
DB 240 RPWYIOGAASPKDMLILVDVSGSVGLTLKLI RTSVSEMLETLDSDDFVNVASFNSI
QY 301 VSCFQHLVQANVRNKKVLDKDAVNNITAKGIDYKGFSAFEPQLLNNVSRANCK
DB 301 VSCFQHLVQANVRNKKVLDKDAVNNITAKGIDYKGFSAFEPQLLNNVSRANCK
QY 361 FTDGGERAEQEIFNKYNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSI
DB 361 FTDGGERAEQEIFNKYNKDKKVRVFRFSGVQHNYERGP:QMAACENKGYIYIPIPSI
QY 421 INTOEYLDVLGRPMVLADGAKAKQVQNTNVLDALELGLVITGTLVPFNITGQENK
DB 421 INTOEYLDVLGRPMVLADGAKAKQVQNTNVLDALELGLVITGTLVPFNITGQENK
QY 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPENGIVLLHPNLQPNPKSQE
DB 481 NQLILGVMGVDVSLIEDIKRLTPRFTLCPNGYFAIDPENGIVLLHPNLQPNPKSQE
QY 541 DFLDALENDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGI
DB 541 DFLDALENDIKVEIRNKMIDGESGKFTLTKVKSQDERVIDKGNRTYTWTPVNGI
QY 600 LALVLPTYSFYIYKAKLBETITQARSKKGMKDSITLKPDMFEESGYTFIAPREY
DB 600 LALVLPTYSFYIYKAKLBETITQARSKKGMKDSITLKPDMFEESGYTFIAPREY
QY 660 LSDNNTFELLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNI
DB 660 LSDNNTFELLNNEFIDRKTNNPNSCNADLINRVLLDAGFTNELLVQNTWSKORNI
QY 720 RFVVTDDGITRYYPKEAGENWOENPETYEDSFYKSLDNDNTVFTAPFNKSGPGI
DB 720 RFVVTDDGITRYYPKEAGENWOENPETYEDSFYKSLDNDNTVFTAPFNKSGPGI
QY 780 INVSKAVELYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCCKNSD
DB 780 INVSKAVELYIOGKLLKPAVGIKIDVNSWIENFTKTSIRDPKAGVPCCKNSD
QY 840 ILDDGGFLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSIDYQSVCEP
DB 840 ILDDGGFLMANHDDVTNOIGRFFGIDPSLMRHLVNI SVYAFNKSIDYQSVCEP
QY 900 QGAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFT
DB 900 QGAGHRSAYVPSVADILQIGWATAAAMSILQOFLSLTPRLLLEAVEMEDDDFT
QY 960 QSCITTEQTOYFFNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCP
DB 960 QSCITTEQTOYFFNDKSPSGVLDGNCRSRI FHGEKLMNTNLI FIMVESKGTCP
QY 1020 IOAEQTSDDGNPCDMVK 1036
DB 1020 IOAEQTSDDGNPCDMVK 1036

```


[illegible]

RESULT 4

T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 20-Jun-1999
C:Accession: T30256
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A>Title: Molecular diversity of the calcium channel alpha2delta subunit
A:Reference number: Z20794
A:Accession: T30256
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1091 <KLU>
A:Cross-references: EMBL:AF010949; PIDN:CAA09423.1
A:Experimental source: brain
C:Superfamily: calcium channel alpha-2 chain

T30256
calcium channel alpha-2-delta-C chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_rev150 22-Oct-1999 #text_change 20-Jun
C:Accession: T30256
R:Klugbauer, N.; Lacinova, L.; Marais, E.; Hobom, M.; Hofmann, F.
J. Neurosci. 19, 648-691, 1999
A:Title: Molecular diversity of the calcium channel alpha2delta subunit
A:Reference number: Z20794
A:Accession: T30256
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1091 <KLU>
A:Cross-references: EMBL:AJ010949; PIDN:CAA09423.1
A:Experimental source: brain
C:Superfamily: calcium channel alpha-2 chain

Query Match	19.9%;	Score 1085;	DB 2;	Length 1091;
Best Local Similarity	28.7%;	Pred. No. 3.5e-57;		
Matches 309;	Conservative 222;	Mismatches 416;	Indels 128;	G
QY	3	AGC A T T L Q S L I G S E E P P S A V I K S W D R Q E D L V T A K T A S G V N Q V		
Db	14	AS A L L A T A L L Y A A L G D V V R S E Q I P U S V V K U S A F G G E I K S I A K Y T S G S Q L L C		
QY	63	KY Q D L Y T V E P N N A R Q L V I A R D I E K L S N R S K A L V S I A E A E K V O A A H Q W R E F F		

[illegible]

- *Caenorhabditis elegans*
habditis elegans

habditis elegans
95 #sequence revision 20-Feb-1995 #text_change 30-Jun-2001

```

C:Accession: S44617
R:Favella, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans comid C50C3.
A:Reference number: S44627
A:Accession: S44617
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-734 <F>A>
A:Cross-references: EMBL:L14433; NID:g289649; PID:g289650
C:Genetics:
A:Introns: 24/2; 87/3; 175/1; 259/1; 290/3; 346/3; 460/3; 538/3

Query Match      11.2%; Score 607; DB 2; Length 734;
Best Local Similarity 26.6%; Pred. No. 1.2e-28;
Matches 180; Conservative 127; Mismatches 258; Indels 112; G:

QY 47 LAKTAGVGNQLVDIYEKYQDLYTVPENNAQVLEIARDEIKLLSNRS-----KALV:
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
36 MKETPSKISHETILKQNYEKLVEEQQDPRAELKSKGRIEDYLUKVSQPAYAKALI:
QY 103 EAEKVOAAHQWRDEPNASVYVYNAKDDLDPK-NDSEPGSQRIKP-----VFIE
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
94 EARSVRNDSTVNDPQSKSFRFMSAKQNGDTIYESNHLGKRLKLVETKSFNLTLQ
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
156 -GRQISYQHAHVHTPTDIYEGSTIVLNEIWNLTSDALDFVKQKREDEPSLLWVQFS
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
154 YTLPTSSVSSAVHTPTLYDRNEDLLRKIDW-SDIDAVYRTNRRETKDLAPQFCS
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
215 ARYYPASPMV-DNSRTPNKIDLDYDVRPPWYIQGAASPKDMLILVDVSGSGSLTLL
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
213 MRYYPAAASFWNDQ--DEHLDLDFCRNTWYINSATNSKVLIMLDMSGSLMGQRY
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
274 TGSVEMKLTLDSDDFVNVAFSNSNA---QDVSGCFQHLVOAVNRNKKVLKDAVNMT
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
271 QTTEALLETLSHNDYENIMTFSKNTFLLDGCGNGTNGLLQATWRNKALKRRKMDTYQ
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
331 TDYKKGFSFAPELLNYN-----VSRANCKIIMLPTDGGEBRAOEIENKYNKDKK
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
331 AEYKALPLAFSLVDLTNGGGDNNRGACENVIMLTIDGAPNAYKKIEDMTNADK3
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
386 RFSVQGHNYERGPQIMACENKGYTTEIPISGAIIRINTOEYL-----DVLGRPMVL
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
391 TFLVGDSEALDFNEVREMACNNRGYMVHVANMADVDEKIHYYIRMRSRVVGSRHYKEE
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
442 KOVQNTNLYLDALELGL--VITGTLPVFNITGQFENKTN-----
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
451 ---WMTGVYRRLYLPRPEIFAEFVPTITNGSFAVMNKMASRRKIRLOKSEARSMI
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
479 ---LKNQLILGVMGVDSLSLDIKRLTPRTCLPCNGYIFAIIDPNGVLLHLNPLQPI
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
508 SYPVIVNETFMGVAANVPLTEVAKQHPANIGSKSYFFMLDQNGFWMTHPQLPR:
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
533 --KSQSFVTLDLFD-----AELENDIKVEIR
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
568 KYHKQYNNMDLLELVGQNGQNVRSQKSAVSDLVCEGSANYAEVCDLIRKAVI
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
562 GESGEKTFRLVKSDERY---IDK--GNRTVTWTPVNGTDYSIALVLPTYSF:
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
628 CDNSD-----VQQLDVLVATELLORVYPTQNTYYAEINHANFVLGLAVAKGDD
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
615 KLBETITQARSKKGRMK 631
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
682 K-----QKKYDFGRVK 692
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
T18770
Probable calcium channel protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18770; T25249
R:Sulston, J.

```

RESULT 6

T18770
probable calcium channel protein - *Caenorhabditis elegans*
C1Species: *Caenorhabditis elegans*
C1Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct
C1Accession: T18770; T25249
R:Sulston, J.
R:Sulston, J.

A-Map position: 3p13-3p12
 A-Superfamily: inter-alpha-tryptin inhibitor complex component II
 C-Superfamily: chondroitin sulfate proteoglycan; glycoprotein; heterodimer
 K-words: Chondroitin sulfate proteoglycan; glycoprotein; heterodimer
 F-1-20/29/Domain: signal sequence #status predicted <SIG>
 F-19-29/Domain: propeptide #status predicted <PRO>
 F-15-29/Domain: propeptide #status predicted <PRO>
 F-16-487/Product: inter-alpha-tryptin inhibitor heavy chain 3 #status e:
 F-1648-887/Domain: inter-alpha-tryptin inhibitor heavy chain 3 #status e:
 F-1648-887/Domain: carboxyl-terminal propeptide #status predicted <CNP>
 F-187-576/Binding site: carboxylate (asn) (covalent) #status predicted
 F-1647/Modified site: chondroitin sulfate ester carboxyl end (asp) (in m:
 F-1647/Modified site: chondroitin sulfate ester carboxyl end (asp) (in m:

Query Match 3.4%; Score 185; DB 2; Length 885;
Best Local Similarity 20.4%; Pred. No. 0.0045;
Matches 133; Conservative 106; Mismatches 243; Indels 170; Gaps

QY 27 FPSAVTIKSWDKRQEDLVTLAKTAGUNQLVDIYEKYQDLYTVEPNNAQLVEIAA
|||:|
28 VDCATVCEVIAKYVEKAVSQCKTAG-----LVKASG

DB 97 IFGNVASEKAVANQVLEKGVQKQKARS

QY 87 EKLLSNRSKAL---VSLALEAEKVQAAHQWREDFASNEVVVYNAKODLDPEKNDSEP

Db	132	EKPTSVNVAAGSKVTFLTYBELLKRHKGK-----YEMYLKVQPK-----
QY	144	RIKPVFIEDANFGRQISYQHAAWHIPTDIYEGSTIVNLNWTLSALDEVFKQKREED

Db 174 LVKHFEB-----VDIFPQISMLDAEASFITNDLL-----

DQ

204 LKQVFGSAIGAKATLALFSLTINSGE
| : | : | : ||||
DB

209 LTKSFSGKKGHVSFKS---LDQRSCTDLSLINGDFITTYDVNRESPGNVQIVN

```

QY      245 I-----QG-AASPKOMILLVDVSGSVGLTKLIRTSVSEMLETLSDDDDFVNVAFF
DB      266 VHFPAQGLFWVPKNVAFVIDISGSMAGRKLEQTKEALLRILEDMQEEDYLNFILFE

```

QY
299 QDVSCF-QHLVQANVRNKKVLKDAVNNTAKGITDYKKGFSPAQEQLLNYNSR---
||| : |||| : | : : ||| : | : | :
204 TYSMSTW VQA TDENT-CEAKTFYKSMEIDKGNTINDELLRGISML--NKAREEI

```

DB      324  -DVSIAWAGNLIQAIFENDQZMAA 110.28211111111111
QY      352  ANCNKIIMLFTDG----GEERAQETFNKYNK--DKKRVFRPSVGOHNYERGPIQM

```

DB 380 ERSTSVIMLTGDANDVGSERPEKIQENVRNAIGGKFPFLYNLGF-----
QY 406 NKGYTTEIPSGAIRINTQEYLDVLGRPMVLGDKAKQVQNTNVLDALE-----

DB
439 NHGFARRIYEDSADLQLQGFEVAVANPL-LTGVEMEYPE--NAILDLTONTYQH.

```

QY 457 GLVITGTEFVNILGQFENKINER---KQZLZGVSF---
DB 496 EIVVAGRL-VDEDMNSP--KADVKGHGATNDL---TFTEEDVMKEMEK-----ALQ

```

uncharacterized protein, probably surface-located [imported] - Clostridium acetobutylicum

uncharacterized protein, probably surface-located [imported] - Clostridium acetobutylicum

C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C; Accession: D97033
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.
P; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001
A. Title: Genome Sequence and Comparative Analysis of the Solvent-Produc-
ing Bacteria *Clostridium acetobutylicum* ATCC 25690 and *Clostridium pasteurianus*
ATCC 6974.
A. Reference number: A96900; MUID:21359325; PMID:21359325
J. Daily, M.S.; Bennett, G.N.; Robinson, D.W.; Smith, J.L.

A;Accession: D97033
A;Status: preliminary
A:Molecule type: DNA

<ROW>
EMBL:Y13402; PIDN:CAA73831.1
re: strain IT 4/25/5

3.0%; Score 161; DB 2; Length 2706;
rity 18.2%; Pred. No. 0.74;
nservative 137; Mismatches 345; Indels 338; Gaps 46;
QEDLVTLAKTAGSNQVLDIVKYQDLYTYEPNNA-----EPNNKYCSGDHCKRTYLDKNTIP 358
AEFECTRKI-----KLENNKCEKD-----
RDIEKLSNRSKALVSLAEKQVAAHQWREDPASNEVYVYNAKDDLPKND 138
PRCENACSNYTK-----WIEIQKQPKQK--YNNEI-----KIKTWNINNENDK 408
---PGSORIKPVFIEDANFGQISYQAAVHIPTDIEGSGTIVLNLNWTSALE 191
LDKKGYSTIN--TFLESJNHGKQCO-----DN 438
REEDPSLLWQVFGSATGLARYYPASP-----WVNSRTPNKI 233
KTFNKNL--ETFGP-----SGYCEACPIYGVKCSNEKCTPTVENENSNRLPTDT 493
RRRPWYTOGAASPKMILVDSVSGSLTLKLRISVSEMLETSLDDDFVNVAS 293
N-----ATNIDMLVNDGIGNAI-----515
QDVSCFQHLVQAVNRKK-----VLKDAVNNITAKGIDYKKGFSFAPELL 345
LEKNCTKYGILKTKQKQWCOYLANIDOCKINNVMNSGYFDNKIAFVLFQRL 573
RANCKNIIMLFTDGEERAQEIFNKYNKDKKVRVFRFSGVGHYERGIOMNACE 405
DHNRK-----EKIDVICIKENINENICIKCKTN-----CE 610
YEIPSIGAIRI-----NTQYLDVLRPMVLADGKAKQVQWTVNYLDALDELGVIT 461
ILEKKEAWDKINQHYNNKHIMFILIPYIITGFYEK--ITFPNDFKALE-----DV 665
/FNITQOFENKMLKNQILGVNGVDSLEDKLTPRTPLCPNGYFAIDPNGVY 521
/LDTLKECD--THCKTEKIRSI--DVLDIKEIISWLNQNKIEVCKS--HHDEKHEYC 721
VLOPKNPKSOEPTVTLDFDLAELENDIKVEIRNRMDGESGECT-----FRT 571
JILPKSVDDDEDD--BEVDEKEESSQTTKRN--ISQGGTKSASCVKGACAIKVG 775
JDBRYID-----KGNRTYTM-----TPVNGTD-----YSLALVLPYISF 609
KSNGSIDNCAKNRKKNEMQCKNXTFDGNEGVCMPPRRSICIHNLTEEOQKNK 835
--YIKALET--ITOARSKGKMSOTLK-----PDNFEB--SGVTFTIAPDYC--N 656
EAFIKCAAKETNLLMDYKNDKNEABELLKKGIKIPEDFMIMFYTFGDFDPCLEN 895
---KISDNTEFLINFNEIDRK-----TPNPNPC--NADLINRVLDDAGFTNEL 703
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Db 1076 ANAKBYLKKKFTASCVTSSGKAQNSATEEVKKNIELLSEEQY-----YDADQY
QY 811 -----ENFTKTSIRDPCAGPVCDCK-----RNSDVMDCVIL 841
Db 1127 TKFIHDDKYSKISGRSNCGLNSDAKKNKIKWRNSDEKDYAPL 1169

RESULT 13
A44396
p-type cation translocating ATPase - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jun-1993
C:Accession: A44396
R:Krishna, S.; Cowan, G.; Meade, J.C.; Wells, R.A.; Stringer, J.R.; Rob J. Cell Biol. 120, 385-398, 1993
A:Title: A family of cation ATPase-like molecules from Plasmodium falciparum
A:Reference number: A44396; MUID:93132070; PMID:8421054
A:Accession: A44396
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-1984 <KRI>
A>Note: sequence extracted from NCBI backbone (NCBIP:122678)

Query Match 2.9%; Score 159; DB 2; Length 1984;
Best Local Similarity 17.1%; Pred. No. 0.59;
Matches 179; Conservative 144; Mismatches 359; Indels 366; Gaps 46

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QY 107 VQAAHQWREDPASNEVYVYNAKDDLPKND-----SEPGSORIKPVFIEDANFGI
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QY 161 YQAAVHIPTDIEGSGTIVLNLNW--TSALDEVKKNREEDPSLLWQVFGSATGLAI
Db 240 EYKSNTH-----DLSNKKLCYINNTYDVMKKNKND
QY 220 ASPWVDSNRTPNKKIDLYDVRPRPWIYQGA--ASPKDMLILVDVSGSVGLTKLIRTP
Db 273 ---YNNNNNNKKKKINLN---FVKGTVINSNLLY
QY 279 MLETLSDDDFVNVASFNQAQVSCFQHLVQAVNRKVKLDAVNNITAKGIDYK
Db 304 -----DDKIGVNIPE--DDVNNMKH--KFNORININYNKDNTNL-----EYN
QY 339 FAFEQILNYSRANCKNIIMLFTDGEERAQEIFNKYNKDKKVRVFRFSGVGHY
Db 346 YIYDCLLKVKVEALSQKNKIY-----SNEDINKY
QY 399 IOWMACENKGYEIPISGAIRINTQYLDVLRPMVLG-----DK
Db 375 ---MLYGGTYVLSLYNINKIKYNNKEENRILGL-VIKTGFITTKGKIVNNILYHK
QY 445 QWTVNYLDALDELGVITGTLPVNIYQFENKTNLKNQILG-----IDPNGYVLLHPNLQ-----PKN
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QY 488 MGVDVSLIEDIKLTPRTPLCPNGYFPA-----IDPNGYVLLHPNLQ-----PKN
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QY 536 EPVTLDFDLAELENDIKVEIRNRMDGESGECTFRTLKVSQDERYIDKGNRTYTW
Db 548 NMLS-DFIHLK-----EMNTESYIHSKDDNMHNKN-----SETLKPDNE
QY 596 TDYSLALVLPYISFYIKAKLEETITOARSKKGGKND-----DNV- 762
Db 578 -----SIISYYIKDNMKNLHTSSK-KKSIKERSNPLVQTIKSCLDKQHY
QY 646 YTFIAPDYCNDLKISDN--TEFLN-----FNEF--IDRKTPNPNPCNADLINR

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in b2270 - Escherichia coli (strain K-12)
chla coli
7 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
8 Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
au, B.; Shao, Y.
1462, 1997
ete genome sequence of Escherichia coli K-12.
8 A64720; MUID:97426617; PMID:9278503
ary; nucleic acid sequence not shown; translation not shown
NA
<BLAT>
rce: GB:AE000317; GB:U00096; NID:91788605; PIDN:AACT5330.1; PID:91788606;
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arity 21.6%; Pred.No.0.1; 206; Indels 105; Gaps 25;
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KND-----SEPGSRIKPVFIEDANFGQISYQHA--VHIPTDI 172
LQEAFTFAAAKAKATHIANPGTARYQF---DDNPVQVAQNPLATSLDVTGS 132
TIVLNE-----LNWTSALDEVFKNREEDPSLLWQVFGSATGLARY 218
TRFLNQLLPPDPAVRVEIVNFFSDNDI--KDKQSIPASKPIPFAMRYELA--- 187
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KELREQDIAIVTYAGDSRIA-----LPSISGSHKABINAAIDSLDAEGSTNGAGL 296
FEQLLNVNVRANCNKLIMLPTDG-----GEERAQEIFNKYNKDKKVRVFRFSVQ 391
YQQAATK-GFTKGGINR-ILLATDGDENVGIDDPKSIKESMYKKQRESGVILSTFGVN 354

QY 392 HNYERGPIQWMAKCNKGYIYEIPSIGAIRINTQEVLDVLRPMVL--AGDKAKQVO-
Db 355 SNYNEMAMVRIADVGNNGNSYIDTIS-----EAKVLNSEKQMLITVAKDVKAQIEI
QY 446 WTNVYLDALDELGLVITGTLPVENITGQFENKTNLKNQLILGVMGVD--VSLEDI---I
Db 411 WTEY---RQIG-----YE-----KQLRVHEHFNNDVDAGDIGAGI
QY 502 PRFTLCPNGYFFAIDPNGVYLLHPNLOPKPKSQE 536
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E90542
lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug
C;Accession: E90542
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissot
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathog
A;Reference number: A99512; MUID:21267165; PMID:11353084
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A;Experimental source: strain UAB CTIP
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Best Local Similarity 20.0%; Pred.No.0.25; 229; Indels 161; G
Matches 122; Conservative 99; Mismatches 229;
QY 305 QHLVQANVRNKKV-----LKDAVNNTAKGIDYKKGFSFAFQQLLNVRANCNK
Db 91 KRILPSNVNENLDFNSLKILITKNTILGKNIPIKNTYVAFSIDPN-SVENASADN
QY 361 FTDGGEERAQIEFNKYNKDKV---RVFRFSVQGHYERGIQWMAKCNKGYIYEI
Db 146 -TDG-----SMNIIIVLAKDNGVLEKFKIT-----GLLSEL
QY 418 AIRINTQEVLDVLRPMVLAKQVQWTVYLDALGLVITGLP-----
Db 182 DQNLK---VDVPKNENILASSIVEVEQITNE-----KISLSTQGVKVPSTFDLTKY
QY 468 NITQFENKTNLKNQLILGVMG-----VDVSLBDIKR--LTPRFTL-CPNGYIYF
Db 233 HVLSHDDKGLKIRVLSAKSKTSKDFDYTIQFKQSFLEDRISLAKQGVNKL
QY 519 GYVLLHPNLOPKPKSQEPTVLDLDAELENIDKVEIRNKMIDGESGEKTRTLV
Db 292 --IIKSLQLLPSSASSED--KLVNLSAYDISVPDGLKFNFSVPEAKQGT-----
QY 579 RYIDKGNRTYTPWNGTDYSALVLPYSPYIKAKLEETITQARSKKGMKDSH
Db 339 ---DKGLVLYTLQINGTRTTEEVKLDIQTENILIKRYLDETLIKLIDSV--VLKKN
QY 638 --PDNFEESGYTFIAPRDYCNLDKISDNNTBFLNLFNEF-IDRKTPNNPNSCNADLJ
Db 394 SLPSSELVKEI---ENWQNEIELLDSKAKINVKNEFQVSVTSANPEYN-----
QY 695 LDAGFTNE-----LVQNYMSKQNIKGVKARF--VVTDDGITRVYP---KEAGI
Db 443 IDGSLNVEVRISDGIQVQTKRISGLTKLDANLPDWWAKANVSNQLPGLKAKD
QY 743 NPETYE-DSF-----YKRSLDN---DNVVFYAPY---FNKSGPGI
Db 503 GEKTFSTDSFELKPKFNKAKENNSILNLYKLSLENVKLNKPNFSQGVSDVVFTRKGTGI

WEIYIQKLL-----KPAVVGKIDVNSWIENFTXSIRDPCAG 824
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RNSDV 835
| | :
ENDDL 620

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February 20, 2004, 16:59:26
3ECB

7:56:56 2004

us-10-090-827-15.rsp

GenCore version 5.1.6
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1 search, using sw model

quary 20, 2004, 16:48:25 ; Search time 11.5951 Seconds
(without alignments)
4311.242 Million cell updates/sec

10-090-827-15

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SUM62

cp 10.0 , Gapext 0.5

863 seqs, 47026705 residues

s satisfying chosen parameters: 127863

th: 0

th: 2000000000

nimum Match 0%

ximum Match 100%

string first 45 summaries

issProt_41.*

the number of results predicted by chance to have a
than or equal to the score of the result being printed,
d by analysis of the total score distribution.

SUMMARIES

ry	ch	length	DB	ID	Description
0	1	1091	1	CIC2 HUMAN	P54289 homo sapien
3	1	1091	1	CIC2 RAT	P54290 rattus norv
1	1	1106	1	CIC2 RABIT	P13806 corytolagus
0	1	1249	1	Y103 SYNY3	P13874 caenorhabdi
5	1	886	1	ITH3_MOUSE	Q61704 mus musculu
3	1	885	1	ITH3 HUMAN	Q66033 homo sapien
2	1	887	1	ITH3 RAT	Q63416 rattus norv
9	1	886	1	ITH3 MESAU	P97280 mesocricetu
9	1	1829	1	DPOL_THBST	Q33845 thermococcu
8	1	1956	1	ATX1_PLAFA	Q04956 plasmodium
8	1	575	1	YFBK_ECOLI	P76481 escherichia
8	1	946	1	ITH2 HUMAN	P19823 homo sapien
7	1	1290	1	EXCI_CLOBO	P18640 clostridium
7	1	420	1	Y103 SYNY3	Q55874 synechocyst
7	1	921	1	ITH4_PIG	P79263 sus scrofa
7	1	654	1	MCPQ_BACSU	P54576 bacillus su
7	1	930	1	ITH4_HUMAN	Q14624 h inter-alp
6	1	964	1	DPOL_CBEFP	P30319 choristoneu
6	1	1087	1	YXNX_CLOTH	P38535 clostridum
6	1	946	1	ITH2 MESAU	P97279 mesocricetu
5	1	1169	1	SMC_METJA	Q59037 methanococc
5	1	1251	1	RBP2_PLAVB	Q00799 plasmodium
5	1	935	1	ITH2_PIG	Q02668 sus scrofa
5	1	2710	1	TOXA_CLODI	P16154 clostridium
5	1	3305	1	APLP_MANSE	Q25490 manduca sex
5	1	764	1	PAG_BACAN	P13423 bacillus an
5	1	1513	1	STU1_YEAST	P38198 saccharomyc
5	1	1180	1	C4AA_BACTI	P16480 bacillus th
5	1	3063	1	CAIC_HUMAN	Q99715 homo sapien
4	1	946	1	ITH2 MOUSE	Q61703 mus musculu
4	1	2077	1	TEGU_HSV6U	P52340 human herpe
4	1	862	1	MUTS_BORBU	O51737 borrelia bu
4	1	1323	1	ADRI_YEAST	P07248 saccharomyc

34	132.5	2.4	547	1	SYM_BUCAL	P57210 buchne
35	132.5	2.4	929	1	CAIC_NOTVI	Q91145 notop
36	132.5	2.4	1679	1	Y109_YEAST	P40457 sacch
37	132	2.4	697	1	YE9C_SCHPO	Q13773 schiz
38	131.5	2.3	1018	1	YCL4_METJA	Q58611 metha
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ALIGNMENTS

RESULT 1	CIC2 HUMAN	STANDARD;	PRT; 1091 AA.
ID	CIC2 HUMAN		
AC	P54289;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor.		
DE	CACNA2D1 OR CACNL2A OR CCHL2A.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92110010; PubMed=1309651;		
RA	Williams M.E., Feldman D.H., McCue A.F., Brenner R., Velicelebi G., Ellis S.B., Harpold M.M.;		
RT	"Structure and functional expression of alpha 1, alpha 2, and beta subunits of a novel human neuronal calcium channel subtype.";		
RL	Neuron 8:71-84(1992).		
CC	1- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT RO		
CC	1- EXCITATION-CONTRACTION COUPLING.		
CC	1- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUN		
CC	1- ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS		
CC	1- HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).		
CC	1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM, SKELETAL MUSCLE A		
CC	1- AORTA TISSUES.		
CC	1- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED		
CC	1- A PRECURSOR FORM (BY SIMILARITY).		
CC	1- SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.		
CC	1- SIMILARITY: Contains 1 VFMA domain.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a coll		
CC	between the Swiss Institute of Bioinformatics and the EMBL out		
CC	the European Bioinformatics Institute. There are no restriction		
CC	use by non-profit institutions as long as its content is in		
CC	modified and this statement is not removed. Usage by and for c		
CC	entities requires a license agreement (See http://www.isb-sib.ch/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
CC	EMBL; M76559; AAA51903.1; --		
DR	PIR; JH0565; JH0565.		
DR	Genew; HGNC:1399; CACNA2D1.		
DR	MTM; 114204; --		
DR	GO; GO:0005891; C-voltage-gated calcium channel complex; TAS.		
DR	GO; GO:0015270; P-dihydropyridine-sensitive calcium channel a. .		
DR	GO; GO:0006832; P:small molecule transport; TAS.		
DR	InterPro; IPR004010; Cache.		
DR	InterPro; IPR002035; VWF_A.		
DR	Pfam; PF02743; Cache; 1.		
DR	Pfam; PF00092; vwa; 1.		
DR	SMART; SM00327; VWA; 1.		
DR	PROSITE; PS50234; VWF_A; 1.		

Transmembrane; Ion transport; Voltage-gated channel;
 1; Glycoprotein; Phosphorylation; Signal.
 1 24 POTENTIAL.
 5 944 L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
 (BY SIMILARITY).
 5 1091 L-TYPE CALCIUM CHANNEL DELTA SUBUNIT (BY
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 6 469 POTENTIAL.
 16 930 POTENTIAL.
 17 1086 POTENTIAL.
 13 430 VWFA.
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 36 986 N-LINKED (GLCNAC. .) (POTENTIAL).
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 conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 YNAKDDLDPEKNDSEPSQRKIPVFIEDANFGROIYSYQAAVHIPTDIYEGSTIVL 180
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 RESULT 2
 C1C2_RAT STANDARD; PRT; 1091 AA.
 ID_C1C2_RAT
 AC P54290;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
 subunits precursor.
 GN CACNA2D1 OR CACNA2A OR CCHL2A.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92228762; PubMed=1314383;
 RA Kim H.L., Kim H., Lee P., King R.G., Chin H.;
 RT "Rat brain expresses an alternatively spliced form of the
 dihydropyridine-sensitive L-type calcium channel alpha 2 subunit.
 Proc. Natl. Acad. Sci. U.S.A. 89:3251-3255(1992).
 RL
 CC -|- FUNCTION: CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT RC
 EXCITATION-CONTRACTION COUPLING.
 CC -|- SUBUNIT: THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUN
 ALPHA-1, ALPHA-2, BETA AND GAMMA. ALPHA-2 AND DELTA FORMS
 HETERODIMERS THAT ARE DISULFIDE-LINKED (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=2 isoforms are produced;
 CC Name=1;
 CC IsoId=P54290-1; Sequence=Displayed;
 CC -|- PTM: ALPHA-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSE
 A PRECURSOR FORM (BY SIMILARITY).
 CC -|- SIMILARITY: TO OTHER SPECIES' ALPHA-2 SUBUNIT.
 CC -|- SIMILARITY: Contains 1 VWFA domain.
 CC
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informatics Institute. There are no restrictions on its
ofit institutions as long as its content is in no way
is statement is not removed. Usage by and for commercial
has a license agreement (See <http://www.ieb-sib.ch/announce/>
.1 to license@sib-sib.ch).

AA41088.1; -;
14147.
04010; Cache.
02035; VWF_A.
Cache; 1.
vwa; 1.
vwa; 1.
34; VWFA; 1.
Transmembrane; Ion transport; Voltage-gated channel;
1; Glycoprotein; Phosphorylation; Signal;
licig.
1 24
5 944
POTENTIAL.
L-TYPE CALCIUM CHANNEL ALPHA-2 SUBUNIT
(BY SIMILARITY).
5 1091
L-TYPE CALCIUM CHANNEL DELTA SUBUNIT
(BY SIMILARITY).
POTENTIAL.
5 468
POTENTIAL.
6 930
7 1086
POTENTIAL.
2 429
VWFA.
2 92
N-LINKED (GLCNAC. .) (POTENTIAL).
6 136
N-LINKED (GLCNAC. .) (POTENTIAL).
4 184
N-LINKED (GLCNAC. .) (POTENTIAL).
3 323
N-LINKED (GLCNAC. .) (POTENTIAL).
7 347
N-LINKED (GLCNAC. .) (POTENTIAL).
4 474
N-LINKED (GLCNAC. .) (POTENTIAL).
4 584
N-LINKED (GLCNAC. .) (POTENTIAL).
3 593
N-LINKED (GLCNAC. .) (POTENTIAL).
3 663
N-LINKED (GLCNAC. .) (POTENTIAL).
9 769
N-LINKED (GLCNAC. .) (POTENTIAL).
2 812
N-LINKED (GLCNAC. .) (POTENTIAL).
6 876
N-LINKED (GLCNAC. .) (POTENTIAL).
3 883
N-LINKED (GLCNAC. .) (POTENTIAL).
3 973
N-LINKED (GLCNAC. .) (POTENTIAL).
6 986
N-LINKED (GLCNAC. .) (POTENTIAL).
0 500
PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
3 833
PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
1 AA; 123822 MW; 7054907D9D343B34 CRC64;
96.3%; Score 5390; DB 1; Length 1091;
rity 95.8%; Pred. No. 3.8e-315;
nservative 24; Mismatches 19; Indels 2; Gaps 2;

TLALTLTLFQSLIGPSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVNQLVDI 60
TLALTLTLFQSLIGPSEPPPSAVTIKSWVDKMQEDLVTLAKTASGVTLADI 60
DLTYTPNNARQLVIAARDIEKLSNRSKALVSLAEKQVAAHQWREDPASN 120
DLTYTPNNARQLVIAARDIEKLSNRSKALVSLAEKQVAAHQWREDPASN 120
ANAKDLDEKNDSEGSQRIKVPFIEDANFGQISQVHAAVHIPTDIYEGSTIVL 180
ANAKDLDEKNDSEGSQRIKVPFIEDANFGQISQVHAAVHIPTDIYEGSTIVL 180
ATGALDEVFKNREEDPSLWQVFGSATGLARYYPASPDNSRTNPKIDLYDVR 240
ATGALDEVFKNREEDPSLWQVFGSATGLARYYPASPDNSRTNPKIDLYDVR 240
IQGAASPKDMLILVDVSGSVGLTLKLRISVSSEMLETLSDDDDFVNVASFN 300
IQGAASPKDMLILVDVSGSVGLTLKLRISVSSEMLETLSDDDDFVNVASFN 300
QHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAEQILNYSRANCKIIML 360
QHLVQANVRNKKVLKDAVNNITAKGIDYKKGFSFAEQILNYSRANCKIIML 360

361 FTDCGERAEQIFNKYNKDKKVRFSVGOHNYERGPIONMACENKGYIYIPISIG
360 FTDCGERAEQIFNKYNKDKKVRFSVGOHNYERGPIONMACENKGYIYIPISIG
421 INTOEYLDVLRPNMVLADGAKAQVQNTNVLDALELGLVITGTLPVFVNITQGFENKT
420 INTOEYLDVLRPNMVLADGAKAQVQNTNVLDALELGLVITGTLPVFVNITQGFENKT
481 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYYPFADPNNGYVLLHPNLOPKPKSGEP
480 NQLILGVMGVDVSLIEDIKRLTPRTLCPNGYYPFADPNNGYVLLHPNLOPKPKSGEP
541 DFLDAELENDIKVEIRNKMDIGESGEKTRFLVKSQDERYIDKGNRTYTWTPVNGTD
540 DFLDAELENDIKVEIRNKMDIGESGEKTRFLVKSQDERYIDKGNRTYTWTPVNGTD
600 LALVLPYTFYIYAKALETITQARSKKGMKDSSETLXPDNFEESGYTFIAPRYCN
600 LALVLPYTFYIYAKALETITQARSKKGMKDSSETLXPDNFEESGYTFIAPRYCN
660 ISDNNTTEFLNPFIDRKTPNPNPCNADLINRLLDAGFTNELVQNYWSKQNKIKG
660 PSDNNTTEFLNPFIDRKTPNPNPCNADLINRLLDAGFTNELVQNYWSKQNKIKG
720 RPVYTDGGITRVYPKEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAY
720 RPVYTDGGITRVYPKEAGENQENPETYEDSFYKSLDNDNYVFTAPYFNKSGPGAY
780 INVSKAVELIYQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCRKNSDVW
780 INVSKAVELIYQGLKLPVAVGKIDVNSWIENFTKTSIRDPCAGPVCDCRKNSDVW
840 ILDDGGFLMANHDDYTNOIGRFFGEIDPRMVRHLVNTSLYAFNKSVDYQSCVDCPG
840 ILDDGGFLMANHDDYTNOIGRFFGEIDPRMVRHLVNTSLYAFNKSVDYQSCVDCPG
900 QGAGHRSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLEAVEDEDDFTAI
900 QGAGHRSAYVPSVADILQIGWATAAASILQOFLSLTFPRLLEAVEDEDDFTAI
960 QSCITEQTYQFPDNDKSPSGVLDGCGNSRIFHGEKLMNTNLIIFIMVSKGTGCPD
960 QSCITEQTYQFPDNDKSPSGVLDGCGNSRIFHGEKLMNTNLIIFIMVSKGTGCPD
1020 IQAETSQGNPCDMVKQPRYKGPVCFDNNVLEDYTDGGVS 1063
1020 MQAETSQGNPCDMVKQPRYKGPVCFDNNVLEDYTDGGVS 1063

RESULT 3
CIC2_RABIT
ID_CIC2_RABIT STANDARD; PRT; 1106 AA.
AC PI3806;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
DE subunits precursor.
DE CACNA2D1 OR CACNA2A OR CCHL2A.
GN Oryctolagus cuniculus (Rabbit).
OS Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SSOURCE FROM N.A.
RX MEDLINE=98336904; PubMed=2458626;
RA Ellis S.B., Williams M.E., Ways N.R., Brenner R., Sharp A.H.,
RA Leung A.T., Campbell K.P., McKenna E., Koch W.J., Hui A.,
RA Schwartz A., Harpold M.M.;
RT "Sequence and expression of mRNAs encoding the alpha 1 and alpha
RT subunits of a DHP-sensitive calcium channel.";
RL Science 241:1661-1664 (1988).
RN [2]

HAADMEDDDFTASMSKQSCITEQTQYFFDNDKSFSGVLDGCGNSRIFHVEXKLN 1013
 [MVESKGTCPDRLLIQAEQTSQDGNPCDMVQPRYKGPDPVCFDNNVLEDTD 1058
 [MVESKGTCPDRLLIQAEQTSQDGNPCDMVQPRYKGPDPVCFDNNVLEDTD 1073

1063

1078

STANDARD; PRT; 1249 AA.

; P34373;

el. 28, Created)

el. 42, Last sequence update)

el. 42, Last annotation update)

ent calcium channel unc-36 precursor (Uncoordinated

72 OR C50C3.9/C50C3.10/C50C3.11.

elegans.

azoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

eloderinae; Caenorhabditis.

9;

N.A.

N2;

18; PubMed:7906398;

scough R., Anderson K., Baynes C., Berks M., Coulson A.,

urton J., Connell M., Copsey T., Cooper J., Fraser A.,

ar S., Du Z., Durbin R., Favello A., Hillier L., Jier M.,

dner A., Green P., Hawkins J., Halster N.,

ones M., Kershaw J., Kirsten J., Maister N.,

Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

rcy C., Rifken L., Roopra A., Saunders D., Showkhen R.,

lon N., Smith A., Smith M., Sonhammer E., Staden R.,

derry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

Watson A., Weinstock L., Wilkinson-Sproat J.,

iguous nucleotide sequence from chromosome III of C.

38 (1994).

-2002) to the EMBL/GenBank/DBJ databases.

TISSUE SPECIFICITY.

; Sanchez B.M., Kenyon C.J.;

ing sensitivity to serotonin in *Caenorhabditis elegans*."

[219-1230(1996).

um act as an auxiliary subunit of the UNC-2 voltage-

ium channel which appears to trigger calcium-activated

pathways that control the serotonin response. Inhibiting

sensitivity of the vulval muscles results in egg laying

ay act in both neurons and muscle cells to enhance motor

SPECIFICITY: Descendants of the cells AB and AB.p (that give

early all nonpharyngeal neurons), descendants of P1 (that

to body muscle) and cell lineages that give rise to the

juvenile motor neurons.

Y: Contains 1 VWFA domain.

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DR EMBL; L14433; AAA27971.3; --
 DR PIR; S44617; S44617.
 DR WormPep; C50C3.9; CE32168.
 DR InterPro; IPR004010; Cache.
 DR InterPro; IPR002035; VWFA.
 DR Pfam; PF02743; Cache; 1.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SM00327; VWFA; 1.
 DR PROSITE; PS0234; VWFA; 1.
 DR Behavior; Ionic channel; Ion transport; Voltage-gated channel;
 KW Calcium channel; Signal; Glycoprotein.
 FT SIGNAL 1 19
 FT CHAIN 20 1249
 FT DOMAIN 250 479
 FT CARBOHYD 100 100
 FT CARBOHYD 140 140
 FT CARBOHYD 146 146
 FT CARBOHYD 302 302
 FT CARBOHYD 520 520
 FT CARBOHYD 558 558
 FT CARBOHYD 757 757
 FT CARBOHYD 838 838
 FT CARBOHYD 903 903
 FT CARBOHYD 923 923
 FT CARBOHYD 1130 1130
 FT SEQUENCE 1249 AA; 144375 MW; 533FF6059D375FB2 CRC64;

Query Match 13.0%; Score 727.5; DB 1; Length 1249;
 Best Local Similarity 23.1%; Pred. No. 1e-35;
 Matches 284; Conservative 201; Mismatches 467; Indels 275; Gc

QY 47 LAKTAGVNLVDIYEKQDLYTVFPNARQVETAAARDIEKLSNRS---KALV
 DB 36 MKETFSKISHETILKQNEKLVSEEFQDPRAELKSKKHRIEDYLVKRSOFAYAKI
 QY 103 EAKYQAAHQWEDFASNEVYVYNAKDDLDPEK-NDSEPGSORIKP-----VFIE
 DB 94 EARSVRNDSTVNDPQSKSFIRFMSAKQNGDGTIYESHLGKRLKYNKTSFNLQ
 QY 156 -GRQSYQAAVHPITDIYEGSTIVLNLNWTSLADVEFKKREEDPSLLMQVFGSI
 DB 154 YLPTSSVSSAVHPTPLDYDRNEDLLRKIDW-SDIDAVYRTNRETKDLAFQFCSI
 QY 215 ARYPASPWV-DNSRTPNKIDYVRRRPWYTCGAASPKDMLILDVSSVSGLTIL
 DB 213 MRYTPAASWFDNQ--DEHLDLFDCNTEWYINSATNSKNVLIMLDMSGMLGQRYI
 QY 274 TSVSEMLETLSDDDFVNVASFNNA---QDVSCFQHLVQANVKNKVLKDAVNNIT
 DB 271 QTTEATLETLSHNDYFNITFTSKNTFLDGCNGTNGLLQATMRNKKALREKMDTYQ
 QY 331 TDYKKGFSFAFQLNLYNVS-----
 DB 331 AEYKALPLAFSVLLDLKGSVALYTKEMSMSANATNEYQFHELPHEVLAATKQ
 QY 351 -----RANKKILMLPTDGEERAQEIFNKYNKKKVRVRSVGVQHNVERG
 DB 391 INNGGGDNNRGACENVIMLITDGNAPYAKKIFDMYNADKKVRVFTFLVGDGADDFN
 QY 402 MACENKGYEIEISGAIRINTQEYL-----DVLGRPMVLADKAKQVQWNTNVLDA
 DB 451 MACNREGYVHVANMADVDEKIHHRMRGRVVRGHRKESGQLS---WVGTVYRER
 QY 458 L--VITGLPVPNITQGFENKTN-----LNQLILG
 DB 508 RPEIPAEFVITWQSPAVMKNKMSRRKIRLQKSEARSRMFVTVTVSVPIVNETPMG
 QY 491 DVSLIEDIKRLTPRTLCPNGYYPFADPNGVVLLHPNLQPNP-----KSQEPVTLDP
 DB 568 NIPLTEVAQKSHPANIGSKSYFFMLDQNGFVMTHPQLRPIDPFTKYHKQNNNDL
 QY 545 -----AELENDIKVEIRNMKIDGESGEKTRFLV

icus (Rat).
tazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
peria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
116;

N.A.
e-Dawley; TISSUE=Liver;
s E.;
C-1994) to the EMBL/GenBank/DBJ databases.
MAY ACT AS A CARRIER OF HYALURONIN IN SERUM OR AS A
ROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
ION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
Y).
I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
O HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
IN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
X-CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN

CC	4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC	SIMILARITY).
CC	- - SIMILARITY: BELONGS TO THE ITHH FAMILY.
CC	- - SIMILARITY: Contains 1 VWFA domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a colla
CC	between the Swiss Institute of Bioinformatics and the EMBL out
CC	the European Bioinformatics Institute. There are no restrictions
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CC	modified and this statement is not removed. Usage by and for cc
CC	entities requires a license agreement (see http://www.ebi.ac.uk/EMBL/1998-01-01/EMBL_1998-01-01.html)
CC	or send an email to license@ebi.ac.uk .
CC	-----
DR	EMBL: X83231; CAA58233.1; --
DR	InterPro: IPR006587; VIT.
DR	InterPro: IPR002035; VWFA_A.
DR	Pfam: PF00092; vwa; 1.
DR	SMART: SM00609; VIT; 1.
DR	SMART: SM00327; VWA; 1.
DR	PROSITE: PS50234; VWFA; 1.
KW	Serine protease inhibitor; Repeat; Signal; Multigene family;
KW	Glycoprotein. 1 21
FT	SIGNAL
FT	PROPEP 22 33
FT	CHAIN 34 647
FT	-----
FT	PROPEP 648 887
FT	DOMAIN 282 442
FT	CARBOHYD 91 91
FT	CARBOHYD 580 580
FT	BINDING 647 647
FT	-----
FT	SEQUENCE 887 AA; 99097 MW; 3B9F0FF6D514096 CRC64;
QY	Query Match 3.2%; Score 180.5; DB 1; Length 887;
QY	Best Local Similarity 18.5%; Pred. No. 0.0037; Indels 275; G;
QY	Matches 173; Conservative 139; Mismatches 350;
QY	-----
QY	27 FPSAVTIKSWDKQBDLVLTAKTASGVNQLDIYEKYQDLYTVPENNARQLVETIA
Db	101 YPGSVKEKEVAQKQEKAVSQGTAG---LVKASGRKLEKFTVSVVAAGSKVIFP
QY	87 EKLLSNRSKALVSLAEAEKQAAHQWRD---FASNEVVVYNKDDLDLPEKNDSEI
Db	157 EEEL--KENKGKEMYLKVPQKQVVRHFEIDAHIFEPQGISMLDA-----
QY	144 RIKPVFTIEDANFCRQISYQHAAVHIPTDIYEGSTIVLNEIWNMTSALDEVFKKNREE
Db	200 -----DASF-----ITNDL-LGSALTKSF-----
QY	204 LMQVFGSATGLAARYPASPWVDNSRT-PNKID-----LYDVRPP-----
Db	218 -----SGKGHGVSKFPLSDQQRSCPTCTDSLNGDFTIVYDVNRESFGNVQIV
QY	245 I-----QG-AASPKDMLILVDVSSVSGVLTKLIRTSVSEMLETSLDDDFVNVASF
Db	270 VHFAPQGLPVFPENIAFVIDVSGSSGSRKIQOTREALLKILDDMKDEYLNILF
QY	299 QDVSCFOHLYQANVRNKKVLKDAVNNITAKGITDYKGFSAFPEQLLNTVNSRAN-
Db	330 --TTMKDHLVKATPANLEEARAFVGNIRDSMTNINDLLRGIEML---NKAREDH
QY	354 -CNKIIMLFTDG---GEERAQEIFNKYNKKVVRFRFSVG-QHNVERGPIQMAA
Db	385 RSTSILVMLTDGANTGESPEKIQENVRNAIRGKPLYNLGFNNLNTVNFLESIA
QY	408 GYYVEIPSIGAIRINTQYILDVLRPVMVLADGKAKQVQMTNVYLDALDELGL--VIT
Db	445 GPARIIYEDSDASIQLOGFYEIVANPL-----INVELEYPENAILDLTR
QY	466 VFNITGOFENKTNLKNQILIGWGVVDVSLSDIIRKLTPTFLTCPNGYYFAIDPNGYV
QY	494 HF-----YDG-----SRIIVAGRLVDNRVN-----FKADVKGKH
Db	-----

VPKQBPVTLDFLDALENDIKVEIRKMDGSGKTF-----RTLVKSQDER 579
 :LTFTEVDMKMDAALK-----EGYIFGDIYIERLWAYLTIBQLLEKKRVAR 574
 :
 NRTYVTPVNGTDYSLA--LVLTPTSPYIYKAKLEETITOARSKKGMKQDSET-- 635
 :
 VIT-----AEALELSLKHYFVPTLTSVMTVPEDNEQTAIAADKPGEAISASTA 629
 :
 VFESGVTFTAPRDCNDLKISDNNTFLNPF--NEFIDRKTNPNSCNADLIN 691
 :
 JSSHSPPYIV-----DGDPHFIIVQFGKNDTICFNIDKPKGTVLSLIQ 677
 :
 AGTNELVQVMSKQKNIKVKARFVVDGTVVYVPEKAGENQWENPETYDSF 751
 :
 IAVTQII-----GEKGNASSRTGKT----- 704
 :
 DNDNYVFTAPYFNKSGFAYESGIMVSKAVEIYIQGLKLPVAVGKIDVNSWIE 811
 :
 -----YFGKLGIANAWMDPRIEVTTEKILGN-----GDALSTFSWLD 742
 :
 SIRDPCAGVCDCKRNSDVMDCVILDG-GFLIMAN-----HDDYTQIGRF 862
 :
 Q-----TGLSVTINRKNMV--VSFEDGISFVILHQVWKHPVHDFLQ 790
 :
 PSLMRHLVNTSVVAFNKSVDYQSV-CEPGAAP 898
 :
 SHRMSAOTGLLQGFQFFDFKVPDVRPGSDP 827

STANDARD; PRT; 886 AA.

el. 36, Created)
 el. 36, Last sequence update)
 el. 41, Last annotation update)
 ypsin inhibitor heavy chain H3 precursor (ITI heavy
 er-alpha-inhibitor heavy chain 3) (HC3).
 uratus (Golden hamster).
 azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 eria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 36;
 N.A.
 88; PubMed=9276673;
 uzuki Y., Yamamoto T., Sinohara H.;
 ning and sequencing of cDNAs encoding three heavy-chain
 the inter-alpha-trypsin inhibitor in Syrian hamster:
 or the evolution of the inter-alpha-trypsin inhibitor
 mily.";
 2:71-82 (1997).

-50; 446-472 AND 504-523, AND SUBUNITS.

41; PubMed=8864857;
 amamoto K., Sinohara H.;
 ypsin inhibitor and its related proteins in Syrian
 and plasma.";
 0:145-152 (1996).
 MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 ROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CON, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
).
 [-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
) HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
 INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
 (N, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND

CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN
 CC -I- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 CC 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY
 CC SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -I- SIMILARITY: Contains 1 VWFA domain.
 CC
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/a>
 CC or send an email to license@isb-sib.ch).
 CC

EMBL; D89287; BAA13940.1; -
 InterPro; IPR006587; VIT.
 DR InterPro; IPR002035; VWFA_A.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SM00609; VIT; 1.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS02334; VWFA; 1.
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 KW Glycoprotein. 1 18
 FT SIGNAL
 FT PROPEP 19 30
 FT CHAIN 31 646
 FT
 FT PROPEP 647 886
 FT DOMAIN 279 439
 FT CARBOHYD 88 88
 FT CARBOHYD 577 577
 FT BINDING 646 646
 FT
 SQ SEQUENCE 886 AA; 99018 MW; AC0594C6852576B8 CRC64;

Query Match 2.9%; Score 164.5; DB 1; Length 886;
 Best Local Similarity 23.2%; Pred. No. 0.034;
 Matches 66; Conservative 56; Mismatches 112; Indels 51; Gs

QY 202 SLLQVFGSATGLARYYPASPMVDNSRT--PNKID-----LYDVRRR--PWYIQ
 DB 208 SALTQSGKGGHVSFKFS---LDQORSCPTDLSLLNGDFIVIVDVNRPESQNVQ
 QY 249 -----ASPKDMLILVDVSGSVSGLTLKLIRTSVSEMLETSLDSDDFVNVAS
 DB 265 YVHFHFAQGLPVVPRNIVFVIDISSMAGRKIQOTRVALLKILDDMKQDDYLNFTI
 QY 297 NAQDVSCFOHLVQAVNRNKKVLKDAVNNTAKGITYDKKGFSAFEQLLN-----YNI
 DB 325 GV--ITWKDSLVOATPANLEEARITFVRSISDQGMNINDGLLRGIRMLTDAREQHT
 QY 353 NCKNKLMLFTDG---GEERAQRIENKYNKKDKKRVFRFSVG--QHNRYERGPQWMA
 DB 383 STSIILML--TDGDANTGESRPEKIQENVRKAIEGRFPLNGLFGNNLNYNLETMAI
 QY 408 GYYPEIPSGAIRINTQEYLDVLGRPMVLGDKAKQVQMTNVILD 452
 DB 442 GVARRIYEDSDANLQIQGFVEEVANPLL-----TNVEVE 475

RESULT 9

DPOL THEST STANDARD; PRT; 1829 AA.
 ID DPOL THEST
 AC Q33875;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 GN POL.
 OS Thermococcus sp. (strain TY).
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcac
 OC Thermococcus.

```

335 LAKLIQSVWDVSRSTGVLVWVYLLAVAVERNELAPKNPDDEBYRRRLRTTYLGG
151 EDANFGRQISYQHAHAHIPTD---IYGGSTIV---LNELNWTLSALDEVFKQREED
395 PERGLMENTAYLDIFRCH-PADTKVIVKVGKIVNISDVKEGDIYTLGIDG-----
204 LMQVFGSAGTLARYYPASPVDNKR---TPN-KIDLYDVRRRPWTYIQGAASPKDMLI
442 -WQ-----RVKVKWKYHYEGKLININGLACTPNHKVPVVTENDRQTRI-----RDSL
260 VSGSVGLTLKLIIRTSVSEMLETISDDDFVNVAFSN-----
492 LSGKVGK---KIITTKL-----FEKIAFEKKPSEBEILKGBLSGILAE
298 -ADVSCF-----OHLVQANW-RNKKVLKDAV-----NNITAGK-
538 LRKDIIEVFSROKKRISHQYVEITIGENEKELLERILYIPDKLGIRSPVKKGD
330 --ITDYKKGFSFAFEQLLANNVSRANCNKIIMLPTDGGEEARAQIIFNKNKOKKVRV
598 LKITTAKKAVVLQIEELLK-NIESLYAPAVLRGF-----PERDATVYNK
388 SV-----GOHNYERGPLOWACENKGY---YYEIPISGAIRINTQEVLDVLGRPMVLP
643 TIVVTOGTNNKWKIDIVAKLDSGLGIPYSRYEYKYIENGKELTKHILEITGRD---
441 AKQVQWTVNYLDALEGLVITGTLVPFNITQCFE-----NKNLKNQLILGVA
696 -----GLILFQTLGVFISSKNEALEKATEVREMRNLKNSFYNLF
492 VSLIEDIKRLTPRTLPCNGYYFAIDPNGVYLLHNPLOPKPKSOEPTVTLDFDLAELI
740 VSSYYKGEVYDITLGNPYIFA-----NG-ILTHNSLSPSIIVTHN-VSPDTLRE-
552 KVEIRNWKIDGESSEKTFRTLKVSQDERYIDKGNRTYTWTPVNGTYSLALVFTY
790 -----GCKYDVAIVG--YKCFCKQFEG--
612 IKAKLEETITTOARSKGKMKDSTLKPDPFESGY-----TFTAPRDYCNDLI
812 IPSILGELITMRQEIKKOKK--ATIDPIEKMDLYRQRAVKLANSLTPNFW---LI
663 NRTPELLNFBEIDRKTTPNPNCSADLINRVLDDAGFTNELVQNVQSKQNKIKGVK
867 NGEVFKVKGIFIDRYMEEQOKKVRTVDNTEVLEVDNIFAFSLNKSCKSEIKKVKY
723 VTDGGITRVYKPEAGE 738
925 -----IRHKYKGEAVE 935

RESULT 10
ATX1_PLAFA
ID_ATX1_PLAFA STANDARD; PRF; 1956 AA.
AC Q04956;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable cation-transporting ATPase 1 (EC 3.6.3.-).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=79/96;
RX MEDLINE=93132070; PubMed=8421054;
RA Krishna S., Cowan G., Meade J.C., Wells R.A., Stringer J.R.,
RA Robson K.J.;
RT *A family of cation ATPase-like molecules from Plasmodium
RL falciparum.";
RL J. Cell Biol. 120:385-398 (1993).
CC -|- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

```

Belongs to the cation transport ATPases family (P-type subfamily V.

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CAA6646.1: -
 01757: ATPase_E1-E2.
 01494: ATPase_P-type; 7.
 54: ATPase_E1 E2; 1.
 55: Membrane; Phosphorylation; Magnesium; ATP-binding.
 1 35 CYTOPLASMIC (POTENTIAL).
 2 58 POTENTIAL.
 3 61 EXTRACELLULAR (POTENTIAL).
 2 80 POTENTIAL.
 1 407 CYTOPLASMIC (POTENTIAL).
 3 427 POTENTIAL.
 3 440 EXTRACELLULAR (POTENTIAL).
 1 462 POTENTIAL.
 3 1818 CYTOPLASMIC (POTENTIAL).
 9 1837 POTENTIAL.
 3 1845 EXTRACELLULAR (POTENTIAL).
 6 1863 POTENTIAL.
 4 1881 CYTOPLASMIC (POTENTIAL).
 2 1905 POTENTIAL.
 6 1928 EXTRACELLULAR (POTENTIAL).
 9 1952 POTENTIAL.
 3 1956 CYTOPLASMIC (POTENTIAL).
 6 496 PHOSPHORYLATION (BY SIMILARITY).
 0 1760 MAGNESIUM (BY SIMILARITY).
 4 1764 MAGNESIUM (BY SIMILARITY).
 6 251 POLY-ASN.
 2 256 POLY-LYS.
 7 941 POLY-ASN.
 4 1347 POLY-LYS.
 3 1372 POLY-ASN.
 0 1684 POLY-ASN.
 6 AA; 230285 MW; AE708AAE9900335 CRC64;

2.8%; Score 159; DB 1; Length 1956;
 rity 17.1%; Pred. No. 0.23;
 nservative 144; Mismatches 359; Indels 366; Gaps 45;

KYQDLTYVEPNARQLVEIARDIEKLSNR-----SKALVSLALEAEK 106
 RYNTSYISS-----ELVPGDIYEIKNNMTIPCDTILSGVTMSHMLTGES 152
 QWRDFASNEVYVYNAKDDLPKND-----SEPGSQRIKPVFIEDANFGQIS 160
 KERLPFGNALINKNNKYSNDERKDLRYNNHAS INMKRNLIEBTICKOR 211
 VHIPTDIYEGSTIVLNELW-TSALDEYFKQKREEDPSLLMQVFGSATGLARYP 219
 TH-----DLCSMNKLCYINNTYDDVHMKNKMD-----244
 TNSRTPNKIDLYDVERRPWYIQA-ASPKDMLILVDVSGSVGLTLKLTIVSVE 278
 INNNKCKKKNNLN-----FVKGTYINNDLLY-----275
 SDDFPNVNASFNASNAQDVSCFOHLYQAVNRNKKVLKDAVNNITAKGTYDKKGS 338
 ---DDKIGVNIPE---DDVNNMKH--KFNQBNINYNKDTNNL-----EYNNKSR 317
 YLNNVSRANCKIIMLTFDGGEERAQEIFNKYNKDKKVRFRFVGQHNVERGP 398
 ILKKEVATSQNKIIV-----SNEDINKY-----346

399 IQWACENKGYEYIPSGAIRINTQBYLDVGRPMVLG-----DKA
 347 ---MLYGGTVLSYLNKIKYNNKEENILGL-VIKTGPITTKGKIVNNILYHK
 445 QMTNVDLDALEGLVITGLTPVFNITQGFENKTNLKNQILG-----
 402 NLINDSYKFLII-LIIVALPSVFIILYITLNNNEYTHIIKCLDITDAIPALPT
 488 MGVDVSLIEDIKRLTPRFTLCPNGYVFA-----IDPNGYVLLHPNLQ-----PKNP
 461 VGIISALRSKKKFSISCLCPHKINIAGQINTWVFDKGT-TLNNLOFQIGIITONK
 536 BPVTLDFDAELNDIKVIRKRMIDGESGKTRTLVKQODERYIDKGNRTYWTTP
 520 NMLS-DFTHIK-----EMNTESIHSKDDNMHNKN-----
 596 TDYSLALVLPYSFYIYKAKLEETITQARSKGGKMKD-----SETLKPNPFE
 550 -----SIIEYYIKONKKNLHTSSK-KKSTIKERSNLFVQTIKSCLLKADHYIK
 646 YFTIAPRDYCNLDKISDNN-TEFLIN-----FNEF--IDRKTNNPNSCNADLINRV
 600 KEYNTNNTYCNLDHINDSTCSSYLLNSETKDAYCEYNNIDH-----LCD--INKK
 697 AGFTNELVONTYMSKQKNIKYKARFVVDGGITRVYPKEAGENWOENPETYEDSFYK
 651 INSKNELMGYSKKNELMGKTIKNELM-----GKYSK
 757 DNDNVFTAPYFNKSGPGAYESGIMVSKAVEIYIOGKLLKPAVVG-----IKIDVK
 685 -----MGYSKKNELMGYSKKNELMGYSKKNELMGYSKKNELMGKTIKNQVGVDTK
 811 ENFTKTSIRD-PCAGPVCDCKRNSDVMDCV-----ILDDGFLMANHDDYTNOIGRF
 738 MNCNDYNDYPCD---YNCNCCNDTYHLEVHNKONSFNIPPEKNKSYNNISEE
 863 -----FGEIDPSLMRHLVMSIVAF-----NKS
 795 NYPLLEALACCHTILSKVNNKIMGVLEILMFNTNCDMLNNNSFIIEKCKGNCSS
 890 SVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAASILQOELLSTLTPRLLEAI
 855 KI---DGDKNIGANDERCHLNN-----NLVSYNLIKRF-----
 950 DDDFTASLSKQSCITEQIQYFPDNDSSK 977
 885 ---EFQSRLOQMSVIVKST-YGNNDNN 909
 RESULT 11
 YPFBK_ECOLI
 ID_YPFBK_ECOLI STANDARD; PRT; 575 AA.
 AC P76481;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yfbk.
 GN YPFBK OR B2270
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KL2 / MG1655;
 RX MEDLINS=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474 (1997).
 CC -!- SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLL0103.

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 8: ail to license@sib-sib.ch).
 9: 1; AAC75330.1; --
 10: 364998.
 11: 395; yfbk.
 12: 102035; VWF_A.
 13: 1; vwa; 1.
 14: 7; VWA; 1.
 15: 234; VWF; 1.
 16: protein; Complete proteome.
 17: 16 394 VWF.
 18: 5 AA; 63634 MW; 7BB6A1A77A2BE111 CRC64;
 19: 2.8%; Score 157.5; DB 1; Length 575;
 20: arity 21.6%; Pred. No. 0.047; Indels 105; Gaps 25;
 21: conservative 93; Mismatches 206; Indels 105; Gaps 25;
 22: ARQLVEIAARDIEKLSNRKALVSLALEAEKQAAHQWREDFASNEVYVYNAKDD 130
 23: KESQQQPSPTTEQVLAAQAAIK--EAEQSA--AKALAQCEVQVQYSDKQA 75
 24: KND-----SFGSQRIPKPVIEDANFGROI SYQHA--VHIPTDI 172
 25: LQEAPTFAAAKAKATHIANEGTAYQOF---DDNPKVQAQNPATFSLDVTG 132
 26: IIVLINE-----LNWTSALDEVFKKREEDPSLLMQVGSATGLARY 218
 27: RRFLNQGLPPPDVAVRVEIVNYPSPDWI--KQKQIPASKPIPPFAWYELA--- 187
 28: WVDSRTFNKIDLDVRRRWYIQGAASPKDMLILVDVSGS-VSLGLTLKIRTSVS 277
 29: ELREQDNIAIVTYAGDSRIA-----LPSISGSHKAEINAAIDSLDAGSTGGAGL 296
 30: EQLLNYSVRANCKNIIMLPDGTG-----GEAAQELFNKYNKKVVRFRVSQ 391
 31: QQATK-GPIKGGIIR-ILLATDGFNVGIDDPKSIEMVKQSGVLTSTFGVGN 354
 32: RGPIQWACENKGYEIPSPGAIIRINTQYLDVLGRPMVL--AGDKAKQVQ---- 445
 33: EAMVRIADVGNVSYIDTSL-----EAQKVLNEMRQMLITVAKDKAQIEFNPA 410
 34: YLDALEGLVITGTLPVNTIGPENKTNLKNQLILVMGYD-VSLEDI---KELT 501
 35: Y---RQIG-----YE-----KRQLRVEHFNNDVNDAGDIGAKGHIT 447
 36: LCPNGYYFAIDPBGVYLLHPLNLPKNPKSQE 536
 37: LTLNGKASIDKLYA--PDNKLAKSDTKYE 480
 38: STANDARD; PRT; 946 AA.
 39: 39; Q15484;
 40: (Rel. 17, Created)
 41: (Rel. 17, Last sequence update)
 42: (Rel. 42, Last annotation update)
 43: (Rel. 42, Last annotation update)
 44: (Rel. 42, Last annotation update)
 45: (Rel. 42, Last annotation update)
 46: (Rel. 42, Last annotation update)
 47: (Rel. 42, Last annotation update)
 48: (Rel. 42, Last annotation update)
 49: (Rel. 42, Last annotation update)
 50: (Rel. 42, Last annotation update)

GN ITIH2 OR IGHEP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=88152237; PubMed=2450046;
 RA Gebhard W., Schreitmuller T., Hochstrasser K., Wachter E.;
 RT "Complementary DNA and derived amino acid sequence of the precurs-
 RT of one of the three protein components of the inter-alpha-trypsin
 RT inhibitor complex";
 RL FEBS Lett. 229:63-67(1988).
 RN [2]
 RP SEQUENCE OF 384-865 FROM N.A.
 RX MEDLINE=88068576; PubMed=2446322;
 RA Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
 RA Benarous R., Okubo I., Kurachi S., Kurachi K., Martin J.P.;
 RT "Isolation and characterization of cDNAs encoding the heavy chain
 RT human inter-alpha-trypsin inhibitor (I alpha II): unambiguous
 RT evidence for multipolypeptide chain structure of I alpha II.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8272-8276(1987).
 RN [3]
 RP SEQUENCE OF 384-766 FROM N.A.
 RX MEDLINE=89076497; PubMed=2462430;
 RA Salier J.-P., Diarra-Mehrpour M., Sesboue R., Bourguignon J.,
 RA Martin J.P.;
 RT "Human inter-alpha-trypsin inhibitor. Isolation and characterizat
 RT of heavy (H) chain cDNA clones coding for a 383 amino-acid sequen
 RT of the H chain.";
 RL Biol. Chem. Hoppe-Seyler 369:15-18(1988).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RA MEDLINE=88024442; PubMed=3663330;
 RA Schreitmuller T., Hochstrasser K., Resinger P.W.M., Wachter E.,
 RA Gebhard W.;
 RT "cDNA cloning of human inter-alpha-trypsin inhibitor discloses th
 RT different proteins.";
 RL Biol. Chem. Hoppe-Seyler 368:963-970(1987).
 RN [5]
 RP SEQUENCE OF 55-74; 116-127; 224-246; 295-307 AND 365-385.
 RX MEDLINE=89380192; PubMed=2476436;
 RA Enghild J.J., Thøgersen I.B., Pizzo S.V., Salvesen G.;
 RT "Analysis of inter-alpha-trypsin inhibitor and a novel trypsin
 RT inhibitor, pre-alpha-trypsin inhibitor, from human plasma.
 RT polypeptide chain stoichiometry and assembly by glycan.";
 RL J. Biol. Chem. 264:15975-15981(1989).
 RN [6]
 RP SEQUENCE OF 55-64.
 RX TISSUE=Plasma;
 RA MEDLINE=9303735; PubMed=1384548;
 RA Malki N., Balduvick M., Maes P., Capon C., Mizon C., Han K.K.,
 RA Tartar A., Fournet B., Mizon J.;
 RT "The heavy chains of human plasma inter-alpha-trypsin inhibitor:
 RT isolation, their identification by electrophoresis and partial
 RT sequencing. Differential reactivity with concanavalin A.";
 RL Biol. Chem. Hoppe-Seyler 373:1009-1018(1992).
 RN [7]
 RP SEQUENCE OF 55-64 AND 681-702. CROSS-LINK STRUCTURE, AND
 RX CARBOHYDRATE-LINKAGE SITES THR-691.
 RA MEDLINE=93232026; PubMed=7682553;
 RA Enghild J.J., Salvesen G., Thøgersen I.B., Valnickova Z.,
 RA Pizzo S.V., Hefta S.A.;
 RT "Presence of the protein-glycosaminoglycan-protein covalent cross
 RT in the inter-alpha-inhibitor-related proteinase inhibitor heavy c
 RT 2/pikunin";
 RL J. Biol. Chem. 268:8711-8716(1993).
 RN [8]
 RP SEQUENCE OF 67-101, AND HYALURONAN BINDING.
 RX TISSUE=Serum;
 RA MEDLINE=94075371; PubMed=7504674;
 RA Huang L., Yoneda M., Kimata K.;

d hyaluronan-associated protein (SHAP) is the heavy
ter alpha-trypsin inhibitor.";
268:26725-26730(1993).

-702, AND COVALENT LINKAGE WITH CHONDROITIN SULFATE.

17; PubMed=7513643;
on C., Baldyck M., Sautiere P., Kouach M.,
Gurnet B., Mizon J.;
alpha covalently cross-links the three polypeptide
-alpha-trypsin inhibitor.";
1. 221:881-888(1994).

IMAGE SITES, AND MASS SPECTROMETRY.

16; PubMed=9677337;
on C., Baldyck M., Ricart G., Sautiere P., Mizon J.;
pattern of human inter-alpha-inhibitor heavy chains.";
1:749-756(1998).

IMAGE SITES, AND DISULFIDE BONDS.

10; PubMed=9425062;
albek-Nielsen H., Thøgersen I.B., Roepstorff P.,
mal modifications of human inter-alpha-inhibitor:

of glycans and disulfide bridges in heavy chains 1 and
of glycans and disulfide bridges in heavy chains 1 and
1:408-416(1998).

WAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
YTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
ON, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
TO CELLS UNDERGOING BIOLOGICAL PROCESSES.
-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
3, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
VD PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
BRIDGE TO THEIR C-TERMINAL ASPARTATE.
ROMETRY: MW=76509; METHOD=MALDI; RANGE=55-702.
: BELONGS TO THE ITIH FAMILY.
: Contains 1 VWFA domain.

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CAA30160.1; ALT_SEQ.

AA60558.1; -

AA59195.1; -

VH2.

P19823; -

67; ITIH2.

; F: plasma glycoprotein; TAS.

06587; VIT.

02035; VWFA_A.

VWA; 1.

; VIT; 1.

; VWA; 1.

34; VWFA; 1.

e inhibitor; Repeat; Signal; Multigene family;

utamic acid; Glycoprotein.

1 18

9 54

5 702

INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN

H2.

13 946

18 468

VWFA.

FT	DISULFID	261	264		
FT	DISULFID	650	651		
FT	CARBOHYD	118	118		
FT	CARBOHYD	666	666		
FT	CARBOHYD	671	671		
FT	CARBOHYD	673	673		
FT	CARBOHYD	675	675		
FT	CARBOHYD	691	691		
FT	CARBOHYD	282	282		
FT	CARBOHYD	283	283		
FT	CARBOHYD	702	702		
FT	CARBOHYD	374	374		
FT	CARBOHYD	674	674		
FT	CARBOHYD	705	705		
FT	CARBOHYD	729	729		
FT	CARBOHYD	731	731		
SQ	SEQUENCE	946	946		

Query Match 2.8%; Score 154.5; DB 1; Length 946;
Best Local Similarity 19.9%; Pred. No. 0.15;
Matches 133; Conservative 106; Mismatches 259; Indels 171; Ga

QY	33	IKSVNDKQEDLVTLAKTAGVGNOLVDIYKQDLTYTVEPNARQLVEIAARDIEKL			
Db	26	LSEFVD--YEDLVEL---APGQFLVAENRRYQSLPGESEEMEEVDQVTLYSYKV			
QY	93	RKALVSLALEAKKQAAHWRRE-----DFASN-----			
Db	81	ITSRMATTMIQSKVNNSPQNVVFDVQIPKGAFISNFSMTVDGKTPRSSIKKKTIV			
QY	123	VYNNAK-----DDLDPKNDSE-----PGSQRKIPFIEDANFGRIQISYOH-			
Db	141	LYAQARAKGTAGLVRRSSALDMENFRTEVNVLPKGAQVQFELHYQEVKWKLGSYEHR			
QY	164	---AAVHIPDIDYEGSTIVLNLNWTSLD-----EVFKKNREE-----DPSLLM			
Db	201	QGRLEKLEHVDVWVIEPQGLRFLHVPDTFGHFGDGVVISKQQKAHVSPKPTVAC			
QY	209	GSATGLARYYPASPVDNSTRPNKIDLYDVRRRP-----WYIOGAAS-----			
Db	259	-----RICHSCR--ETAVDGLVLDYVKREKAGELEVFGYVHFVFPADNLDE			
QY	253	DMLILVDVSGSVGLTKLIRTSVSEMLETSDDDFVNVAASNADVSCFQHLVC			
Db	310	NILFVIDVSGSMGWYKMKQTVEAMKTIILDLRAEDHFSVIDFNQINR--TWNRDLIS			
QY	313	RNKKVLKDAVNNITAKGITDYKKGKGF--SFAPEQLNLYNVSANCKIIMLFTDG--			
Db	368	TOVADAKRYIEKIQPSGGTNINEALLRAIFILNEANNLGLDPSVSLILVSDGDF			
QY	366	BERAQEIFNKYNKDKKVRVFRFSVQO-----HNYERGPQIWM-----AC			
Db	428	ELKLSKIQKNVKENIQDNISLFLGWFVDYDFLKLRLSNENHGAQRIYGNQDTSE			
QY	408	GYYYEI--PSIGAIRIN--TQBYLDVL-----GRPMVLGAG--DKAKQVQWTVN			
Db	488	KFYNOVSTPLLRNVQFPHTSVTDVQNNFNHYFGSGSEIVVAGKFPDAK-----			
QY	453	ALELGLVITGTLPVFNITGQFENKTNLKNQLITLVGMGVDSVLEDI-----KRLTPRFT			
Db	540	QIE--SVITA-----TSANTQLVLETLAQWDDLODPLSKDKHADPFT			
QY	509	NGYYFAIDPNGYVLLHPLMQPNPKSQBPVTLDFLDLAELNDIKVEIRNKMIDGSGC			
Db	583	LWAYLTIN---QLLAERSLAP--TAAAKRRTSRILQMSLDHHIVTPLTSLVIENBAC			
QY	569	FRTLKVSQD 577			

PPQD 647

STANDARD; PRT; 1290 AA.

el. 16, Created)

el. 16, Last sequence update)

el. 41, Last annotation update)

otoxin type C1 precursor (EC 3.4.24.69) (BoNT/C1)

Cl).

tulinum.

idutes; Clostridia; Clostridiales; Clostridiaceae;

1;

N.A.

{87; PubMed=2204031;

und M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,

off M.R.;

quence of Clostridium botulinum C1 neurotoxin.";

Res. 18:4924-4924(1990).

N.A.

Stockholm / C-ST;

{98; PubMed=2222445;

jii N., Tezuka K., Murakami T., Indoh T.,

akeshi K., Syuto B., Oguma K.;

nucleotide sequence of the gene coding for botulinum

in the C-ST phage genome.";

ys. Res. Commun. 171:1304-1311(1990).

-25.

Stockholm / C-ST;

{72; PubMed=2450068;

kosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,

: of a monoclonal antibody recognizing an antigenic site

stridium botulinum type B, C1, D, and E toxins and

.";

. 56:898-902(1988).

N OF SUBSTRATE.

366; PubMed=7901002;

man E.R., Yanaaki S., Binz T., Niemann H., Jahn R.;

rotoxin C1 blocks neurotransmitter release by means of

1/syntaxin.";

21-4828(1993).

BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER

IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED

BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD

CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT

NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC

DASE THAT CLEAVES SYNTAXIN.

ACTIVITY: Limited hydrolysis of proteins of the

ytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No

action on small molecule substrates.

Binds 1 zinc ion per subunit (By similarity).

DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A

IN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY,

N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL

AND TOXIN BINDING, RESPECTIVELY.

AR LOCATION: Secreted.

BOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF

NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

BOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C

CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE

HAGE.

Y: BELONGS TO PEPTIDASE FAMILY M27.

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EMBL; X66433; CAA47060.1; -
 EMBL; X72793; CAA51313.1; -
 EMBL; X53751; CAA37780.1; -
 EMBL; D90210; BAA14235.1; -
 EMBL; X62389; CAA44263.1; -
 HSSP; F10845; 3BTA.
 MEROPS; M27.002; -
 InterPro; IPR000395; Bontoxilysin.
 InterPro; IPR006025; Zn_MTPeptidase.
 Pfam; PF01742; Peptidase M27; 1.
 PRINTS; PR00760; BONTOXILYSIN.
 ProDom; PD001963; Bontoxilysin; 1.
 PROSITE; PS00142; ZINC_PROTEASE; 1.
 Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 INIT MET 0
 CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN
 CHAIN 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN
 METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
 ACT_SITE 229 229 BY SIMILARITY.
 METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
 DISULFID 436 452 INTERCHAIN (PROBABLE).
 CONFLICT 84 84 P -> T (IN REF. 2).
 SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129B8 CRC64;

Query Match 2.7%; Score 152; DB 1; Length 1290;
 Best Local Similarity 20.3%; Pred. No. 0.33;
 Matches 205; Conservative 125; Mismatches 346; Indels 334; G;

QY 106 KVGAAHQRDFASNEVYNAKDDLDPKNDSEPGSQRIK---PVFIEDANFGR-
 DB 138 KTGQNNVKTGSIINPSVIITG-----PRENIIDPETSTFKLTNNTFAAQGEFGAL
 QY 158 -----QISVQHAHVHPTDIYEGS-----TIVLEINWTSALDEVFK---
 DB 193 ISPRFMLTYSNAT---NDVGEGRFSKSEFCMDPILILAHLELN---HAMHLYGIAT
 QY 199 EDFSLLWQVPGSATGLARYYP-----ASPMVDNSRTPNKIDLYDVRPPWYIQGAA
 DB 247 TISVSTSNIFYSQNVKLEYAEIYAFGGPTID--LIPKSARKYFEKALDYYSIA
 QY 254 MLILVDVSG---SVSGLTLMILR-----TSVSEMLETSLDDDFVNVASFNSNAQD
 DB 305 SITANPSSFNKYGKVKQKLRKRVVSSGSEV--TVNRKFVEL--YNELTQI
 QY 305 QHLVQANVRKKV-LKDAVNNITAK-----GITYKKGFSAFQOL-----LNYNVS
 DB 361 NYAKIYNVQRKIYLSNVYTPVTANILDDNVYDIQNGFNIPKGNLNLVLFMGQNLNR
 QY 352 --ANCKNIIMFT-----DGGEERAQEIFNK-----YMKO-----KKV
 DB 421 RKNPENMLYTFKFKCHADG-----RSYKNTLDCRELLVKNTDLPFGIDISDV
 QY 387 FSVGQHNYERGIQWMACENKGYEYIPSGAIRI--NTQY--LDVL-----
 DB 476 FLRCKDINEETVI-----YYPDNVSDVQVILSKNTSEHGQDLILYPSIDSES
 QY 431 GRPMVLADGKAKQVQWNTN--VYLDALGLVITGTLVPFNTIGTFENKTN-----
 DB 527 GENQVFDNRNTQNDYLNYSYILESQKL-----SDNVEDFTFTRSIEBALONSAKVY
 QY 479 -LKNQLILGWG-----VDVSLIEDIKRLTPFTLCPCNGYIFAIDPNGVYLLHPN
 DB 583 TLANKVAGVGGLFLMWANDVVEFTTNIRKOTLDKISDVSAIIP-----YIGPA
 QY 531 NPKSQEPVTLDF-----LDAELENDI-----KVEIRNKWIDGESGKT
 DB 639 NSVERGNFTEAFATVGTVILLAPFTIPALGAFVIYSKVQERNEII-----KT

501

100-106800-1700

RA Garcia-Gil A., Lampreave F., Pineiro A.;

RA Gonzalez-Ramon N., Alava M.A., Sarasa J.A., E

RA Gonzalez-Ramon N., Alava M.A., Sarasa J.A., E

te phase serum protein in pigs is homologous to human
ein sensitive PK-120.",
:227-230(1995).

MAY BE INVOLVED IN ACUTE PHASE REACTIONS.

CIFICITY: Liver-specific.

LEVELS INCREASE SIGNIFICANTLY AFTER CARDIOGENIC

RS TO BE BOTH N- AND O-GLYCOSYLATED (BY SIMILARITY).

ED BY PLASMA KALLIKREIN TO YIELD 55- AND 25-KDA

: BELONGS TO THE ITIH FAMILY.

: Contains 1 VWFA domain.

EF.2 SEQUENCE IS INCORRECT DUE TO FRAMESHIFTS AND OTHER

ERRORS.

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il to license@isb-sib.ch).

AAD00024.1; -;

AAB46821.1; -;

-; NOT_ANNOTATED_CDS.

IC4625.

IO6587; VIT.

IO2035; VWF_A.

vwa; 1.

; VIT; 1.

; VWA; 1.

:34; VWFA; 1.

se inhibitor; Repeat; Signal; Multigene family;

1 27 INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
18 921 H4.

70 428 VWFA.

80 N-LINKED (GLCNAC. .) (POTENTIAL).

80 N-LINKED (GLCNAC. .) (POTENTIAL).

205 N-LINKED (GLCNAC. .) (POTENTIAL).

242 N-LINKED (GLCNAC. .) (POTENTIAL).

513 N-LINKED (GLCNAC. .) (POTENTIAL).

577 N-LINKED (GLCNAC. .) (POTENTIAL).

50 HT -> SK (IN REF. 3).

703 D -> H (IN REF. 1; AA SEQUENCE).

1 AA; 102146 MW; E2BF9525DE8D07C CRC64;

2.7%; Score 150.5; DB 1; Length 921;

arity 19.9%; Pred.No.0.25;

nservative 100; Mismatches 264; Indels 265; Gaps 36;

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-----LVTLAKTASGNQLVDIYEK--YQDIYT-VEPNNAQLVEIAARDIEKL--- 89

KKAFITNFMIDIGVTPGNIKAKAAQEQYSAVARGESAGLVRAUGRTKTEQFOVA 129

SKALVSLALAEKQVAAHQWREDFASNEVYVNAKDDLDPEKNDSEPGSQRIKVPF 149

PAAKVTTELVEELLARH-----LGVYELLKKIQPQ-----QLVKHLQ 171

NFGHQ-LSY-QHAAVHIPTDIYEGSTIVLNE-----LAWTSALDEVPKKNREEDPSL 203

IFEPQIGSFLETSTFTMELAEALTISQNKKAHIFKPTLSQO-QRSPEQGETV 230

-----WQVFGSATG-----LARYYPASFPVDNSRTPNKKIDLYDVRBPWYIQG 247

FIVRYDVNRVTGSGIQIENGYFVHYFAPEVM----- 266

KDMLILVDVSGSVSLTLKILRTSVSEMLETLSDDDFVNVASFNSAQDVSCFQHL 307

Db 267 SAIPKNVIFVIDTSGMEGRKIQQOTREALIILKLDGSRDQPNLVSFSGEAPR-----
QY 308 VOANVRNKKVLKDAVNNTAKGITYDKKGFSAFPAEQLLNNVNSRANCKNI-----
Db 323 VAASAENVEEAKSYAAETHAQGTNINDAMLMAVQLL-----ERANRELLPARSVT
QY 360 LETDG-----GEERAQEIFNKYNDKKVRV-----PRFSVGQHNVERGPIC
Db 378 LITDGDPTVGETNPSKI-----QKNVREADQGHSLFCLGFGFDVPAFLER-----
QY 404 CENKG-----YY-----YEIPSIGAIRINTQEYLDVL-----
Db 427 LENGGLARRIYEDSDSALQLEDIFYQEVANPLRLVAFEPFS-NAVEEVTQDNFRLFE
QY 433 PMVLGAG---DKAQVQWNTNVLDALELGLVITGTLPVFNITQGFENKTNLKNQILIC
Db 486 ELVWAGKLRDQSPDV-----LSAKVRGQLHMENVTFVMSRVAEQAEFLF
QY 487 -----VNGVDVSLEDI--KELTRFTLCPNGYVFAIDPNGVYLLH
Db 535 IFHSPMERLWAYLTITQQLLAQTVSASDAEKKALEARALSLSLNYSFVTPLTSMVITH
QY 528 QPKNPKSQBPVTLDFLDAELNDIKVEIRNKMDIGESGEKTFRTLVKSQDERYIDK
Db 595 QSQSQAERP-----VNGNRQGNTHSGHSF-----QFHSVK
QY 588 YTWTPVNGTDYSLALVLPYTPYFYKAKLEETITQARSKKGKMOSETLKPDPNFEK
Db 631 SRLTGGSSVD-----PVFS-----HRRGNKGOAQ-----GFEKQ
QY 648 FIAPR 652
Db 662 -LPPR 665

Search completed: February 20, 2004, 16:56:17

Job time : 16.5951 secs

6:26:18 2004

us-10-090-827-14.rapb

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(without alignments)
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;404 seqs, 257433775 residues
; satisfying chosen parameters: 1045404

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the number of results predicted by chance to have a
than or equal to the score of the result being printed,
by analysis of the total score distribution.

SUMMARIES

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0	1036	14	US-10-090-827-14	Sequence 14, Appl
0	1063	14	US-10-090-827-15	Sequence 15, Appl
0	1091	9	US-09-875-423-4	Sequence 4, Appl
0	1091	14	US-10-162-012-17	Sequence 17, Appl
0	1091	14	US-10-090-827-16	Sequence 16, Appl
0	1091	15	US-10-162-012-17	Sequence 17, Appl
3	1086	15	US-10-375-253-49	Sequence 49, Appl
0	1084	15	US-10-375-253-53	Sequence 53, Appl
8	1036	14	US-10-090-827-7	Sequence 7, Appl
8	1063	14	US-10-090-827-8	Sequence 8, Appl
8	1069	14	US-10-090-827-9	Sequence 9, Appl
8	1091	14	US-10-090-827-5	Sequence 5, Appl
6	1103	15	US-10-375-253-47	Sequence 47, Appl
2	1079	15	US-10-375-253-51	Sequence 51, Appl
2	1018	14	US-10-090-827-13	Sequence 13, Appl

16	5316	97.7	1091	15	US-10-375-253-20	Sequence 2
17	5288	97.2	1018	14	US-10-090-827-6	Sequence 6
18	2907.5	53.4	1145	14	US-10-116-949-2	Sequence 2
19	2907.5	53.4	1145	14	US-10-116-949-4	Sequence 4
20	2886.5	53.0	1076	14	US-10-116-949-6	Sequence 6
21	1085	19.9	1091	9	US-09-875-423-5	Sequence 5,
22	1085	19.9	1091	14	US-10-162-012-18	Sequence 1
23	1085	19.9	1091	15	US-10-162-012-18	Sequence 1
24	1084	19.9	1091	9	US-09-875-423-2	Sequence 2,
25	1084	19.9	1091	14	US-10-162-012-15	Sequence 1
26	1084	19.9	1091	15	US-10-162-012-15	Sequence 1
27	1063	19.5	1114	12	US-10-257-174-35	Sequence 3
28	1051	19.3	1075	12	US-10-257-174-34	Sequence 3
29	1051	19.3	1090	10	US-09-833-222A-10	Sequence 1
30	1051	19.3	1090	14	US-10-119-624-10	Sequence 1
31	365.5	6.7	223	13	US-10-005-168-2	Sequence 2
32	353.5	6.5	1274	16	US-10-380-727-8	Sequence 8
33	343.5	6.3	1223	10	US-09-964-256A-2	Sequence 2
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35	286	5.3	75	15	US-10-364-049-3575	Sequence 4
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38	190	3.5	35	9	US-09-864-761-38318	Sequence 38
39	187	3.4	74	14	US-10-029-386-28507	Sequence 36
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41	182	3.3	885	9	US-09-828-423-5	Sequence 5
42	171.5	3.2	888	12	US-10-282-122A-57155	Sequence 5
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44	167	3.1	796	15	US-10-369-493-18214	Sequence 1
45	161	3.0	1829	15	US-10-435-766-13	Sequence 1

ALIGNMENTS

RESULT 1
US-10-090-827-14
; Sequence 14, Application US/10090827
; Publication No: US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; FILE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090.827
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-14

Query Match	100.0%	Score 5443;	DB 14;	Length 1036;
Best Local Similarity	100.0%;	Pred. No. 0;		
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Db	121	EWYVYNKDDLDPEKNSEPGSQRIKPVFIEDANFGROIYSQHAHVHPTDIYEGST		
Qy	181	NELNWTSDALDFVFKKREEDPSLLMQFGSATGLARYYPASFPVNDNSRTPNKIDLYD		

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BERAQEIPFNKNDKVRVFRFSVQGHNYERGPQWMACENKGYIYIIPSGAIR 420
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Location US/10090827
IS20030073132A1
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ar-Lambert
[ON: Method for the screening of alpha 2 delta-1 subunit
[ON: binding ligands
179
TION NUMBER: US/10/090,827
DATE: 2002-03-06
ON NUMBER: US/09/397,549
TE: 1999-09-16

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; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-15

Query Match      100.0%; Score 5443; DB 14; Length 1063;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gc

QY 1 MAAGCLLALTTLFQSLIIGPSSEPPFPSSAVTIKSWVDKMQEDLVTLAKTASGVNQI
DB 1 MAAGCLLALTTLFQSLIIGPSSEPPFPSSAVTIKSWVDKMQEDLVTLAKTASGVNQI
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QY 121 EVVYTNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGROI SYOHAAVHIPTDIYEGST
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QY 241 RPYWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSSDDDFVNVAASFNS
DB 241 RPYWYIQAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSSDDDFVNVAASFNS
QY 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNLYNSRANCNKI
DB 301 VSCFOHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFQOLLNLYNSRANCNKI
QY 361 FTDGGEERAQEIFNKYKNDKVRVFRFSVQGHNYERGPQWMACENKGYIYIIPSGI
DB 361 FTDGGEERAQEIFNKYKNDKVRVFRFSVQGHNYERGPQWMACENKGYIYIIPSGI
QY 421 INTQEYLDVLRPMVLGAKAKQVQWNTNLYLDALGLVITGTLPVFNITGQFENKI
DB 421 INTQEYLDVLRPMVLGAKAKQVQWNTNLYLDALGLVITGTLPVFNITGQFENKI
QY 481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPLNLPKNPKSQBI
DB 481 NQLILGVMGVDSLEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPLNLPKNPKSQBI
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRTYTWTPVNGTI
DB 541 DFLDAELENDIKVEIRNKMIDGESGKTPRTLKVSQDERYIDKGNRTYTWTPVNGTI
QY 601 ALVLPYISFYIYKAKLEETITQARSKKGMKQSETLKPDNFESGYTFIAPRDYCNMI
DB 601 ALVLPYISFYIYKAKLEETITQARSKKGMKQSETLKPDNFESGYTFIAPRDYCNMI
QY 661 SDNNTFELNPNFIDRKTNNPNSCNADLINRVLLDAGFTNELVQWYKQKIKGVKAR
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DB 781 MYSKAVEIYIYQGLLKPAPVVGIIKIDVNSWIENTFTKTSIRDPKAGPVCDCRNSDMDVI
QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPGA
DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYOSVCEPGA
QY 901 GAGHRSAYVPSVADILQIGHWATAAAWSILQQFLSLTFPRLLLEAVEMEDDDFTASI
DB 901 GAGHRSAYVPSVADILQIGHWATAAAWSILQQFLSLTFPRLLLEAVEMEDDDFTASI

```

|||||
3AVVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTASLSKQ 960
|||||
JTOYFFDNDSKSGVLDGNCNSRI FHGKLMNTNLI FIMVESKGTCPDCTRLII 1020
|||||
JTOYFFDNDSKSGVLDGNCNSRI FHGKLMNTNLI FIMVESKGTCPDCTRLII 1020
|||||

3DGNPCDMVK 1036
|||||

3DGNPCDMVK 1036
|||||

ation US/09875423

081657A1

3, Rory A.J.

JN: 21784, A NOVEL HUMAN CALCIUM CHANNEL

JN: FAMILY MEMBER AND USES THEREOF

10448-059001

ION NUMBER: US/09/875,423

ATE: 2001-06-05

Y NUMBER: US 60/209,257

3: 2000-06-05

NOS: 6

2 for Windows Version 4.0

sapiens

100.0%; Score 5443; DB 9; Length 1091;

ity 100.0%; Pred. No. 0;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

GLALTTLFQSLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60

GLALTTLFQSLIGPSSSEPPFSAVTIKSWVDKMQEDLVTLAKTAGSVNQLVDI 60

OLYTVENPNARQOLVEIAARDIEKLLSNRKALVSLALEAEKVQAAHQRDEFSAN 120

OLYTVENPNARQOLVEIAARDIEKLLSNRKALVSLALEAEKVQAAHQRDEFSAN 120

YAKDDLPENKNDSEPGSORIKPVFIEDANFCROISYQHAHVHPTDIYEGSTIVL 180

YAKDDLPENKNDSEPGSORIKPVFIEDANFCROISYQHAHVHPTDIYEGSTIVL 180

ISALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNPKIDLYDVR 240

ISALDEVFKKNREDDPSLLMQVFGSATGLARYYPASPWDNSRTPNPKIDLYDVR 240

QGAASPKDMLILDVSGSVSGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300

QGAASPKDMLILDVSGSVSGLTKLIRTSVSEMLETSLDDDFVNVASFNSNAQD 300

HLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQQLNLYNVRANCNKIIML 360

HLVQANVRNKKVLDKADANNITAKGIDYKKGFSFAFQQLNLYNVRANCNKIIML 360

EERAQEIFNKYNKDKKVVFRFVSQGHNYERGPQIWMACENKGYIYIPISGAIR 420

EERAQEIFNKYNKDKKVVFRFVSQGHNYERGPQIWMACENKGYIYIPISGAIR 420

YLDVLRPMVLGAKQKQVQWNTNYLDALELGLVITGTLPVFNITGQFENKTNLK 480

YLDVLRPMVLGAKQKQVQWNTNYLDALELGLVITGTLPVFNITGQFENKTNLK 480

GMVGVDVSLIEDIKLTLRFTLCPNGYYFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540

GMVGVDVSLIEDIKLTLRFTLCPNGYYFAIDPNGYVLLHPNLQPKNPKSQEPVTL 540

QY 541 DFLDAELENDIKVEIRNKMIDGESSEKTFRTLVSQDERYIDKGNRTYTWTVPNGTD
DB 541 DFLDAELENDIKVEIRNKMIDGESSEKTFRTLVSQDERYIDKGNRTYTWTVPNGTD
QY 601 ALVLPYTSFYIYKAKLEBETITQARSKKGKMKDSETLKPDNFEESGYTFIAPRDYCN
DB 601 ALVLPYTSFYIYKAKLEBETITQARSKKGKMKDSETLKPDNFEESGYTFIAPRDYCN
QY 661 SDNTEFLLNENEFIDRKTNNPCSNADLINRVLLDAGFTNELLVQNYWSKQKNIKGV
DB 661 SDNTEFLLNENEFIDRKTNNPCSNADLINRVLLDAGFTNELLVQNYWSKQKNIKGV
QY 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKXSLDNNDNTVFTAPYFNKSGPGAYE
DB 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKXSLDNNDNTVFTAPYFNKSGPGAYE
QY 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVM
DB 781 MYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKRNSDVM
QY 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPDLMLRHLVNIISVYAFNKSVDYQSVCEPGAA
DB 841 LDDGGFLLMANHDDYTNQIGRFFGEIDPDLMLRHLVNIISVYAFNKSVDYQSVCEPGAA
QY 901 GAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTASL
DB 901 GAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLLEAVEMEDDDFTASL
QY 961 SCITEQTOYFFDNDSKSGVLDGNCNSRI FHGKLMNTNLI FIMVESKGTCPDCTR
DB 961 SCITEQTOYFFDNDSKSGVLDGNCNSRI FHGKLMNTNLI FIMVESKGTCPDCTR
QY 1021 QAEQTS DGNPCDMVK 1036
DB 1021 QAEQTS DGNPCDMVK 1036

RESULT 4

US-10-162-012-17
; Sequence 17, Application US/10162012
; Publication No. US20030051660A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY M
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15

ON NUMBER: US 60/226,770
 TE: 2000-08-21
 ON NUMBER: US 09/934,421
 TE: 2001-08-21
 ON NUMBER: PCT/US01/26096
 TE: 2001-08-21
 ON NUMBER: US 60/279,281
 TE: 2001-03-28
 ON NUMBER: US 10/109,029
 TE: 2002-03-28
 ON NUMBER: PCT/US02/09728
 TE: 2002-03-28
 ON NUMBER: US 60/290,288
 TE: 2001-05-11
 ON NUMBER: US (not assigned)
 TE: 2002-05-13
 D NOS: 48
 EQ for Windows Version 4.0

sapiens

100.0%; Score 5443; DB 14; Length 1091;
 arity 100.0%; Pred. No. 0;
 conservative 0; Mismatches 0; Indels 0; Gaps 0;

CLLALTLTQLSLLIGPSSPEPPPSAVTIKSWVDKMOEDLVTLAKTAGVNLVDI 60
 |||||
 CLLALTLTQLSLLIGPSSPEPPPSAVTIKSWVDKMOEDLVTLAKTAGVNLVDI 60
 |||||

QDLVTEPNARQVETAAARDIEKLLSNRSLVSLALEAEKVQAAHOWREDFASN 120
 |||||
 QDLVTEPNARQVETAAARDIEKLLSNRSLVSLALEAEKVQAAHOWREDFASN 120
 |||||

YNKADLDPEKNSEPGSQIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
 |||||
 YNADLDPEKNSEPGSQIKPVFIEDANFGRQISYQHAHVHIPTDIYEGSTIVL 180
 |||||

ATSALDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
 |||||
 ATSALDEVFKNREEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLYDVR 240
 |||||

IQGAASPKMLILVDVSGSGVTLKLIKRTSVSEMLETLSDDDFVNVASFNNAQD 300
 |||||
 IQGAASPKMLILVDVSGSGVTLKLIKRTSVSEMLETLSDDDFVNVASFNNAQD 300
 |||||

JHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSAFEQLLNNVSRANCKIIML 360
 |||||
 JHLVQANVRNKKVLKDAVNNITAKGITDYKKGFSAFEQLLNNVSRANCKIIML 360
 |||||

IERAQEIFNKYNKDKVRVFRFSVQGHNYERGIQWMAKNGYIYEIPSGAIR 420
 |||||
 IERAQEIFNKYNKDKVRVFRFSVQGHNYERGIQWMAKNGYIYEIPSGAIR 420
 |||||

YLDVLGRPMVLADGAKQVQWNTNVLDLLEGLVITGTLPVNIQGFENKTNLK 480
 |||||
 YLDVLGRPMVLADGAKQVQWNTNVLDLLEGLVITGTLPVNIQGFENKTNLK 480
 |||||

JGVMGVDVSLDIKRLTPRTLCNPGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
 |||||
 JGVMGVDVSLDIKRLTPRTLCNPGYFAIDPNGYVLLHPNLQPNKPSQEPVTL 540
 |||||

IELNDIKVIRNMKIDGESGKFTRLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 |||||
 IELNDIKVIRNMKIDGESGKFTRLVKSQDERVIDKGNRTYTWTPVNGTDYSL 600
 |||||

PTYSFYIKAKLETTQAKSKGKMDSETLKPDPFESGYTFIAPROYCNDLKI 660
 |||||
 PTYSFYIKAKLETTQAKSKGKMDSETLKPDPFESGYTFIAPROYCNDLKI 660
 |||||

TEFLNFEFIDRKTNNPSCNADLNRLVDAGFTNELVQVYWSKQKNIKGKAR 720
 |||||

Db 661 SDNTEFLNFEFIDRKTNNPSCNADLNRLVDAGFTNELVQVYWSKQKNIKG
 |||||

QY 721 FVNTDGGITRVYKPEAGENWQENPETYEDSYKESLONDNYVFTAPYFNKSGPGAY
 |||||

Db 721 FVNTDGGITRVYKPEAGENWQENPETYEDSYKESLONDNYVFTAPYFNKSGPGAY
 |||||

QY 781 MVSKAVEIYIQGKLLKPAVVIGIKIDVNSWIENFTKTSIROPCAGPVCDCCKRNSDVW
 |||||

Db 781 MVSKAVEIYIQGKLLKPAVVIGIKIDVNSWIENFTKTSIROPCAGPVCDCCKRNSDVW
 |||||

QY 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGA
 |||||

Db 841 LDDGGFLLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKS YDYQSVCEPGA
 |||||

QY 901 GAGHRSAYVPSVADILQIGWATAAASIIQQOFLLSITFPRLLEAVEMEDDDFTAS
 |||||

Db 901 GAGHRSAYVPSVADILQIGWATAAASIIQQOFLLSITFPRLLEAVEMEDDDFTAS
 |||||

QY 961 SCITEQTQYFFDNDKSKFSGLDCGNCGRIFHGKELMNTNLI FIMVESKGTCPCDT
 |||||

Db 961 SCITEQTQYFFDNDKSKFSGLDCGNCGRIFHGKELMNTNLI FIMVESKGTCPCDT
 |||||

QY 1021 QAEQTSQGNPCDMVK 1036
 |||||

Db 1021 QAEQTSQGNPCDMVK 1036
 |||||

RESULT 5
 US-10-090-827-16
 ; Sequence 16, Application US/10090827
 ; Publication No. US20030073132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warner-Lambert
 ; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
 ; FILE REFERENCES: 179
 ; CURRENT APPLICATION NUMBER: US/10/090,827
 ; CURRENT FILING DATE: 2002-03-06
 ; PRIOR APPLICATION NUMBER: US/09/397,549
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patencin ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 1091
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-090-827-16

Query Match 100.0%; Score 5443; DB 14; Length 1091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1036; Conservative 0; Mismatches 0; Indels 0; G

QY 1 MAAGCCLLALTTLTQLSLLIGPSSPEPPPSAVTIKSWVDKMOEDLVTLAKTAGVNC
 |||||

Db 1 MAAGCCLLALTTLTQLSLLIGPSSPEPPPSAVTIKSWVDKMOEDLVTLAKTAGVNC
 |||||

QY 61 YEKYQDLVTEPNARQVETAAARDIEKLLSNRSLVSLALEAEKVQAAHOWREDI
 |||||

Db 61 YEKYQDLVTEPNARQVETAAARDIEKLLSNRSLVSLALEAEKVQAAHOWREDI
 |||||

QY 121 EVVYNAKDDLDPEKNSEPGSQIKPVFIEDANFGRQISYQHAHVHIPTDIYEGS
 |||||

Db 121 EVVYNAKDDLDPEKNSEPGSQIKPVFIEDANFGRQISYQHAHVHIPTDIYEGS
 |||||

QY 181 NELNWTSAIDVFKKREEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLYI
 |||||

Db 181 NELNWTSAIDVFKKREEDPSLLWQVFGSATGLARYYPASPWVDNSRTNPKIDLYI
 |||||

QY 241 RPYWYIQGAASPKMLILVDVSGSGVTLKLIKRTSVSEMLETLSDDDFVNVASFNNS
 |||||

Db 241 RPYWYIQGAASPKMLILVDVSGSGVTLKLIKRTSVSEMLETLSDDDFVNVASFNNS
 |||||

'DGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 'DGGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
 'JAVEIYIQGLKLPKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
 'JAVEIYIQGLKLPKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVMDCVI 840
 'KQFLMANHDDYTNOIGRFFGBIDPDLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 'KQFLMANHDDYTNOIGRFFGBIDPDLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
 'RSAYVPSVADILQIGWATAAASWILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 'RSAYVPSVADILQIGWATAAASWILQOFLSLTPRLLLEAVEMEDDDFTASLSKQ 960
 'EQTOYFFNDNKSFGVLDCGNCRSRIFHGEKLMNTNLI FIMVESKGTCPCTRLLI 1020
 'EQTOYFFNDNKSFGVLDCGNCRSRIFHGEKLMNTNLI FIMVESKGTCPCTRLLI 1020
 'TSDGPNPCDMVK 1036
 'TSDGPNPCDMVK 1036

lication US/10375253

US20040018510A1

ION:

SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ION: METHODS

SD9813DA

TION NUMBER: US/10/375,253

DATE: 2003-02-27

ON NUMBER: 08/450,273

TE: 1995-05-25

ON NUMBER: 08/404,354

TE: 1995-02-15

ON NUMBER: 07/914,231

TE: 1992-07-13

ON NUMBER: 08/314,083

TE: 1994-09-28

ON NUMBER: 07/914,231

TE: 1992-07-13

ON NUMBER: 07/603,751

TE: 1990-11-09

ON NUMBER: 08/290,012

TE: 1994-08-11

ON NUMBER: 08/149,097

TE: 1993-11-05

ON NUMBER: 08/105,536

TE: 1993-08-11

ON NUMBER: 08/149,097

TE: 1993-11-05

Application data removed - See File Wrapper or PALM.

D NOS: 65

EQ for Windows Version 4.0

a

arity 99.3%; Score 5403.5; DB 15; Length 1086;

onservative 0; Mismatches 0; Indels 5; Gaps 1;

CLLALTLTQSLIGSPSEPPPSAVTIKSWVDKMOEDLVTLAKTAGVNLVDI 60

CLLALTLTQSLIGSPSEPPPSAVTIKSWVDKMOEDLVTLAKTAGVNLVDI 60

QY 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLNRSKALVSLALEAEKVQAAHOREI
 DB 61 YEKYQDLTYVEPNNAQOLVEIAARDIEKLLNRSKALVSLALEAEKVQAAHOREI
 QY 121 EVVYNKADLDPEKNDSEPGSQRIPKPVFIEDANFGROI SYQHAAVHIPTDIYEG
 DB 121 EVVYNKADLDPEKNDSEPGSQRIPKPVFIEDANFGROI SYQHAAVHIPTDIYEG
 QY 181 NELNWTSDALDEVFKKNREDEPSLLWQVFGSATGLARYYPASVWDNSRTPNKIDLA
 DB 181 NELNWTSDALDEVFKKNREDEPSLLWQVFGSATGLARYYPASVWDNSRTPNKIDLA
 QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDDFVNVSFNE
 DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETSLDDDDFVNVSFNE
 QY 301 VSCQHLVQANVRKVKULKDAVNNITAKGITDYKKGPSFAPEQLLNYNVSRANCN
 DB 301 VSCQHLVQANVRKVKULKDAVNNITAKGITDYKKGPSFAPEQLLNYNVSRANCN
 QY 361 FTDGGEERAQBEIFNKYNKDKKVRFRFSVGOHNYERGPIONMACENKGYIYEIPSI
 DB 361 FTDGGEERAQBEIFNKYNKDKKVRFRFSVGOHNYERGPIONMACENKGYIYEIPSI
 QY 421 INTOEYLDVLGRPMVLADGKAKQVWNTVYLDLLELGLVITGTLPVFNITQGFENK
 DB 421 INTOEYLDVLGRPMVLADGKAKQVWNTVYLDLLELGLVITGTLPVFNITQGFENK
 QY 481 NQLILGVWGVDSLEDIKRLTPRTLCPNGYFAIDPNGYVLLHPNLOPKPKSQE
 DB 481 NQLILGVWGVDSLEDIKRLTPRTLCPNGYFAIDPNGYVLLHPNLOPKPKSQE
 QY 541 DFLDAELENDIKVEIRNMKIDGSGEKTFTLVKSQDERYIDKGNRTVTWTPVNGT
 DB 536 DFLDAELENDIKVEIRNMKIDGSGEKTFTLVKSQDERYIDKGNRTVTWTPVNGT
 QY 601 ALVLPYTSFYIYKAKLETTITQARSKGKMKDSETLKPDPNFEESGYTIFAPRDYCK
 DB 596 ALVLPYTSFYIYKAKLETTITQARSKGKMKDSETLKPDPNFEESGYTIFAPRDYCK
 QY 661 SDNNTFLLNFEEDIRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKG
 DB 656 SDNNTFLLNFEEDIRKTPNNPSCNADLINRVLLDAGFTNELVQNYWSKQKNIKG
 QY 721 FVVTDDGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAY
 DB 716 FVVTDDGITRVYPKEAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAY
 QY 781 MVSXAVEIYIQGLKLPKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVM
 DB 776 MVSXAVEIYIQGLKLPKPAVVGKIDVNSWIENFTKTSIRDPKAGVPCDCKRNSDVM
 QY 841 LDDGGFLMANHDDYTNOIGRFFGBIDPDLMRHLVNI SVYAFNKSVDYQSVCEPGA
 DB 836 LDDGGFLMANHDDYTNOIGRFFGBIDPDLMRHLVNI SVYAFNKSVDYQSVCEPGA
 QY 901 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTPRLLLEAVEMEDDDFTAS
 DB 896 GAGHSAYVPSVADILQIGWATAAASWILQOFLSLTPRLLLEAVEMEDDDFTAS
 QY 961 SCITEQTOYFFNDNKSFGVLDCGNCRSRIFHGEKLMNTNLI FIMVESKGTCPCDT
 DB 956 SCITEQTOYFFNDNKSFGVLDCGNCRSRIFHGEKLMNTNLI FIMVESKGTCPCDT
 QY 1021 QASQTS DGNPCDMVK 1036
 DB 1016 QASQTS DGNPCDMVK 1031

RESULT 8

US-10-375-253-53

; Sequence 53, Application US/10375253

; Publication No. US20040018510A1

ION:
ALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
ION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ION: METHODS

SD9813DA

ION NUMBER: US/10/375,253

DATE: 2003-02-27

ION NUMBER: 08/450,273

TE: 1995-05-25

ION NUMBER: 08/404,354

TE: 1995-02-15

ION NUMBER: 07/914,231

TE: 1992-07-13

ION NUMBER: 08/314,083

TE: 1994-09-28

ION NUMBER: 07/914,231

TE: 1992-07-13

ION NUMBER: 07/603,751

TE: 1990-11-09

ION NUMBER: 08/290,012

TE: 1994-08-11

ION NUMBER: 08/149,097

TE: 1993-11-05

ION NUMBER: 08/105,536

TE: 1993-08-11

ION NUMBER: 08/149,097

TE: 1993-11-05

Application data removed - See File Wrapper or PALM.

ION NOS: 65

IQ for Windows Version 4.0

99.0%; Score 5386.5; DB 15; Length 1084;

Identity 99.2%; Pred. No. 0;

inservative 0; Mismatches 1; Indels 7; Gaps 1;

LLALTLTFLQSLIGPSSSEPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

LLALTLTFLQSLIGPSSSEPPSAVTIKSWDKMQEDLVTLAKTAGVNLVDI 60

DLTYTVPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRWEDPASN 120

DLTYTVPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRWEDPASN 120

NAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

NAKDDLDPEKNDSEPGSQRIKPVFTEDANFGRQISYQHAHVHPTDIYEGSTIVL 180

TSALDEVKKREEDPSLLQWVFGSATGLARYYPASPMVDNSRTNPKIDLDVRR 240

TSALDEVKKREEDPSLLQWVFGSATGLARYYPASPMVDNSRTNPKIDLDVRR 240

QGAAPKMDLIIIVDVSGVSGITLKLRTSVSEMLETLSDDDFVNVSFNSNAQD 300

QGAAPKMDLIIIVDVSGVSGITLKLRTSVSEMLETLSDDDFVNVSFNSNAQD 300

HLVQANVRNKKVLKDVANNITAKGTTDYKGFSPAFEQLLNLYNVRANCKIIML 360

HLVQANVRNKKVLKDVANNITAKGTTDYKGFSPAFEQLLNLYNVRANCKIIML 360

IERAQEIEFNKNDKKVVRFRFVSQHNRYERGPIQWACENKGYIYEIPTSIGAIR 420

IERAQEIEFNKNDKKVVRFRFVSQHNRYERGPIQWACENKGYIYEIPTSIGAIR 420

YLDVLGRPMVLADGKAKQVQWNTVYLDLLEGLVITGLPVFNITGQENKTNLK 480

YLDVLGRPMVLADGKAKQVQWNTVYLDLLEGLVITGLPVFNITGQENKTNLK 480

QWGMVDVSLSDIKRUTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNPKSQBFVTL 540

481 NQILGVMGVDSLEDIKRLTTPRFTLCPNGYYFAIDPNGYVLLHPNLQPKNPKSQE

541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGT

541 DFLDAELENDIKVEIRNKMIDGESGKFTFTLVKSQDERYIDKGNRTYTWTPVNGT

601 ALVLPYTSFYIYKAKLEETITOARSKGKMKDSETLKPDPNFESGYTFIAPRDYCN

601 ALVLPYTSFYIYKAKLEETITOARSKGKMKDSETLKPDPNFESGYTFIAPRDYCN

661 SDNNTFLLNFEFIDRKTPNNFSCNADLINRVLLDAGFTNELVQNYWSKQKNIKG

654 SDNNTFLLNFEFIDRKTPNNFSCNADLINRVLLDAGFTNELVQNYWSKQKNIKG

721 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNDYVFTAPYFNKSGPGAY

714 FVYTDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNDYVFTAPYFNKSGPGAY

781 MVSKAVEIYIQGLLPAVVGIIKIDVNSWIENTFTKTSIRDPCCAGPVCDCRNSDVM

774 MVSKAVEIYIQGLLPAVVGIIKIDVNSWIENTFTKTSIRDPCCAGPVCDCRNSDVM

841 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLWRHLVNIISVYAFNKSVDYQSVCEPGA

834 LDDGGFLLMANHDDYTNQIGRFFGEIDPSLWRHLVNIISVYAFNKSVDYQSVCEPGA

901 GAGHRSAVPSVADIIQIGHWATAAAWSILQOFLLSLTFPRILEAVEMEDDDFTAS

894 GAGHRSAVPSVADIIQIGHWATAAAWSILQOFLLSLTFPRILEAVEMEDDDFTAS

961 SCITEQTYFFDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCPCDT

954 SCITEQTYFFDNDKSFSGVLDCGNCRIFFHGEKLMNTNLIIFIMVESKGTCPCDT

1021 QAEQTSQGNPCDMVK 1036

1014 QAEQTSQGNPCDMVK 1029

RESULT 9

US-10-090-827-7

; Sequence 7, Application US/10090827

; Publication No. US20030073132A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert

; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub

; FILE REFERENCE: 179

; CURRENT APPLICATION NUMBER: US/10/090,827

; PRIOR FILING DATE: 2002-03-06

; PRIOR APPLICATION NUMBER: US/09/397,549

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 1036

; TYPE: PRT

; ORGANISM: Sus scrofa

US-10-090-827-7

Query Match 98.8%; Score 5380; DB 14; Length 1036;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 1023; Conservative 6; Mismatches 7; Indels 0; G

QY 1 MAAGCLLALTLTFLQSLIGPSSSEPPSAVTIKSWDKMQEDLVTLAKTAGVNLQI

DB 1 MAAGCLLALTLTFLQSLIGPSSSEPPSAVTIKSWDKMQEDLVTLAKTAGVNLQI

QY 61 YEKYQDLYTVEPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRWEDI

DB 61 YEKYQDLYTVEPNNARQLVEIARDIEKLSNRKALVSLALEAEKVQAAHQRWEDI

:ON: binding ligands

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; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-8

Query Match          98.8%; Score 5380; DB 14; Length 1063;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; G

QY 1 MAAGCLLALTLTQSLILGPSSERPPPSAVTIKSWDKMQEDLVTLAKTASGVNQ
DB 1 MAAGCLLALTLTQSLILGPSSERPPPSAVTIKSWDKMQEDLVTLAKTASGVNQ

QY 61 YEKYQDLYTVEPNNAQQLVEIARDDTEKLLSNRSKALVSLALEAEKQVAAHQWRD
DB 61 YEKYQDLYTVEPNNAQQLVEIARDDIEKLLSNRSKALVSLALEAEKQVAAHQWRD

QY 121 EYVYTNAKDLDPEKNDSEPGSORIKPVPIDEDANFGROIISYQHAANHPTDIIYEGS
DB 121 EYVYTNAKDLDPEKNDSEPGSORIKPVIDEDANFGROIISYQHAANHPTDIIYEGS

QY 181 NELNWTSSALDEVFKKREEDPSLLMQVGSATGLARYVPASPWVDNRSRTPNKKIDLY
DB 181 NELNWTSSALDEVFKKREEDPSLLMQVGSATGLARYVPASPWVDNRSRTPNKKIDLY

QY 241 RPWYIQGAASPDKMLILVDVSGSVSGLTCLKLIRTSVSEMLETLSDDDFVNVSASFNS
DB 241 RPWYIQGAASPDKMLILVDVSGSVSGLTCLKLIRTSVSEMLETLSDDDFVNVSASFNS

QY 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGTTDYKKGFSFAFEQLLNNVNSRANCK
DB 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGTTDYKKGFSFAFEQLLNNVNSRANCK

QY 361 FTDGGERAEQIEFNKNKOKKVRVRFSGVGHNTYBERGPIQMWACENKGYIYEIPISTI
DB 361 FTDGGERAEQIEFNKNKOKKVRVRFSGVGHNTYBERGPIQMWACENKGYIYEIPISTI

QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVNYLDALGLVITGTLFVFNITGQFENK
DB 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVNYLDALGLVITGTLFVFNITGQFENK

QY 481 NQLILGWGVQDVLSLEDIKRLTPRFTLCPNGYYFAIDPNGVYLLHPNLQPKPKSQEI
DB 481 NQLILGWGVQDVLSLEDIKRLTPRFTLCPNGYYFAIDPNGVYLLHPNLQPKPKSQEI

QY 541 DFLDAELNDIKVEIERNKMI DGESEKFTRLTVKSKQDERYTDKGNRTYTWTPVNGTI
DB 541 DFLDAELNDIKVEIERNKMI DGESEKFTRLTVKSKQDERYTDKGNRTYTWTPVNGTI

QY 601 ALVLPTYSFYIYIKAKLEETITQARSKGKMKDSETLXPDNFEESSGYTFFIAPRDYCN
DB 601 ALVLPTYSFYIYIKAKLEETITQARSKGKMKDSETLXPDNFEESSGYTFFIAPRDYCN

QY 661 SDNNTFELNPFNFIDRKTTPNPNPCNAOLINRVLLDAGFTNQLVQYVWSKQKNIKGI
DB 661 SDNNTFELNPFNFIDRKTTPNPNPCNTDOLINRVLLDAGFTNQLVQYVWSKQKNIKGI

QY 721 FVWTDGGITRVYPKEAGENQSNPETYEDSFVKESLNDNDNVVFTAPVFNKSGPGAYI
DB 721 FVWTDGGITRVYPKEAGENQSNPETYEDSFVKESLNDNDNVVFTAPVFNKSGPGAYI

QY 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEFNFTKTSIRDFPCAGPVCDCRNSDVM
DB 781 MVSKAVEIYIQGKLLKPAVVGIKIDVNSWIEFNFTKTSIRDFPCAGPVCDCRNSDVM

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FLLMANHDDYTNQIGRPFGEIDPSLMRHLVNIISVYAFNKSVDYOSVCEPGAAPKQ 900
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XQTYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNLIIFIMVESKGTCTPCDTRLII 1020
XQTYFFDNDKSFSGVLDCGNCRSIFHVEKLMNTNLIIFIMVESKGTCTPCDTRLII 1020
SDGNPCDMVK 1036
SDGPDPCDMVK 1036

cation US/10090827
IS20030073132A1
ON:
x-Lambert
ON: Method for the screening of alpha 2 delta-1 subunit
ON: binding ligands
179
ION NUMBER: US/10/090, 827
ATE: 2002-03-06
N NUMBER: US/09/397,549
E: 1999-09-16
NOS: 21
In Ver. 2.1

crofa

98.8%; Score 5380; DB 14; Length 1069;
rity 98.7%; Pred. No. 0;
nservative 6; Mismatches 7; Indels 0; Gaps 0;

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DLYTVEPNNAQLVEIAARDIEKLSNRSKALVRLALEAEKVQAAHQRDPASN 120
NAKDDLPEKNDSEPGSQRIKPVFTEDANFGRIQISYQAAVHIPTDIYEGSTIVL 180
NAKDDLPEKNDSEPGSQRIKPVFTEDANFGRIQISYQAAVHIPTDIYEGSTIVL 180
TSALDEVEKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLDVRR 240
TSALDEVEKKNREEDPSLLMQVFGSATGLARYYPASPWDNSRTPNKIDLDVRR 240
QGAAPSKDMLILVDVSGVSLTGLKIRTSVSEMLETLSDDDFVNVAFSNNAQD 300
QGAAPSKDMLILVDVSGVSLTGLKIRTSVSEMLETLSDDDFVNVAFSNNAQD 300
JHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
JHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
JERAQEIIFKNYKDKKRVFPFVSVCHYERGPICQMACENKGYIYEIPSGAIR 420
JERAQEIIFAKYKDKKRVFTFVSGQHNVDGPIQMACENKGYIYEIPSGAIR 420
YLDVLGRPWLAGDKAKQVQNTNVYLDALGLVITGLPVFNITQGFENKTNLK 480
YLDVLGRPWLAGDKAKQVQNTNVYLDALGLVITGLPVFNITQGFENKTNLK 480

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QY 481 NOLILGVMGVDSLEIDIKLTPRFTLCPNGYFPAIDPENGVLVLLHPNLQPKPKSQE
DB 481 NOLILGVMGVDSLEIDIKLTPRFTLCPNGYFPAIDPENGVLVLLHPNLQPKPKSQE
QY 541 DFLDABLENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNRTYTWTPVNGT
DB 541 DFLDABLENDIKVEIRNKMIDGESGKTFRTLVKSDERYIDKGNRTYTWTPVNGT
QY 601 ALVLPYSPYIYKAKLEETITQARSKKGKMKDSETLKPDNFESGYTFFIAPRDYCN
DB 601 ALVLPYSPYIYKAKLEETITQARSKKGKMKDSETLKPDNFESGYTFFIAPRDYCN
QY 661 SDNNTFLLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNIKG
DB 661 SDNNTFLLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQVWSKQKNIKG
QY 721 FVVTGGITRVYPPKEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGFGAYI
DB 721 FVVTGGITRVYPPKEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGFGAYI
QY 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENTFTKTSIRDPACAGPVCDCKRNSDVM
DB 781 MYSKAVEIYIOGKLKPAVVGKIDVNSWIENTFTKTSIRDPACAGPVCDCKRNSDVM
QY 841 LDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNIISVYAFNKSVDYOSVCEPGA
DB 841 LDGGFLLMANHDDYTNQIGRPFGEIDPSLMRHLVNIISVYAFNKSVDYOSVCEPGA
QY 901 GAGHSAYVPSVADILIQIGWATAAASLILQOFLSLITPRLLLEAVEMEDDDFTAS
DB 901 GAGHSAYVPSIADILHIGWATAAASLILQOFLSLITPRLLLEAVEMEDDDFTAS
QY 961 SCITEQTYFFDNDKSFSGVLDCGNCRSIFHGEKLMNTNLIIFIMVESKGTCTPCDTI
DB 961 SCITEQTYFFDNDKSFSGVLDCGNCRSIFHVEKLMNTNLIIFIMVESKGTCTPCDTI
QY 1021 QAEQTSDDGNPCDMVK 1036
DB 1021 QAEQTSDDGPDPCDMVK 1036

RESULT 12
US-10-090-827-5
; Sequence 5, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-090-827-5

Query Match 98.8%; Score 5380; DB 14; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 6; Mismatches 7; Indels 0; G

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QY 1 MAAGCLLALTLTLFQSLILGPSSEBPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLQI
DB 1 MAAGCLLALTLTLFQSLILGPSSEBPPPSAVTIKSWVDKMQEDLVTLAKTAGVNLQI
QY 61 YEKYQDLYTVEPNNAQLVEIAARDIEKLSNRSKALVSLALEAEKVQAAHQRDP

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 22AKADLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGSTIVL 180
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 40TEFLLPNFEIDRKTNNPSCNADLINRVLLDAGFTNELVQYWSKQKNIKGVKAR 720
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 44AVEIYIOGKLLKPAVVGKIDVNSWIENTFKTSIRDPACAPVCDCKRNSDVMDCVI 840
 45FLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSQYDQVCEPFGAAPKQ 900
 46FLLMANHDDYTQIGRFFGEIDPSLMRHLVNI SVYAFNKSQYDQVCEPFGAAPKQ 900
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 49JQTYFFDNDKSGFSGVLDGCGNSRIFPHGKLMNTNLI FIFMVESKGTCPCDTFLLI 1020
 50JQTYFFDNDKSGFSGVLDGCGNSRIFPHGKLMNTNLI FIFMVESKGTCPCDTFLLI 1020
 51TSDGPNPCDMVK 1036
 52TSDGPNPCDMVK 1036

lication US/10375253
 JS20040018510A1

ION:

SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
 ; TITLE OF INVENTION: METHODS
 ; FILE REFERENCE: SD9813DA
 ; CURRENT APPLICATION NUMBER: US/10/375,253
 ; CURRENT FILING DATE: 2003-02-27
 ; PRIOR APPLICATION NUMBER: 08/450,273
 ; PRIOR FILING DATE: 1995-05-25
 ; PRIOR APPLICATION NUMBER: 08/404,354
 ; PRIOR FILING DATE: 1995-02-15
 ; PRIOR APPLICATION NUMBER: 07/914,231
 ; PRIOR FILING DATE: 1992-07-13
 ; PRIOR APPLICATION NUMBER: 08/314,083
 ; PRIOR FILING DATE: 1994-09-28
 ; PRIOR APPLICATION NUMBER: 07/914,231
 ; PRIOR FILING DATE: 1992-07-13
 ; PRIOR APPLICATION NUMBER: 07/603,751
 ; PRIOR FILING DATE: 1990-11-09
 ; PRIOR APPLICATION NUMBER: 08/290,012
 ; PRIOR FILING DATE: 1994-08-11
 ; PRIOR APPLICATION NUMBER: 08/149,097
 ; PRIOR FILING DATE: 1993-11-05
 ; PRIOR APPLICATION NUMBER: 08/105,536
 ; PRIOR FILING DATE: 1993-08-11
 ; PRIOR APPLICATION NUMBER: 08/149,097
 ; PRIOR FILING DATE: 1993-11-05
 ; Remaining Prior Application data removed - See File Wrapper or PALM
 ; NUMBER OF SEQ ID NOS: 65
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 47
 ; LENGTH: 1103
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-10-375-253-47

Query Match 98.6%; Score 5367; DB 15; Length 1103;
 Best Local Similarity 97.4%; Pred. No. 0;
 Matches 1020; Conservative 0; Mismatches 1; Indels 26; G:

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 Qy 61 YEKYQDLYTVEPNARQLVEIARDEIEKLISNRKALVRLALEAEKVQAAHQWRE
 Db 61 YEKYQDLYTVEPNARQLVEIARDEIEKLISNRKALVRLALEAEKVQAAHQWRE
 Qy 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGS
 Db 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGQISYQHAHVHPTDIYEGS
 Qy 181 NELNWTSAALDEVFKNREEDPSLLWQVFGSATGLARYYPASPMWVNSRTPNKIDLY
 Db 181 NELNWTSAALDEVFKNREEDPSLLWQVFGSATGLARYYPASPMWVNSRTPNKIDLY
 Qy 241 RPYIIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDFVNVASFN
 Db 241 RPYIIOGAASPKDMLILVDVSGVSGTLKLRISVSEMLETLSDDDFVNVASFN
 Qy 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANCKN
 Db 301 VSCFQHLVQANVRNKKVLKDAVNNTAKGIDYKKGFSFAFEQLLNYSRANCKN
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 Qy 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITGQENK
 Db 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVLDALEGLVITGTLPVFNITGQENK
 Qy 481 NQLILGVMGVDSLEDIKRLTPRTFLCPNGYYPFAIDPNGYVLLHPNLOPKNPKSQEP
 Db 481 NQLILGVMGVDSLEDIKRLTPRTFLCPNGYYPFAIDPNGYVLLHPNLOPKNPKSQEP

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TYWTPVNGTDSYALVLPYVSFYIYKAKLEETITQARY-----SETLKPONF 653
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ication US/10375253
S20040018510A1
ON:
ALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
ON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ON: METHODS
SD9813DA
ION NUMBER: US/10/375,253
ATE: 2003-02-27
N NUMBER: 08/450,273
E: 1995-05-25
N NUMBER: 08/404,354
E: 1995-02-15
N NUMBER: 07/914,231
E: 1992-07-13
N NUMBER: 08/314,083
E: 1994-09-28
N NUMBER: 07/914,231
E: 1992-07-13
N NUMBER: 07/603,751
E: 1990-11-09
N NUMBER: 08/290,012
E: 1994-08-11
N NUMBER: 08/149,097
E: 1993-11-05
N NUMBER: 08/105,536
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N NUMBER: 08/149,097
E: 1993-11-05
Application data removed - See File Wrapper or PALM.
NOS: 65
Q for Windows Version 4.0

LENGTH: 1079
TYPE: PRT
ORGANISM: Human
US-10-375-253-51
Query Match 98.2%; Score 5347; DB 15; Length 1079;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1023; Conservative 0; Mismatches 1; Indels 12; Gs
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Db 1 MAAGCLLALTITLTFOSLIGSSSEPPFSAVTIKSWDKMQEDVTLAKTAGVNOI
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Db 61 YEKYQDLTVPENNARQOLVEIARDEIKLLSNRSKALVSLALEAEKVQAAHQWREDE
QY 121 EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEGST
Db 121 EVVYNKADDDLPKNDSEPGSQRIKPVFIEDANFGRQISYOHAAVHIPTDIYEGST
QY 181 NELNWTSALEDEVFKKREDEPSLLMQVFGSATGLARYYPASPWVNSRTPNKIDLYI
Db 181 NELNWTSALEDEVFKKREDEPSLLMQVFGSATGLARYYPASPWVNSRTPNKIDLYI
QY 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLIRTSVSEMLETLSDDDFVNVASFNSN
Db 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLIRTSVSEMLETLSDDDFVNVASFNSN
QY 301 VSCFQHLVQAVNRNKKVKADAVNNITAKGITYKKGSPFAFQOLLNINVSANCNKI
Db 301 VSCFQHLVQAVNRNKKVKADAVNNITAKGITYKKGSPFAFQOLLNINVSANCNKI
QY 361 FTDGGEERAQEIFNKYNKDKKVRVERFVSQGHNYERGPIONWACENKGYIYIETPSIC
Db 361 FTDGGEERAQEIFNKYNKDKKVRVERFVSQGHNYERGPIONWACENKGYIYIETPSIC
QY 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLGLVITGTLPVFNITGQFENKI
Db 421 INTQEYLDVLGRPMVLADGKAKQVQWNTVYLDALGLGLVITGTLPVFNITGQFENKI
QY 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOPNKPSQEE
Db 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYYFAIDPNGYVLLHNPLOPNKPSQEE
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTI
Db 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTI
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Db 596 ALVLPYTSFYIYKAKLEETITQARY-----SETLKPONFEESGYTFIAPRDYCN
QY 661 SDNTEFLLNPNFIDRKTPNNPSCNADLINRVLLDAGFTNLTAPYFNKSKQKNIKGV
Db 649 SDNTEFLLNPNFIDRKTPNNPSCNADLINRVLLDAGFTNLTAPYFNKSKQKNIKGV
QY 721 FVVTDDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYE
Db 709 FVVTDDGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNYFTAPYFNKSGPGAYE
QY 781 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCRNSDVM
Db 769 MYSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCDCRNSDVM
QY 841 LDDGGFLMANHDDYTNOIGRFFGEIDPISLMRHLVNI SVYAFNKSQYQSVCEPGAA
Db 829 LDDGGFLMANHDDYTNOIGRFFGEIDPISLMRHLVNI SVYAFNKSQYQSVCEPGAA
QY 901 GAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPRLLLEAVEMEDDDFTASL
Db 889 GAGHRSAYVPSVADILQIGWATAAAWSILOQFLLSLTTPRLLLEAVEMEDDDFTASL

QTQVFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIIFIMVESKGTCPDTRLLI 1020
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'SDGNPCDMVK 1036
 'SDGNPCDMVK 1024

ication US/10090827
 IS20030073132A1

ON: binding ligands
 ON: Method for the screening of alpha 2 delta-1 subunit
 179
 TON NUMBER: US/10/090,827
 DATE: 2002-03-06
 N NUMBER: US/09/397,549
 E: 1999-09-16
 NOS: 21
 In Ver. 2.1

sapiens

98.2%; Score 5346; DB 14; Length 1018;
 ivity .100.0%; Pred. No. 0;
 nservative 0; Mismatches 0; Indels 0; Gaps 0;
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 JLYTVEPNNAQQLVEIAARDTEKLSNRSKALVSLALEAEKVQAAHWRDPASN 120
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 TSALDEVPKKNREEDPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLYDVR 240
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 QGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVSFNSNAQD 300
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 JHLVQANVRNKKVLDKAVNNITAKGITDYKKGFSFAFEQLLNNVSRANCKIIML 360
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 IERAQEIENKYNKKKVVFRFVSQHNRYERGPIQMACENKGYIYEIPSIGAIR 420
 YLDVLGRPMVLADGKAKOVQWNTNVDLDALEGLVITGTLPVFNITGQFENKTNLK 480
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 GWMGVDVSLEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPNLQPKNPKSQBPVTL 540
 GWMGVDVSLEDIKRLTPFTLCPNGYYPFAIDPNGYVLLHPNLQPKNPKSQBPVTL 540
 ILENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600
 ILENDIKVEIRNKMIDGESGKTFRTLKVSQDERYIDKGNRTYTWTPVNGTDYSL 600

601 ALVLPYSPYIYKAKLEETITQARSKKGKMDSETLKPDNFEESGYTFIAPRDYCN
 601 ALVLPYSPYIYKAKLEETITQARSKKGKMDSETLKPDNFEESGYTFIAPRDYCN
 661 SDNNTFFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKG
 661 SDNNTFFLLNFNEFIDRKTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQKNIKG
 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYFTAPYFNKSGPGAY
 721 FVVTGGITRVYPKEAGENWQENPETYEDSFYKRSILDNDNYFTAPYFNKSGPGAY
 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPCAGPVCDCKRNSDVM
 781 MYSKAVEIYIQGLKLPVAVGKIDVNSWIENTFTKTSIRDPCAGPVCDCKRNSDVM
 841 LDGGFLLMANHDDVTNQIGRFEGEIDPSLMRHLVNIISVYAFNKSVDYQSVCEPGAJ
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 901 GAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTPTPRLLLEAVEMEDDDFTASI
 901 GAGHRSAYVPSVADILQIGMWATAAASILQOFLLSLTPTPRLLLEAVEMEDDDFTASI
 961 SCITTEQTOYFFDNDKSFSGVLDGNCNRSIFHGEKLMNTNLIIFIMVESKGTCPDTR
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Search completed: March 17, 2004, 20:26:54
 Job time : 39.8932 secs

;DGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

ication US/10090827

320030073132A1

DN:

r-Lambert

DN: Method for the screening of alpha 2 delta-1 subunit

DN: binding ligands

179

ION NUMBER: US/10/090,827

ATE: 2002-03-06

N NUMBER: US/09/397,549

E: 1999-09-16

NOS: 21

In Ver. 2.1

sapiens

rity 100.0%; Score 5599; DB 14; Length 1091;

nservative 0; Mismatches 0; Indels 0; Gaps 0;

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HLVQANVRNKKVLKDAVNNITAKGITDYKGFSPAFQOLLNLYNVSRAKNIIML 360

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YLDVLRPMVLGADKAKQVQNTVYLDALGLVITGTLPVFNITGQFENKTNLK 480

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661 SDNTEFLNFEFIDRKTNNPSCNADLINRVLLDAGFTNQLVQYWSKQKNGV

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721 FVVTDDGGITRVYKPEAGRWQENPETVEDSPYKSLDNDNVFTAPYENKSGPGAYE

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841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPAA

841 LDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPAA

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1021 QAEQTSQGNPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

RESULT 5

US-10-162-102-17

; Sequence 17, Application US/10162102

; Publication No. US2003023236A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY M

; FILE REFERENCE: 10448-190001

; CURRENT APPLICATION NUMBER: US/10/162,102

; CURRENT FILING DATE: 2003-04-04

; PRIOR APPLICATION NUMBER: US 60/209,845

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: US 09/875,321

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: PCT/US01/18340

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: US 60/209,257

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,423

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18398

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/209,238

; PRIOR FILING DATE: 2000-06-05

; PRIOR APPLICATION NUMBER: US 09/875,363

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: PCT/US01/18247

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US 60/227,068

; PRIOR FILING DATE: 2000-08-22

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 1091

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-162-102-17

Query Match 100.0%; Score 5599; DB 15; Length 1091;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps

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LYTVFPNNARQVETAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDFASN 120
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RESULT 6
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; Sequence 49, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Human
US-10-375-253-49
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Query March 99.3%; Score 5559.5; DB 15; Length 1086;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1058; Conservative 0; Mismatches 0; Indels 5; Ga

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Qy 61 YEKYQDLYTVFPNNARQVETAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDF
Db 61 YEKYQDLYTVFPNNARQVETAARDIEKLLNSRKALVSLALEAEKVQAAHQWREDF

Qy 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIIYSGST
Db 121 EVVYVNAKDDLDPEKNDSEPGSORIKPVFIEDANFGROI SYQHAHVHPTDIIYSGST

Qy 181 NELNWTLSALDEVFKKNEEDPSLLWQVFGSAGTLARYYPASFPWVDSNRTPNKIDLYD
Db 181 NELNWTLSALDEVFKKNEEDPSLLWQVFGSAGTLARYYPASFPWVDSNRTPNKIDLYD

Qy 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASFNSN.
Db 241 RPWYIOGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVASFNSN.

Qy 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQOLLNVNVRANCNKI.
Db 301 VSCFQHLVQANVRNKKVLDKAVNNITAKGIDYKKGFSFAFEQOLLNVNVRANCNKI.

Qy 361 FTDGGEERAQEIFNKYNKDKKVRFRFSVGHNYERGPIONMACENKGYEYIIPSIG.
Db 361 FTDGGEERAQEIFNKYNKDKKVRFRFSVGHNYERGPIONMACENKGYEYIIPSIG.

Qy 421 INTQEYLDVLGRPMVLADGKAKQVQWNTNYYLDALGLVITGTLPVENITQGFENK.
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FLLMANHDDYTNOIGRPFGEIDPSLMRHLVNI SYVAFNKS YDYQSVCEPGAAPKQ 900
SAYVPSVADILQIGWATAAWSILOQFLSLTFRLLLEAVEMEDDFTASLSKQ 960
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SDGNPNCDMVQPRYKPGDPVCFDNNVLEDTDCGGVS 1063
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cation US/10090827
IS20030073132A1
:ON:
:R-Lambert
:ON: Method for the screening of alpha 2 delta-1 subunit
:ON: binding ligands

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; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Sus scrofa
; US-10-090-827-5

Query Match      98.8%; Score 5532; DB 14; Length 1091;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gai

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Db 61 YEKYODLYTVEPNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDEF
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Db 121 EVVYVNAKDDLDPEKNDSEPGSQRKIPVLEDFANFGQISYQHAHVHIPTDIYEGST
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Db 181 NELNMTSALDEVFKKNEDEPSSLWQVFGSATGLARYYPASPWVDSNRTNPKIDLYD
Qy 241 RPWTIQGAASPKMDLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSN
Db 241 RPWTIQGAASPKMDLILVDVSGSVGLTLKIRTSVSEMLETSLDDDFVNVASFNSN
Qy 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITYKKGFSFAFEQQLLNVNVRANCKI
Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGITYKKGFSFAFEQQLLNVNVRANCKI
Qy 361 PTDGGESEAAQIFAKYKNDKKVRVFRFSVGQHYNERGPIQWACENKGYYYEIPSGI
Db 361 PTDGGESEAAQIFAKYKNDKKVRVFRFSVGQHYNERGPIQWACENKGYYYEIPSGI
Qy 421 INTQBYLDVLRGPMVLADGKAKQVQWNTVNYLDALGLHVIITGTLPVFNITGQFNKT
Db 421 INTQBYLDVLRGPMVLADGKAKQVQWNTVNYLDALGLHVIITGTLPVFNITGQFNKT
Qy 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLPKPKSQDEF
Db 481 NQLILGVNGVDVSLIEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPNLPKPKSQDEF
Qy 541 DFLDAELENLIKVEIRNKMIDGESGKFTRLVKSQDERYIDKGNRTYTWTVPNGTCL
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Qy 601 ALVLPYTFYIKAKLEETITQARSKKGMKDETLKPDNFEESGYTFIAPRDYCNL
Db 601 ALVLPYTFYIKAKLEETITQARSKKGMKDETLKPDNFEESGYTFIAPRDYCNL
Qy 661 SDNNTFEFLNFEFDRTKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNIKGK
Db 661 SDNNTFEFLNFEFDRTKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNIKGK
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CON NUMBER: US/10/375,253
ATE: 2003-02-27
NUMBER: 08/450,273
NUMBER: 08/404,354
NUMBER: 07/914,231
NUMBER: 08/314,083
NUMBER: 07/914,231
NUMBER: 07/603,751
NUMBER: 08/290,012
NUMBER: 08/149,097
NUMBER: 08/105,536
NUMBER: 08/149,097
application data removed - See File Wrapper or PALM.
NOS: 65
for Windows Version 4.0

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reservative 0; Mismatches 1; Indels 12; Gaps 2;

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DB 536 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGTDSL
QY 601 ALVLPYTSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRDYCNL
DB 596 ALVLPYTSFYIYKAKLEETITQARY-----SETLKPDPNFESGYTFIAPRDYCNL
QY 661 SDNNTEFLNPFIDRKTNNPNSCNADLNRLVLLDAGFTNVLQNTWSKQKNIKGV
DB 649 SDNNTEFLNPFIDRKTNNPNSCNADLNRLVLLDAGFTNVLQNTWSKQKNIKGV
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DB 709 FVVTDDGGITRYPKAGENWQENPETYEDSFYKESLNDNNTVFTAPYFNKSGPGAYE
QY 781 MVSXAVIYIQGLKLLKPAVVGKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSDVMD
DB 769 MVSXAVIYIQGLKLLKPAVVGKIDVNSWIENFTKTSIRDPFCAGPVCDCCKNSDVMD
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DB 829 LDDGGFLLMANHDDYTNOIGRFFGEIDPSPMLMRHLVNI SVTAFNKSIDYQSVCEPAA
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RESULT 13
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; Sequence 20, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
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; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1091
; TYPE: PRT

97.7%; Score 5472; DB 15; Length 1091;
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; Sequence 14, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-14
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; Gaps
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.cation US/10090827
IS20030073132A1
:ON:
xr-Lambert
:ON: Method for the screening of alpha 2 delta-1 subunit
:ON: binding ligands
179
:ION NUMBER: US/10/090,827
:ATE: 2002-03-06
:ON NUMBER: US/09/397,549
:RE: 1999-09-16
: NOS: 21
:In Ver. 2.1

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arity 98.7%; Pred. No. 0;
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1021 QAEQTS DGNPNPCDMVK 1036

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Job time : 41.8547 secs

26:18 2004

us-10-090-827-15.rapb

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GenCore version 5.1.6
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the number of results predicted by chance to have a
than or equal to the score of the result being printed,
i by analysis of the total score distribution.

SUMMARIES

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0	1091	9	US-09-875-423-4	Sequence 4, Appli	
0	1091	14	US-10-162-012-17	Sequence 17, Appl	
0	1091	14	US-10-090-827-16	Sequence 16, Appl	
0	1091	15	US-10-162-102-17	Sequence 17, Appl	
3	1086	15	US-10-375-253-49	Sequence 49, Appl	
0	1084	15	US-10-375-253-53	Sequence 53, Appl	
8	1063	14	US-10-090-827-8	Sequence 8, Appli	
8	1069	14	US-10-090-827-9	Sequence 9, Appli	
8	1091	14	US-10-090-827-5	Sequence 5, Appli	
6	1103	15	US-10-375-253-47	Sequence 47, Appl	
3	1079	15	US-10-375-253-51	Sequence 51, Appl	
7	1091	15	US-10-375-253-20	Sequence 20, Appl	
2	1036	14	US-10-090-827-14	Sequence 14, Appl	
1	1036	14	US-10-090-827-7	Sequence 7, Appli	

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19	3004.5	53.7	1145	14	US-10-116-949-4	Sequence 4
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ALIGNMENTS

RESULT 1
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; Sequence 15, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-15

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6:26:18 2004

us-10-090-827-15.rapb

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cation US/09875423
0081657A1
ON:
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ON: 21784, A NOVEL HUMAN CALCIUM CHANNEL
ON: FAMILY MEMBER AND USES THEREOF
10448-059001
TON NUMBER: US/09/875, 423
ATE: 2001-06-05
N NUMBER: US 60/209,257
E: 2000-06-05

NUMBER OF SEQ ID NOS: 6
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; SEQ ID NO 4
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-423-4
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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ication US/10162102
 320030232336A1
 3N: RORY A.J.
 3: -Santiago, Inmaculada
 fei

3N: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS

10448-190001

ION NUMBER: US/10/162,102

ATE: 2003-04-04

3: 2000-06-06

3: 2000-06-06

3: 2001-06-06

3: 2001-06-06

3: 2000-06-05

3: 2001-06-05

3: 2000-06-05

3: 2001-06-05

3: 2000-08-22

Application data removed - See File Wrapper or PALM.

2 for Windows Version 4.0

apiens

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RESULT 4

US-10-162-012-17

; Sequence 17, Application US/10162012

; Publication No. US20030051660A1

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; APPLICANT: Silos-Santiago, Inmaculada

; APPLICANT: Gu, Wei

; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY M

; FILE REFERENCE: 10448-190001

; CURRENT APPLICATION NUMBER: US/10/162,012

; CURRENT FILING DATE: 2002-06-04

; PRIOR APPLICATION NUMBER: US 60/209,845

; PRIOR FILING DATE: 2000-06-06

; PRIOR APPLICATION NUMBER: US 09/875,321

; PRIOR FILING DATE: 2001-06-06

[illegible]

ication US/09875423
20081657A1

ION:
is, ROY A. J.
ION: 21784. A NOVEL HUMAN CALCIUM CHANNEL
ION: FAMILY MEMBER AND USES THEREOF
10448-050001
TION NUMBER: US/09/875,423
DATE: 2001-06-05
ON NUMBER: US 60/209,257
TE: 2000-06-05

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;	SOFTWARE: FastSeq for Windows Version 4.0	
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US-09-875-423-4		
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Matches 1063;	Conservative 0;	Mismatches 0; Indels 0; G
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Db	121	EVVYTNAKDDLDEPKNDSPGSGQRIPKPIEDANFGROI SYQHAAVHIPTDIYEVS
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Db	241	RPWYIQGAASPDKMLILVDVSGSVGLTKLIRTSVSEMLTLDGDDPFVNVASFNS
QY	301	VSCFQHLVQANVRNKKVLDXAVNNITAKGITDYKKGFSAFEQLLNTVNSRANCNK
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QY	541	DFLDARELNDIKVEIENKMDGSEGEKFTRLTVKSQDERYIDKGNRYITWTTPVNGT
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17:56:55 2004

us-10-090-827-15.rapb

GenCore version 5.1.1.6
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n search, using sw model

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10-090-827-15

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SUM62

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than or equal to the score of the result being printed,
ed by analysis of the total score distribution.

SUMMARIES

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1.0	1063	15	US-10-090-827-15	Sequence 15, Appl
1.0	1091	9	US-09-875-423-4	Sequence 4, Appl
1.0	1091	12	US-10-162-102-17	Sequence 17, Appl
1.0	1091	15	US-10-162-012-17	Sequence 17, Appl
1.0	1091	15	US-10-090-827-16	Sequence 16, Appl
1.3	1086	12	US-10-375-253-49	Sequence 49, Appl
1.0	1084	12	US-10-375-253-53	Sequence 53, Appl
1.8	1063	15	US-10-090-827-8	Sequence 8, Appl
1.8	1069	15	US-10-090-827-9	Sequence 9, Appl
1.8	1091	15	US-10-090-827-5	Sequence 5, Appl
1.6	1103	12	US-10-375-253-47	Sequence 47, Appl
1.3	1079	12	US-10-375-253-51	Sequence 51, Appl
1.7	1091	12	US-10-375-253-20	Sequence 20, Appl
1.2	1036	15	US-10-090-827-14	Sequence 14, Appl
1.1	1036	15	US-10-090-827-7	Sequence 7, Appl

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17	5288	94.4	1018	15	US-10-090-827-6	Sequence
18	3004.5	53.7	1145	15	US-10-116-949-2	Sequence
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37	185	3.3	35	9	US-09-864-761-36461	Sequence 3
38	182	3.3	885	9	US-09-828-423-5	Sequence 5
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45	159.5	2.8	173	12	US-10-154-678-100	Sequence

ALIGNMENTS

RESULT 1

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; Sequence 15, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
; FILE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1993-09-16
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 15
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 1063
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-15

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; G;
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DB 61 YEKYQDLYTFVFNNAQVLEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDI
QY 121 EYVYVYNAKDDLPKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGS
DB 121 EYVYVYNAKDDLPKNDSEPGSQRIKPVIEDANFGRQISYQHAHVHPTDIYEGS
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1 NUMBER: US 60/209,257
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2: 2001-06-05
1 NUMBER: US 60/227,068
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1 NUMBER: US 60/226,770
2: 2000-08-21
1 NUMBER: US 09/934,421
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1 NUMBER: US 60/279,281
2: 2001-03-28
1 NUMBER: US 10/109,029
2: 2002-03-28
1 NUMBER: PCT/US02/09728
2: 2002-03-28
1 NUMBER: US 60/290,288
2: 2001-05-11
1 NUMBER: US (not assigned)
2: 2002-05-13
NOS: 48
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sapiens

100.0%; Score 5599; DB 15; Length 1091;
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nservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 16, Application US/10090827
; Publication NO. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 1091
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-16
Query Match 100.0%; Score 5599; DB 15; Length 1091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1063; Conservative 0; Mismatches 0; Indels 0; Gaps

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; Sequence 49, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT FILING DATE: 2003-02-27
; PRIOR FILING DATE: 2003-02-27
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1086
; TYPE: PRT
; ORGANISM: Human
US-10-375-253-49

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ication US/10375253
IS20040018510A1
ON:
ALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
ON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
ON: METHODS
SD9813DA
TON NUMBER: US/10/375, 253
DATE: 2003-02-27
IN NUMBER: 08/450, 273
E: 1995-05-25
IN NUMBER: 08/404, 354
E: 1995-02-15
IN NUMBER: 07/914, 231
E: 1992-07-13
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E: 1990-11-09
IN NUMBER: 08/290, 012
E: 1994-08-11
IN NUMBER: 08/149, 097
E: 1993-11-05
IN NUMBER: 08/105, 536
E: 1993-08-11

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; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 1084
; TYPE: PRT
; ORGANISM: Human
US-10-375-253-53

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Best Local Similarity 99.2%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 1; Indels 7; Gc

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QY 421 INTQEYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKI
DB 421 INTQEYLDVLGRPMVLGADKAKQVQWNTVYLDALGLVITGTLPVFNITGQFENKI
QY 481 NQLILGVMGVDVLSLEDIKELTTPRFTLCPNGYFPAIDPNGYVLLHPNLQPNPKSQEI
DB 481 NQLILGVMGVDVLSLEDIKELTTPRFTLCPNGYFPAIDPNGYVLLHPNLQPNPKSQEI
QY 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTKVKSQDERYIDKGNRTYTWTPVNGTI
DB 541 DFLDAELENDIKVEIRNKMIDGESGKFTLTKVKSQDERYIDKGNRTYTWTPVNGTI
QY 601 ALVLPTYSFYIKAKLEETITQARSKGKMKOSETLKPONFESGYTFTAPRDYCNM
DB 601 ALVLPTYSFYIKAKLEETITQARSKGKMKOSETLKPONFESGYTFTAPRDYCNM
QY 661 SDNNTTEFLNPNFEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIKGV
DB 661 SDNNTTEFLNPNFEDIRKTPNPNPCNADLINRVLLDAGFTNELVQYWSKQNKIKGV
QY 721 FVYVTDGGITRVYKPEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYE
DB 721 FVYVTDGGITRVYKPEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGAYE
QY 781 MYSKAVEIYIQGLLKPAPVIGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVM
DB 781 MYSKAVEIYIQGLLKPAPVIGIKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVM
QY 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAP
DB 841 LDDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAFNKSVDYOSVCEPGAP

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FLMANHDDYTNQIGRFGEIDPSLMRHLVNISVIAFNKSYDYQSVCEPGAAPKQ 893
SAVPSVADILQIGWATAAAWSILOQFLSLTFPRLLLEAVEMEDDDFTASLSQ 960
SAVPSVADILQIGWATAAAWSILOQFLSLTFPRLLLEAVEMEDDDFTASLSQ 953
SAVPSVADILQIGWATAAAWSILOQFLSLTFPRLLLEAVEMEDDDFTASLSQ 953
2QYFFNDNDSKSGVLDGNCNRSIFHGEKLMNTNLIIFMVESKGTGTCPCDTRLII 1020
2QYFFNDNDSKSGVLDGNCNRSIFHGEKLMNTNLIIFMVESKGTGTCPCDTRLII 1013
3DGNPCDMVKQPRYKRGPDVCFDNNVLEDDYTDGCGVS 1063
3DGNPCDMVKQPRYKRGPDVCFDNNVLEDDYTDGCGVS 1056

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cation US/10090827

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20030073132A1

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DN:

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c-Lambert

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DN: Method for the screening of alpha 2 delta-1 subunit

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DN: binding ligands

```

```

179

```

```

ION NUMBER: US/10/090,827

```

```

ATE: 2002-03-06

```

```

NUMBER: US/09/397,549

```

```

3: 1999-09-16

```

```

NOS: 21

```

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In Ver. 2.1

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:rofa

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ity 98.8%; Score 5532; DB 15; Length 1063;

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servative 6; Mismatches 8; Indels 0; Gaps 0;

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ALALTTLFQSLILIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLYDI 60
ALALTTLFQSLILIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQLYDI 60
LYTVBPNNARQLVEAARDIEKLSNRKALVSLALEAEKVAQAQHWEDFASN 120
LYTVBPNNARQLVEAARDIEKLSNRKALVSLALEAEKVAQAQHWEDFASN 120
IAKDDLDPEKNDSEPGSRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
IAKDDLDPEKNDSEPGSRIKPVFIEDANFGROIYSQHAHVHPTDIYEGSTIVL 180
SALDVRPKKREEDPSLLWQVFGSATGLARYYPASPVWDSNRTNPKIDLYDVR 240
SALDVRPKKREEDPSLLWQVFGSATGLARYYPASPVWDSNRTNPKIDLYDVR 240
XGAASPKDMLILVDVSGVSLTKLIRTSVSEMLETLSDDDFNVNVSFNSNAQD 300
XGAASPKDMLILVDVSGVSLTKLIRTSVSEMLETLSDDDFNVNVSFNSNAQD 300
ILVQANVRNKKVLKDAVNNITAKITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
ILVQANVRNKKVLKDAVNNITAKITDYKKGFSFAFEQLLNYNVSRANCKIIML 360
IERAQEIFKNYKNDKKVRVFRSVGOHNYERGIOMWACENKGYIYEISGAIR 420
IERAQEIFKNYKNDKKVRVFRSVGOHNYERGIOMWACENKGYIYEISGAIR 420
LDVLRGPMVLGDKAKQVQWNTNVLDALEGLVITGTLPVNITGQFNKNLX 480
LDVLRGPMVLGDKAKQVQWNTNVLDALEGLVITGTLPVNITGQFNKNLX 480
WGVNDVLSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLQPKNPKSQEPVTL 540

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481 NQLILGWGVDSLEDIKRLTPRFTLCPNGYFFAIDPNGYVLLHPLQPKNPKSQE
541 DFLDAELNDIKVEIRNMIDGESGEKTRTLVKSQDERYIDKGNRTYTTWTPVNGTI
541 DFLDAELNDIKVEIRNMIDGESGEKTRTLVKSQDERYIDKGNRTYTTWTPVNGTI
601 ALVLPTYSFYIKAKLEETITQARKSKGKMDSETLKPDPNFEESGYTFAIPRDYCN
601 ALVLPTYSFYIKAKLEETITQARKSKGKMDSETLKPDPNFEESGYTFAIPRDYCN
661 SDNNTFLLNFNEFIDRKTNNPSCNADLINRVLLDAGFTNELLVQNYWSKQKNIKG
661 SDNNTFLLNFNEFIDRKTNNPSCNADLINRVLLDAGFTNELLVQNYWSKQKNIKG
721 FVVTGGITRYVPKEAGENWQENPETTEDSYFKRSLNDNDNTVFTAPYFNKSGPGAYE
721 FVVTGGITRYVPKEAGENWQENPETTEDSYFKRSLNDNDNTVFTAPYFNKSGPGAYE
781 MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKNSDVMD
781 MVSKAVEIYIOGKLLKPAVVGIKIDVNSWIENFTKTSIRDPGAGVCDCKNSDVMD
841 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNISVIAFNKSYDYQSVCEPGA
841 LDDGGFLLMANHDDYTNQIGRFGEIDPSLMRHLVNISVIAFNKSYDYQSVCEPGA
901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLSLTFPRLLLEAVEMEDDDFTASL
901 GAGHSAYVPSVADILQIGWATAAAWSILOQFLSLTFPRLLLEAVEMEDDDFTASL
961 SCITEQTYFFDNDKSGFSGVLDGNCNRSIFHGEKLMNTNLIIFMVESKGTGCPDTR
961 SCITEQTYFFDNDKSGFSGVLDGNCNRSIFHGEKLMNTNLIIFMVESKGTGCPDTR
1021 QAEQTSQDGNPDMVKQPRYKRGPDVCFDNNVLEDDYTDGCGVS 1063
1021 QAEQTSQDGNPDMVKQPRYKRGPDVCFDNNVLEDDYTDGCGVS 1063

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RESULT 9

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US-10-090-827-9

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; Sequence 9, Application US/10090827

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```

; Publication No. US20030073132A1

```

```

; GENERAL INFORMATION:

```

```

; APPLICANT: Warner-Lambert

```

```

; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 subu

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```

; FILE REFERENCE: 179

```

```

; CURRENT APPLICATION NUMBER: US/10/090,827

```

```

; PRIOR FILING DATE: 2002-03-06

```

```

; PRIOR APPLICATION NUMBER: US/09/397,549

```

```

; PRIOR FILING DATE: 1999-09-16

```

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; NUMBER OF SEQ ID NOS: 21

```

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; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 9

```

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; LENGTH: 1069

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; TYPE: PRT

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; ORGANISM: Sus scrofa

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US-10-090-827-9

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Query Match 98.8%; Score 5532; DB 15; Length 1069;

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Best Local Similarity 98.7%; Pred. No. 0;

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Matches 1049; Conservative 6; Mismatches 8; Indels 0; Gai

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Qy 1 MAAGCLALTLTLFQSLILIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQL

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Db 1 MAAGCLALTLTLFQSLILIGSSSEPPPSAVTIKSWDKMQEDLVTLAKTASGVNQL

```

```

Qy 61 YEKYQDLYTVEPNARQLVEAARDIEKLSNRKALVSLALEAEKVAQAQHWEDF

```

```

Db 61 YEKYQDLYTVEPNARQLVEAARDIEKLSNRKALVSLALEAEKVAQAQHWEDF

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NAKDDLDPEKNDSEPGSORIKPFIEDANFGRQISYQAAVHIPTDIEGSTIVL 180
NAKDDLDPEKNDSEPGSORIKPFIEDANFGRQISYQAAVHIPTDIEGSTIVL 180
NAKDDLDPEKNDSEPGSORIKPFIEDANFGRQISYQAAVHIPTDIEGSTIVL 180
TSALDEVFKKNNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTNPKILDYDVR 240
TSALDEVFKKNNREEDPSLLWQVFGSATGLARYYPASPWVDSNRTNPKILDYDVR 240
QGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVAFSNSAQD 300
QGAASPKDMLILVDVSGSVGLTKLIRTSVSEMLETLSDDDFVNVAFSNSAQD 300
HLVQANVRNKKVLXDAVNNITAKGITDYKGFSPAFEQLLNLYNVRANCKIIML 360
HLVQANVRNKKVLXDAVNNITAKGITDYKGFSPAFEQLLNLYNVRANCKIIML 360
EERAQEI FNKNKOKKRVFRFVSQOHNYERGP IOWMACENKGYVIEIPSIGAIR 420
EERAQEI FNKNKOKKRVFRFVSQOHNYERGP IOWMACENKGYVIEIPSIGAIR 420
YLDVLRGPMVLGAKAKOVQWNTVLDALGLVITGLTPVFNITQGFENKTNLK 480
YLDVLRGPMVLGAKAKOVQWNTVLDALGLVITGLTPVFNITQGFENKTNLK 480
GVMGVDVSLIEDIKRLTPRTLCPNGYYPFAIDPNGVYLLHPNLOPKNPKSQBPVTL 540
GVMGVDVSLIEDIKRLTPRTLCPNGYYPFAIDPNGVYLLHPNLOPKNPKSQBPVTL 540
ELENDIKVEIRNKMIDGSGSEKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDSL 600
ELENDIKVEIRNKMIDGSGSEKFTRTLKVSQDERYIDKGNRTYTWTPVNGTDSL 600
TYSYFYIIKAKLEETITQARKKGMKDSITLKPDPNEESGYTFIAPRDYCNDLKI 660
TYSYFYIIKAKLEETITQARKKGMKDSITLKPDPNEESGYTFIAPRDYCNDLKI 660
TEFLNLFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720
TEFLNLFNEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQKNIKGVKAR 720
OGGITRVPYKBAGENQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPGAYESGI 780
OGGITRVPYKBAGENQENPETYEDSFYKSLDNDNVYFTAPYFNKSGPGAYESGI 780
AVEIYIYQGLLKPAVVGIIKDVSNIENFTKTSIRDP CAGPVCDCRNSDVMDCVI 840
AVEIYIYQGLLKPAVVGIIKDVSNIENFTKTSIRDP CAGPVCDCRNSDVMDCVI 840
3FLLMANHDDYTNQIGRFEGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
3FLLMANHDDYTNQIGRFEGEIDPSLMRHLVNI SVYAFNKSVDYQSVCEPGAAPKQ 900
RSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLAEVEMDDDFTLASLSKQ 960
RSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLAEVEMDDDFTLASLSKQ 960
EQTOYFPDNDKSPSGVLDQNCNSRI PHGEKMLNTLLIFIMVESKGTCPDCTRLLI 1020
EQTOYFPDNDKSPSGVLDQNCNSRI PHGEKMLNTLLIFIMVESKGTCPDCTRLLI 1020
TSDGPNPCDMVKQPYRKRGPDVCFDNNVLEDTDCGGYS 1063
TSDGPNPCDMVKQPYRKRGPDVCFDNNVLEDTDCGGYS 1063

FLMANHDDVTNOLIGRFFGEIDPSLMRHLVNIISVYAFNKSYDYQSVCEPGAAPKQ 900
 FLMANHDDVTNOLIGRFFGEIDPSLMRHLVNIISVYAFNKSYDYQSVCEPGAAPKQ 900
 SAYVPSVADILQIGWATAAAMSILQOFLLSLTPPRLEAVEVEMEDDDFTASLSKQ 960
 SAYVPSIADILHIGWATAAAMSILQOFLLSLTPPRLEAVEVEMEDDDFTASLSKQ 960
 QTOYFFNDNDSKSFSGVLDGNCRSIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
 QTOYFFNDNDSKSFSGVLDGNCRSIFHGEKLMNTNLIFIMVESKGTCPDTRLLI 1020
 SDGNPCDMVKQPRYKGPVCFDNNVLEDYTDGCGVS 1063
 SDGPDPCDMVKQPRYKGPVCFDNNVLEDYTDGCGVS 1063

ication US/10375253
 S20040018510A1

ON: ALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
 ON: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

ON: METHODS
 SD9813DA
 ION NUMBER: US/10/375,253

ATE: 2003-02-27
 N NUMBER: 08/450,273

E: 1995-05-25

N NUMBER: 08/404,354

E: 1995-02-15

N NUMBER: 07/914,231

E: 1992-07-13

N NUMBER: 08/314,083

E: 1994-09-28

N NUMBER: 07/914,231

E: 1992-07-13

N NUMBER: 07/603,751

E: 1990-11-09

N NUMBER: 08/290,012

E: 1994-08-11

N NUMBER: 08/149,097

E: 1993-11-05

N NUMBER: 08/105,536

E: 1993-08-11

N NUMBER: 08/149,097

E: 1993-11-05

Application data removed - See File Wrapper or PALM.

NOS: 65

Q for Windows Version 4.0

urity 98.6%; Score 5523; DB 12; Length 1103;
 nservative 0; Mismatches 1; Indels 26; Gaps 2;

LLALTLTLFQSLIGPSEPPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60

LLALTLTLFQSLIGPSEPPPSAVTIKSWYDKMQEDLVTLAKTASGVNQLVDI 60

DLTYTEPNNAQLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDPASN 120

DLTYTEPNNAQLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDPASN 120

DLTYTEPNNAQLVIAARDIEKLLSNRSKALVSLALEAEKVQAAHQWREDPASN 120

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

ANAKDLDPKNDSEPGSQRIKPVFIEDANFGQISVQHAHVHIPTDIYEGSTIVL 180

181 NELNWTSSALDEYFKKONREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYI
 181 NELNWTSSALDEYFKKONREEDPSLLMQVFGSATGLARYYPASPWVDNSRTPNKIDLYI
 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLIRTSVSEMLETISDDDFVNVASFNS
 241 RPWYIQGAASPKDMLILVDVSGSVSGLTLKLIRTSVSEMLETISDDDFVNVASFNS
 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITYDKKGFSAFAPQLLNYNVSRANCKI
 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGITYDKKGFSAFAPQLLNYNVSRANCKI
 361 FTDGGEERAQEIIFNKYNKDKKVRVFRFVSGQNYERGPIONMACENKGYIYIIPSI
 361 FTDGGEERAQEIIFNKYNKDKKVRVFRFVSGQNYERGPIONMACENKGYIYIIPSI
 421 INTQBYLDVLGRPMVLGDKAKQVQNTNVLDALELGLVITGTLPVFNITGQFENKI
 421 INTQBYLDVLGRPMVLGDKAKQVQNTNVLDALELGLVITGTLPVFNITGQFENKI
 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNCGYVLLHPLNLPK-
 481 NOLILGVMGVDVSLIEDIKRLTPRFTLCPNGYIFAIDPNCGYVLLHPLNLPKIGVGI
 531 -----NPKSQBPVTILDFAELENDIKVEIRNKMIDGESGKTFRTLKVSQDI
 541 LKRRPNIQNPKSQBPVTILDFAELENDIKVEIRNKMIDGESGKTFRTLKVSQDI
 582 DKGNRTYTWTPVNGTDYSLALVLPYSPYIKAKLEETITQARSKKGKMKDSETLKI
 601 DKGNRTYTWTPVNGTDYSLALVLPYSPYIKAKLEETITQARSKKGKMKDSETLKI
 642 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPNSCNADLNRLVLLDA
 654 EESGYTFIAPRDYCNLDKISDNNTFLLNFEFIDRKTNNPNSCNADLNRLVLLDA
 702 ELVQNTWSKQKNIKGVKARFVVTDDGITRVYKPEAGENQENPETYEDSFYKRSLDI
 714 ELVQNTWSKQKNIKGVKARFVVTDDGITRVYKPEAGENQENPETYEDSFYKRSLDI
 762 VTTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTS
 774 VTTAPYFNKSGPGAYESGIMVSKAVEIYIQGKLLKPAVVGIKIDVNSWIENFTKTS
 822 CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI
 834 CAGPVCDCKRNSDVMDCVILDDGGFLMANHDDYTNOIGRFFGEIDPSLMRHLVNI
 882 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSL
 894 FNKSYDYQSVCEPGAAPKQAGHRSAYVPSVADILQIGWATAAAMSILQOFLLSL
 942 LLEAVEVEMEDDDFTASLSKOSCTEQYFDFDNDKSFSGVLDGNCNSRIFHGEKLM
 954 LLEAVEVEMEDDDFTASLSKOSCTEQYFDFDNDKSFSGVLDGNCNSRIFHGEKLM
 1002 IFIMVESKGTCPDTRLLIQAESQTSQPNPCDMVKQPRYKGPVCFDNNVLEDYTI
 1014 IFIMVESKGTCPDTRLLIQAESQTSQPNPCDMVKQPRYKGPVCFDNNVLEDYTI
 1062 VS 1063
 1074 VS 1075

RESULT 12

US-10-375-253-51

; Sequence 51, Application US/10375253

; Publication No. US20040018510A1

; GENERAL INFORMATION:

; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES

; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND

; TITLE OF INVENTION: METHODS

SD9813DA
ION NUMBER: US/10/375,253
DATE: 2003-02-27
N NUMBER: 08/450,273
E: 1995-05-25
N NUMBER: 08/404,354
E: 1995-02-15
N NUMBER: 07/914,231
E: 1992-07-13
N NUMBER: 08/314,083
E: 1994-09-28
N NUMBER: 07/914,231
E: 1992-07-13
N NUMBER: 07/603,751
E: 1990-11-09
N NUMBER: 08/290,012
E: 1994-08-11
N NUMBER: 08/149,097
E: 1993-11-05
N NUMBER: 08/105,536
E: 1993-08-11
N NUMBER: 08/149,097
E: 1993-11-05

Application data removed - See File Wrapper or PALM.
NOS: 65
3Q for Windows Version 4.0

98.3%; Score 5503; DB 12; Length 1079;
arity 98.8%; Pred. No. 0;
onservative 0; Mismatches 1; Indels 12; Gaps 2;

CLALATLTLFQSLIGSSSEPPSPSAVTKSWDKQEDLVTLAKTASGVNQLVDI 60
CLALATLTLFQSLIGSSSEPPSPSAVTKSWDKQEDLVTLAKTASGVNQLVDI 60
QDLVTPPNARQVETAAEDIEKLNRSKALVSLALEAKVQAAHQRWEDFASN 120
QDLVTPPNARQVETAAEDIEKLNRSKALVSLALEAKVQAAHQRWEDFASN 120
YNAKDDLDPKNDSEPSQRIKPVFIEDANFGRQISYCHAAVHIPTDIYEGSTIVL 180
YNAKDDLDPKNDSEPSQRIKPVFIEDANFGRQISYCHAAVHIPTDIYEGSTIVL 180
WTSALDEVFKQREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
WTSALDEVFKQREEDPSLLWQVFGSATGLARYYPASPWDNSRTPNKIDLYDVR 240
IQGAASPKDMLILDVSGSVGLTKLIRTSVSEMLETSLDDDFNVASFNNAQD 300
IQGAASPKDMLILDVSGSVGLTKLIRTSVSEMLETSLDDDFNVASFNNAQD 300
QHLVQANVRNKKVLDKAVNNITAKGITDYKGFSAFEQLLNYSRANCNKIIML 360
QHLVQANVRNKKVLDKAVNNITAKGITDYKGFSAFEQLLNYSRANCNKIIML 360
GEERAQEIFNKNKKVRFPSVQGHYERGPQWACENKGYVEIPIGAI 420
GEERAQEIFNKNKKVRFPSVQGHYERGPQWACENKGYVEIPIGAI 420
EYLDVGLRPMVLADKAKQVQWNTVLDALGLVITGLPVFNITGOFENKTNLK 480
EYLDVGLRPMVLADKAKQVQWNTVLDALGLVITGLPVFNITGOFENKTNLK 480
LGVMGVDSLEDIKELTRFTLCPNGYFAIDPNNGYVLLHPNLPKSPQSVTL 540
LGVMGVDSLEDIKELTRFTLCPNGYFAIDPNNGYVLLHPNLPKSPQSVTL 540
AELENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGT 600

Db 536 DELDALENDIKVEIRNKMIDGESGEKTRTLVKSQDERYIDKGNRTYTWTPVNGT
QY 601 ALVLPITYSYIYKAKLEETITQARSKKGMKODSETLKPONFESGYTFIAPRDYCN
Db 596 ALVLPITYSYIYKAKLEETITQARY-----SETLKPONFESGYTFIAPRDYCN
QY 661 SONNTEFLNFNEFIDRKTTPNPNPCNADLINVLDDAGFTNELVQVWSKQKNIKG
Db 649 SONNTEFLNFNEFIDRKTTPNPNPCNADLINVLDDAGFTNELVQVWSKQKNIKG
QY 721 FVVDGCIITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAFYFNKSGPGAY
Db 709 FVVDGCIITRVYPKEAGENQENPETYEDSFYKRSILDNDNYVFTAFYFNKSGPGAY
QY 781 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVM
Db 769 MYSKAVEIYIQGKLLKPAVVGKIDVNSWIENFTKTSIRDPCAGPVCDCKRNSDVM
QY 841 LDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAPNKS YDYOSVCEPGA
Db 829 LDGGFLLMANHDDYTNQIGRPFGEIDPSIMRHLVNI SVYAPNKS YDYOSVCEPGA
QY 901 GAGHRSAVPSVADILOIGWATAAAWSIIQQFLLSLTFPRLLLEAVEMEDDDFTAS
Db 889 GAGHRSAVPSVADILOIGWATAAAWSIIQQFLLSLTFPRLLLEAVEMEDDDFTAS
QY 961 SCITEQTQYFFDNDKSFSGVLDCGNCRI FHGEKLMNTNLIIFIMVESKGTCPCDT
Db 949 SCITEQTQYFFDNDKSFSGVLDCGNCRI FHGEKLMNTNLIIFIMVESKGTCPCDT
QY 1021 QAEQTSQDGNPCDMVKQPRYKGPDYCFDNNVLEDYTDCCGVS 1063
Db 1009 QAEQTSQDGNPCDMVKQPRYKGPDYCFDNNVLEDYTDCCGVS 1051

RESULT 13

US-10-375-253-20
; Sequence 20, Application US/10375253
; Publication No. US20040018510A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE BIOTECHNOLOGY/INDUSTRIAL ASSOCIATES
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: SD9813DA
; CURRENT APPLICATION NUMBER: US/10/375,253
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 08/450,273
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/404,354
; PRIOR FILING DATE: 1995-02-15
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 08/314,083
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/914,231
; PRIOR FILING DATE: 1992-07-13
; PRIOR APPLICATION NUMBER: 07/603,751
; PRIOR FILING DATE: 1990-11-09
; PRIOR APPLICATION NUMBER: 08/290,012
; PRIOR FILING DATE: 1994-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; PRIOR APPLICATION NUMBER: 08/105,536
; PRIOR FILING DATE: 1993-08-11
; PRIOR APPLICATION NUMBER: 08/149,097
; PRIOR FILING DATE: 1993-11-05
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1091
; TYPE: PRT

1
195-
C
B
M
ity 97.7%; Score 5472; DB 12; Length 1091;
naervative 0; Mismatches 0; Indels 32; Gaps 2;
XIALTLTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
XIALTLTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
XIALTLTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVNQLVDI 60
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DLTYVPPNARQLVEIAARDIEKLSNRKALVSLALEAEKVAQAHHQWREDPASN 120
NAKDDLPKNDSEPGSORIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
NAKDDLPKNDSEPGSORIKPVFIEDANFGQISYQHAHVHIPTDIYEGSTIVL 180
TSALDEVEKQNEEDPSLLWQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240
TSALDEVEKQNEEDPSLLWQVFGSATGLARYYPASPVVDNSRTPNKIDLYDVR 240
QGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 300
-GAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNSNAQD 284
JHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAPEQLLNNVNSRANCKIIML 360
JHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAPEQLLNNVNSRANCKIIML 344
HERRAQEIEFNKYNKDKKKVFRFVSQGHVYERGPQIOWMACEN----- 406
HERRAQEIEFNKYNKDKKKVFRFVSQGHVYERGPQIOWMACENKIDLYDVRPPWY 404
TYEIPSGAIRINTOEYLDVGRPMVLADGKAKQVQWTVNVLDALELGLVITGTL 464
TYEIPSGAIRINTOEYLDVGRPMVLADGKAKQVQWTVNVLDALELGLVITGTL 464
TGORENKNLKNQLILGVMGVDSLEDKLITPRTLCPNGYFFAIDNGVVLH 524
TGORENKNLKNQLILGVMGVDSLEDKLITPRTLCPNGYFFAIDNGVVLH 524
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WTPVNGTDYSALVLPITYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPFES 644
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APRDYCNLDKISDNNTEFLNPFIDRKTNNPNSCNADLNRVLLDAGFTNELV 704
APRDYCNLDKISDNNTEFLNPFIDRKTNNPNSCNADLNRVLLDAGFTNELV 704
KQKNIKGKARFVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNVFT 764
KQKNIKGKARFVVTGGITRVYPKEAGENQENPETYEDSFYKRSLDNDNVFT 764
KSGPGAYESGIMWKAIVYIQGLKLLPAVVGKIDVNSWIENFTKTSIRDPACG 824
KSGPGAYESGIMWKAIVYIQGLKLLPAVVGKIDVNSWIENFTKTSIRDPACG 824
XKNSDVMDCVILDDGGFLMANHDDYTNOIGRPFGEIDPSLRHLVNI SVYAFNK 884
XKNSDVMDCVILDDGGFLMANHDDYTNOIGRPFGEIDPSLRHLVNI SVYAFNK 884
JSVCEGAAPKQAGHRSAYVPSVADILQIGHWATAAAMSILQOFLLSITFPRLLE 944
JSVCEGAAPKQAGHRSAYVPSVADILQIGHWATAAAMSILQOFLLSITFPRLLE 944
TDDFTASLSKQSCITEQTQYFPDNDKSFSGVLDGCGNCSRIFFHGEKLMNTNFI 1004

Db 945 AVEMEDDDFTASLSKQSCITEQTQYFPDNDKSFSGVLDGCGNCSRIFFHGEKLMNTN
Qy 1005 MVESKGTCTCDTRLLIQASQTSQGNPCDMVKQPRYRKGPDPVCFDNNVLEDDYDQCG
Db 1005 MVESKGTCTCDTRLLIQASQTSQGNPCDMVKQPRYRKGPDPVCFDNNVLEDDYDQCG
RESULT 14
US-10-090-827-14
; Sequence 14, Application US/10090827
; Publication No. US20030073132A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert
; TITLE OF INVENTION: Method for the screening of alpha 2 delta-1 sub
; TITLE OF INVENTION: binding ligands
; FILE REFERENCE: 179
; CURRENT APPLICATION NUMBER: US/10/090,827
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US/09/397,549
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-090-827-14
Query Match 97.2%; Score 5443; DB 15; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1036; Conservative 0; Mismatches 0; Indels 0; G
Qy 1 MAAGCLLALTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVN
Db 1 MAAGCLLALTLFQSLILGPSSEPPPSAVTIKSWDKMOEDLVTLAKTASGVN
Qy 61 YEKYQDLYTVPEPNARQLVEIAARDIEKLSNRKALVSLALEAEKVAQAHHQWRED
Db 61 YEKYQDLYTVPEPNARQLVEIAARDIEKLSNRKALVSLALEAEKVAQAHHQWRED
Qy 121 EYVYNAKDDLPKNDSEPGSORIKPVFIEDANFGQISYQHAHVHIPTDIYEGS
Db 121 EYVYNAKDDLPKNDSEPGSORIKPVFIEDANFGQISYQHAHVHIPTDIYEGS
Qy 181 NELNWTSLDDEVEKQNEEDPSLLWQVFGSATGLARYYPASPVVDNSRTPNKIDLY
Db 181 NELNWTSLDDEVEKQNEEDPSLLWQVFGSATGLARYYPASPVVDNSRTPNKIDLY
Qy 241 RPYWIOGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNS
Db 241 RPYWIOGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETLSDDDFVNVASFNS
Qy 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAPEQLLNNVNSRANCKI
Db 301 VSCFQHLVQANVRNKKVLKDAVNNITAKGIDTYKKGFSFAPEQLLNNVNSRANCKI
Qy 361 FTDGGEERAQEIFNKNYKDKKVRFRFVSQGHVYERGPQIOWMACENKGYIYIIPSI
Db 361 FTDGGEERAQEIFNKNYKDKKVRFRFVSQGHVYERGPQIOWMACENKGYIYIIPSI
Qy 421 INTQEYLDVGRPMVLADGKAKQVQWTVNVLDALELGLVITGTLPVFNITGQFENKI
Db 421 INTQEYLDVGRPMVLADGKAKQVQWTVNVLDALELGLVITGTLPVFNITGQFENKI
Qy 481 NQLILGVMGVDSLEDKLITPRTLCPNGYFFAIDNGVYLLHLPNLPKNPKSQE
Db 481 NQLILGVMGVDSLEDKLITPRTLCPNGYFFAIDNGVYLLHLPNLPKNPKSQE
Qy 541 DFLDAELENDIKVEIRNKMIDGESGKFTLVKQSDERYIDKGNRTYTWTPVNGTI
Db 541 DFLDAELENDIKVEIRNKMIDGESGKFTLVKQSDERYIDKGNRTYTWTPVNGTI
Qy 601 ALVLPITYSFYIYKAKLEETITQARSKKGMKDSSETLKPDPFESGYTFTAPRDYCN

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In search, using sw model

February 20, 2004, 16:51:31 ; Search time 38.1957 Seconds
 (without alignments)
 7181.696 Million cell updates/sec

10-090-827-15

MAAGCLLALTTLFQSLIG.....PDVCFDNNVLEDYDCGVS 1063

SUM62

top 10.0 , Gapext 0.5

1525 seqs, 258052604 residues

5 satisfying chosen parameters: 830525

hch: 0

hch: 2000000000

Minimum Match 0%

Maximum Match 100%

Using first 45 summaries

TREMBL-23:*

sp_archaea:*

sp_bacteria:*

sp_fungi:*

sp_human:*

sp_invertebrate:*

sp_mammal:*

sp_mhc:*

sp_organelle:*

sp_phase:*

sp_plant:*

sp_rodent:*

sp_virus:*

sp_vertebrate:*

sp_unclassified:*

sp_virus:*

sp_bacteriopl:*

sp_archaeap:*

the number of results predicted by chance to have a
 . than or equal to the score of the result being printed,
 d by analysis of the total score distribution.

SUMMARIES

ID	Length	DB	Description
4	1110	Q9UIU0	Q9uiuo homo sapien
8	1091	6	O77773 aus acrofa
3	1091	11	Q9ERS3
2	1084	11	Q8CFG7
1	1103	11	Q08532
6	1079	11	Q8VHS9
3	745	4	Q9UDQ3
4	1150	4	Q9NY47
9	1143	4	Q9NY48
9	1156	11	Q9EQG2
8	1157	11	Q8CFG6
8	1148	11	Q8C8R8
7	1145	4	Q9Y268
5	1098	11	Q8CHE9
4	1084	11	Q920H6
3	1076	4	Q9UEW0

ID	Length	DB	Description
17	2814	50.3	975
18	1124.5	20.1	1085
19	1119.5	20.0	1091
20	1114.5	19.9	1091
21	1112	19.9	1120
22	1045.5	18.7	997
23	1009	18.0	1218
24	1000.5	17.9	1170
25	937	16.7	2190
26	891.5	15.9	1255
27	882.5	15.8	1120
28	875	15.6	170
29	738.5	13.2	519
30	658	11.8	317
31	580.5	10.4	1148
32	541.5	9.7	842
33	526.5	9.4	394
34	514.5	9.2	104
35	506	9.0	100
36	498.5	8.9	121
37	482	8.6	98
38	465	8.3	97
39	462.5	8.3	223
40	459	8.2	100
41	402	7.2	77
42	344	6.1	1185
43	237.5	4.2	978
44	227	4.1	43
45	223	4.0	1449

ALIGNMENTS

RESULT 1

Q9UIU0

ID Q9UIU0 PRELIMINARY; PRT; 1110 AA.

AC Q9UIU0;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Dihydropyridine receptor alpha 2 subunit.

GN CACNA2D1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20005942; PubMed=10534405;

RT Schleithoff L., Mehrke G., Reutlinger B., Lehmann-Horn F.;

RT "Genomic structure and functional expression of a human alpha (2) /

RT calcium channel subunit gene (CACNA2).";

RL Genomics 61:201-209(1999).

DR EMBL; AF083854; AAF03259.1; JOINED.

DR EMBL; AF083817; AAF03259.1; JOINED.

DR EMBL; AF083818; AAF03259.1; JOINED.

DR EMBL; AF083819; AAF03259.1; JOINED.

DR EMBL; AF083820; AAF03259.1; JOINED.

DR EMBL; AF083821; AAF03259.1; JOINED.

DR EMBL; AF083822; AAF03259.1; JOINED.

DR EMBL; AF083823; AAF03259.1; JOINED.

DR EMBL; AF083824; AAF03259.1; JOINED.

DR EMBL; AF083825; AAF03259.1; JOINED.

DR EMBL; AF083826; AAF03259.1; JOINED.

DR EMBL; AF083827; AAF03259.1; JOINED.

DR EMBL; AF083828; AAF03259.1; JOINED.

DR EMBL; AF083829; AAF03259.1; JOINED.

DR EMBL; AF083830; AAF03259.1; JOINED.

DR EMBL; AF083831; AAF03259.1; JOINED.

DR EMBL; AF083832; AAF03259.1; JOINED.

DR EMBL; AF083833; AAF03259.1; JOINED.

DR EMBL; AF083834; AAF03259.1; JOINED.


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mservative 6; Mismatches 8; Indels 0; Gaps 0;
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|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 120
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 180
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 180
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 240
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 240
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 300
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 300
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 360
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 360
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 420
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 420
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|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 540
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 540
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|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 780
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 840
|||||LTLT|FQSL|LIGPSS|EPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QL|VDI 840
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RESULT 3
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ID Q9ERS3 PRELIMINARY; PRT; 1091 AA.
AC Q9ERS3;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Voltage-gated calcium channel alpha2/delta-1 subunit.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rati
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Superior cervical ganglion;
RA Lin Y., Lipscombe D.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP286488; AAG28164.1; -
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; WVF_A.
DR Pfam; PF02743; Cache; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWA; 1.
FT VARIANT 209 212 GSAT -> AADR.
FT VARIANT 338 338 S -> T.
FT VARIANT 599 600 SL -> RY.
FT VARIANT 869 869 S -> R.
SQ SEQUENCE 1091 AA; 123467 MW; C155088971628E19 CRC64;

Query Match 97.3%; Score 5447; DB 11; Length 1091;
Best Local Similarity 96.5%; Pred. NO. 0;
Matches 1026; Conservative 22; Mismatches 15; Indels 0; G

QY 1 MAAGCLLALTLTLFQSLIGPSSSEPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QI
DB 1 MAAGCLLALTLTLFQSLIGPSSSEPPS|AVTT|KSW|DVK|MQED|LVT|LAKT|AS|GN|QI
QY 61 YKYQDLYTVPEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDI
DB 61 YKYQDLYTVPEPNNAQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRREDI
QY 121 EVVYNAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGS'
DB 121 EVVYNAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGS'
QY 121 EVVYNAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGS'
DB 121 EVVYNAKDDLPKNDSEPGSORIKPVFIEDANFGROI SYQHAAVHIPTDIYEGS'
QY 181 NELNWT|SALD|VFKK|NR|EED|PS|LL|WQV|FSG|AT|GL|ARY|YPAS|PW|D|NS|RT|PNK|IDL|YI
DB 181 NELNWT|SALD|VFKK|NR|EED|PS|LL|WQV|FSG|AT|GL|ARY|YPAS|PW|D|NS|RT|PNK|IDL|YI
QY 241 RPY|Y|OGA|ASP|KDM|L|IL|VDV|SGV|SGL|TL|KL|RT|SV|SEM|ET|L|S|DD|D|FVN|VAS|FNSI
DB 241 RPY|Y|OGA|ASP|KDM|L|IL|VDV|SGV|SGL|TL|KL|RT|SV|SEM|ET|L|S|DD|D|FVN|VAS|FNSI
QY 301 VSCFQ|HL|VQ|AN|VR|NK|V|K|AD|V|NN|IT|AK|GI|TDY|K|KG|FS|FA|FQ|LL|N|Y|N|S|R|AN|CN|KI
DB 301 VSCFQ|HL|VQ|AN|VR|NK|V|K|AD|V|NN|IT|AK|GI|TDY|K|KG|FS|FA|FQ|LL|N|Y|N|S|R|AN|CN|KI
QY 361 FTDGGE|RAQ|E|F|NK|Y|K|D|K|V|VR|F|S|VG|Q|H|N|Y|E|RG|P|I|Q|W|A|C|E|N|K|G|Y|Y|E|I|P|S|I|C
DB 361 FTDGGE|RAQ|E|F|NK|Y|K|D|K|V|VR|F|S|VG|Q|H|N|Y|E|RG|P|I|Q|W|A|C|E|N|K|G|Y|Y|E|I|P|S|I|C
QY 421 INTQ|EY|LDV|LGR|PMV|LAGD|K|AK|Q|VQ|W|TNV|YL|DA|LE|GLV|IT|GT|LPV|FN|IT|GQ|F|EN|KI
DB 421 INTQ|EY|LDV|LGR|PMV|LAGD|K|AK|Q|VQ|W|TNV|YL|DA|LE|GLV|IT|GT|LPV|FN|IT|GQ|F|EN|KI
QY 481 NQ|L|L|G|V|M|G|V|D|V|S|L|E|D|I|K|E|L|T|P|R|F|L|C|P|N|G|Y|Y|F|A|D|P|N|G|Y|V|L|L|H|P|N|L|Q|P|N|K|S|Q|E|I
DB 481 NQ|L|L|G|V|M|G|V|D|V|S|L|E|D|I|K|E|L|T|P|R|F|L|C|P|N|G|Y|Y|F|A|D|P|N|G|Y|V|L|L|H|P|N|L|Q|P|N|K|S|Q|E|I
QY 541 DF|L|D|A|E|L|E|N|D|I|K|V|E|I|R|N|K|N|I|D|G|E|S|G|E|K|T|P|L|V|K|S|Q|D|E|R|Y|I|D|K|G|N|R|T|Y|T|W|T|P|V|N|G|T|I

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181 NELNWTSDALDEVFKQNRBEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDL
 181 NELNWTSDALDEVFKQNRBEDPSLLQVFGSATGLARYYPASVPWVDSNRTPNKIDL
 241 RPYITQGAASPKOMLILVDVSGSVGLTLKLRISVSSEMLTSLDDDDFVNVSFNE
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 301 VSCFOHLVQANVRNKKVLKDAVNITAKGITDYKKGSFAESOLLNYSRANCN
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 361 FTDGGEERAQBIENKYNKKVRVFRFVSGQHNRYERGERPIQWACENKGYEIPESJ
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 421 INTQBYLDVGRPMVLADGKAKQVQWNTVYLDALGLVITGTLFVFNVTQSENI
 421 INTQBYLDVGRPMVLADGKAKQVQWNTVYLDALGLVITGTLFVFNVTQSENI
 481 NQILILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNGYVLLHNPLOPKPKSOI
 481 NQILILGVMGVDSLEDIKRLTPRFTLCPNGYVFAIDPNGYVLLHNPLOPKPKSOI
 541 DFLDALENDIKVEIRNKKMIDGESSEKTFRTLVKSQDERYIDKGNRTYTTPVNGI
 541 DFLDALENDIKVEIRNKKMIDGESSEKTFRTLVKSQDERYIDKGNRTYTTPVNGI
 601 ALVLPYTSFYIKAKLESTIIOAKSKKGMKOSLTKPDNFEESGYTFIAPRDYCT
 601 ALVLPYTSFYIKAKLESTIIOAKSKKGMKOSLTKPDNFEESGYTFIAPRDYCT
 661 SDNTEFLNNEFTDRKTPNNPSCNADLINRVLDDAGFTNELVQYWSKOKNIK
 661 SDNTEFLNNEFTDRKTPNNPSCNADLINRVLDDAGFTNELVQYWSKOKNIK
 721 FVVDGGITRVYPKEAGENWOENPETEYDSFYKSLDNDNYVFTAPYFNKSGPGAI
 721 FVVDGGITRVYPKEAGENWOENPETEYDSFYKSLDNDNYVFTAPYFNKSGPGAI
 781 MYSKAVELIYIOGKLLKPAVIGIKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDVN
 781 MYSKAVELIYIOGKLLKPAVIGIKIDVNSWIENFTKTSIRDPGAPVCDCKRNSDVN
 841 LDDGGFLIMANHDDVTNOIGRFFGEIDPISLMRHLVNSVYAFNKSVDYQSVCEPGP
 841 LDDGGFLIMANHDDVTNOIGRFFGEIDPISLMRHLVNSVYAFNKSVDYQSVCEPGP
 901 CAGHSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFPRLLAEVEMEDDDFTAE
 901 CAGHSAYVPSVADILQIGMWATAAAMSILQOFLLSLTFPRLLAEVEMEDDDFTAE
 961 SCITEQTYFFDNDKSPSGVLDGNCNSRIEFGKLMNTNLIIFIMVBSKGTCPDI
 961 SCITEQTYFFDNDKSPSGVLDGNCNSRIEFGKLMNTNLIIFIMVBSKGTCPDI
 1021 QAEQTSQGNPCDMVKOPRYKGPVCFDNNVLEDTDCGGVS 1063
 1021 QAEQTSQGNPCDMVKOPRYKGPVCFDNNVLEDTDCGGVS 1063
 1014 QAEQTSQGNPCDMVKOPRYKGPVCFDNNVLEDTDCGGVS 1056
 1014 QAEQTSQGNPCDMVKOPRYKGPVCFDNNVLEDTDCGGVS 1056
 RESULT 5
 O08532
 ID O08532 PRELIMINARY; PRT: 1103 AA.
 AC O08532; O08533; O08534; O08535; O08536;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta
 subunits precursor.
 GN CACNA2D1 OR CACNA2.
 OS Mus musculus (Mouse).

RELIMINARY; PRT: 1084 AA.

Tremblrel. 23, Created
 Tremblrel. 23, Last sequence update)
 Tremblrel. 23, Last annotation update)
 el alpha-2 delta-1 subunit isoform e.
 icus (Rat).
 tazioa; Chordata; Craniata; Vertebrata; Euteleostomi;
 heria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 116;

N.A.
 e-Dawley; TISSUE=Heart atrium;
 st P.M.;
 gicus voltage-dependent calcium channel alpha-2 delta-1
 rm e (CACNA2D1e) mRNA."
 B-2002) to the EMBL/GenBank/DBJ databases.
 6; AA014652.1; --
 84 AA; 122711 MW; 6269592D8F1657FF CRC64;

96.2%; Score 5386.5; DB 11; Length 1084;

arity 95.7%; Pred. No. 0;

conservative 23; Mismatches 16; Indels 7; Gaps 1;

CLLALTLTFLQSLIGPSSPPSPSAVTKSWDKMQEDLVTLAKTAGVGNQLVDI 60

CLLALTLTFLQSLIGPSSPPSPSAVTKSWDKMQEDLVTLAKTAGVGNQLVDI 60

QDLVTEPNNAQRLVEIAARDIEKLLNSRKALVSLALAEKVAQAHOHREDPASN 120

QDLVTEPNNAQRLVEIAARDIEKLLNSRKALVSLALAEKVAQAHOHREDPASN 120

YNAKDDLDPEKNDSEPGSQRTKPFVIEDANFGROI SYQHAHVHIPTDIYEGSTIVL 180

YNAKDDLDPEKNDSEPGSQRTKPFVIEDANFGROI SYQHAHVHIPTDIYEGSTIVL 180

azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mollusca; Nemertea; Platyhelminthes; Sciarognathi; Muriidae; Murinae; Mus.
190;

N.A.

514; PubMed=8955374;

Hofmann F.;

7:331-337(1996).

CALCIUM CHANNEL PROTEIN WHICH PLAYS AN IMPORTANT ROLE IN
A-CONTRACTION COUPLING.

THE L-TYPE CALCIUM CHANNEL IS COMPOSED OF FOUR SUBUNITS:

ALPHA-2, BETA AND GAMMA.

ALPHA-2 AND DELTA FORM HETERODIMERS THAT ARE DISULFIDE-

BR LOCATED: INTEGRAL MEMBRANE PROTEIN.

VE PRODUCTS: 5 ISOFORMS; 2A (SHOWN HERE), 2B, 2C, 2D AND

3CIFICITY: ISOFORM 2A IS EXPRESSED

IN SKELETAL MUSCLE AND

IS EXPRESSED IN BRAIN, 2C IS EXPRESSED IN HEART, 2D IS

IN HEART AND SMOOTH MUSCLE, AND 2E IS EXPRESSED IN

SCLE. ALL FIVE ISOFORMS ARE EXPRESSED IN THE

JULAR SYSTEM.

1-2 AND DELTA SUBUNITS ARE PROTEOLYTICALLY PROCESSED FROM

OR FORM.

(; TO OTHERS SPECIES ALPHA-2 SUBUNIT.

AAB50139.1; -

AAB50140.1; -

AAB50138.1; -

AAB50141.1; -

AAB50142.1; -

; Caccna2d1.

04010; Cache.

02035; VWF_A.

; Cache; 1.

; vwa; 1.

; VWA; 1.

; VWA; 1.

; VWA; 1.

; VWA; 1.

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; VWA; 1.

; VWA; 1.

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QY 1063
DB 1075

PRELIMINARY; PRT; 1079 AA.
(TREMBLrel. 20, Created)
(TREMBLrel. 20, Last sequence update)
(TREMBLrel. 21, Last annotation update)
um channel alpha2/delta subunit.
icus (Rat).
kazo; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1116;

1 N.A.
; TISSUE=Heart;
730; PubMed=11604404;
gashima M., Tsutsuura M., Kobayashi T., Seki S.,
rio Y., Tohee N.;
functional splice variant of L-type calcium channel
from rat heart";
1. 276:47163-47170(2001).
12; AAL47093.1; -.
1004010; Cache.
1002035; VWF A.
1; Cache; 1.
1; vwa; 1.
179 AA; 122172 MW; DC4A3641195B546C CRC64;

arity 95.6%; Score 5351; DB 11; Length 1079;
onservative 22; Mismatches 16; Indels 12; Gaps 2;

KLLALTLTFLQSLIGPSEPPFPSPAVTKSWVDKMQEDLVLTAKTASGVNQLVDI 60
KLLALTLTFLQSLIGPSEPPFPSPAVTKSWVDKMQEDLVLTAKTASGVNQLVDI 60
QDLYTVENNAQRLVEIARDIEKLLNSKALVSLAEAKVQAHHQWREDFASN 120
QDLYTVENNAQRLVEIARDIEKLLNSKALVSLAEAKVQAHHQWREDFASN 120
YNAKDDLPKNDSPGSRQIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
YNAKDDLPKNDSPGSRQIKPVFIEDANFGRQISYQHAHVHPTDIYEGSTIVL 180
WTSALDEVFKKREDDPSLLMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
WTSALDEVFKKREDDPSLLMQVFGSATGLARYYPASPWVNSRTPNKIDLYDVR 240
TQGAASPKDMLILVDVSGVSGSLTKLRTSVSEMLETLSDDDFVNVAFSNQAQ 300
TQGAASPKDMLILVDVSGVSGSLTKLRTSVSEMLETLSDDDFVNVAFSNQAQ 300
QHLVQANVRNKKVLKDAVNNITAKGITDYKGFSPAFQQLNLYNVRANCKNIML 360
QHLVQANVRNKKVLKDAVNNITAKGITDYKGFSPAFQQLNLYNVRANCKNIML 360
XGEERAQEI PNKYNKDKVRFRFVSQGNHYERGPIQWMAKNGYIYIPISGAIR 420
XGEERAQEI PNKYNKDKVRFRFVSQGNHYERGPIQWMAKNGYIYIPISGAIR 420
BYLDVLRGPMVLADKAKOVQWNTVYLDALGLVITGLPVFNITGQFENKTNLK 480
BYLDVLRGPMVLADKAKOVQWNTVYLDALGLVITGLPVFNITGQFENKTNLK 480
LGVMGVDVSLIEDIKLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPK-----
481 NQLLIGVMGVSVSLEDIKLTPRFTLCPNGYYFAIDPNGYVLLHPNLQPK-----
541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKQSDERYIDKGNRTYTWTPVNG
536 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKQSDERYIDKGNRTYTWTPVNG
601 ALVLTYSFYIYKAKLETTIQAARKKMKDSETLKPDNPFESGYTFIAPRDYCI
596 ALVLTYSFYIYKAKLETTIQAARKKMKDSETLKPDNPFESGYTFIAPRDYCI
661 SNNTFEFLNFEFFIDRKTNNPNSCNADLINEVLVDAGFTNELVONYYSKQNKIK
649 SNNTFEFLNFEFFIDRKTNNPNSCNTDLINKILLDAGFTNELVONYYSKQNKIK
721 FVVTDDGTRVYPKEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
709 FVVTDDGTRVYPKEAGENQWENPETYEDSFYKRSILDNDNYVFTAPYFNKSGPGA
781 MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCCKRNSDV
769 MYSKAVEIYIQGLKLPKPAVVGIKIDVNSWIENFTKTSIRDPKAGPVCCKRNSDV
841 LDDGGFLMANHDDVTNOIGRPFGEIDPSLMRHLVNIISYAFNKSVDYQSVCEPGI
829 LDDGGFLMANHDDVTNOIGRPFGEIDPSLMRHLVNIISYAFNKSVDYQSVCEPGI
901 GAGHSAYVPSVADILQIGWATAAASILQQLLSLTFPRLEAVEMEDDDFTAI
889 GAGHSAYVPSVADILQIGWATAAASILQQLLSLTFPRLEAVEMEDDDFTAI
961 SCITEQTQYFFDNDSKFSGLVDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPD
949 SCITEQTQYFFDNDSKFSGLVDCGNCRSRIFHGEKLMNTNLIFIMVESKGTCPD
1021 QAEQTSDDGNPCDMVKQPRYKGPVDFDNNVLEDYTDGCGVS 1063
1009 QAEQTSDDGNPCDMVKQPRYKGPVDFDNNVLEDYTDGCGVS 1051

RESULT 7
Q9UDQ3 PRELIMINARY; PRT; 745 AA.
AC Q9UDQ3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE WUGSC:H_DJ0560014.1 protein (fragment).
GN WUGSC:H_DJ0560014.1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=99063792; PubMed=9847074;
RA Sulston J.E., Waterston R.;
RT "Toward a complete human genome sequence.";
RL Genome Res. 8:1097-1108(1998).
RN [2]
RN SEQUENCE FROM N.A.
RX
RA Mead K., Bauer C.;
RT
RL
RN [3]
RN SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006145; AAD20938.1; -.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; VWF A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR PROSITE; PSS0234; VWF A; 1.

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1 1
AA; 84396 MW; BC07B53484B71EA4 CRC64;
68.3%; Score 3823; DB 4; Length 745;
urity 99.7%; Pred. No. 9.3e-232; Indels 0; Gaps 0;
nservative 1; Mismatches 1;
ANCNKIIMLFTDGGERAQEIFPNKYKDKKVRVFSVQGHNYRGPQIOMACEN 406
ANCNKIIMLFTDGGERAQEIFPNKYKDKKVRVFSVQGHNYRGPQIOMACEN 60
EIPSGAIRINTQBYLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGLPV 466
EIPSGAIRINTQBYLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGLPV 120
QPENKTNLKNOLILGVMGVDSLEDIKLTTPRTLCPNGYYPADIPNGVLLHPN 526
QPENKTNLKNOLILGVMGVDSLEDIKLTTPRTLCPNGYYPADIPNGVLLHPN 180
PKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNR 586
PKSQEPVTLDFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNR 240
PVNGTDYSLALVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGY 646
PVNGTDYSLALVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGY 300
RDYCNLDKISDNNTFEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVN 706
RDYCNLDKISDNNTFEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVN 360
KNIKGVKARFVVDGGITRVVPKEAGENQWNPETYEDSFYKRSLDNDNYFTAP 766
KNIKGVKARFVVDGGITRVVPKEAGENQWNPETYEDSFYKRSLDNDNYFTAP 420
GPGAYESGIMYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTKTSIRDPAGPV 826
GPGAYESGIMYSKAVEIYIOGKLLKPAVVGIKIDVNSWIENTFTKTSIRDPAGPV 480
NSDVMDCVILDDGGFLMANHDDYTNQIGRFEGEIDPSLMRHLVNIYSVAFNKS 886
NSDVMDCVILDDGGFLMANHDDYTNQIGRFEGEIDPSLMRHLVNIYSVAFNKS 540
CEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLSLTPRLEAV 946
CEPGAAPKQAGHRSAYVPSVADILQIGWATAAAWSILOQFLSLTPRLEAV 600
DPTASLSKQSCITQTQYFFDNDSKPSGVLDGCGNCSRIFHGEKLMNTNLFIMV 1006
DPTASLSKQSCITQTQYFFDNDSKPSGVLDGCGNCSRIFHGEKLMNTNLFIMV 660
CPCDTRLLIOAEQTSIDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
CPCDTRLLIOAEQTSIDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 717

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ELIMINARY; PRT; 1150 AA.

REMBLrel. 15, Created)

REMBLrel. 15, Last sequence update)

REMBLrel. 23, Last annotation update)

1, alpha 2/delta subunit 2.

Human).

azoa; Chordata; Craniata; Vertebrata; Euteleostomi;

eria; Primates; Catarrhini; Hominidae; Homo.

6;

N.A.

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RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Hobom M., Dai S., Marais E., Lacinova L.;
RT "Neuronal distribution and functional characterization of the cal-
channel alpha2delta-2 subunit."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ251368; CAB86193.1; -
DR InterPro; IPR004010; Cache.
DR InterPro; IPR002035; WVF.A.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00327; vwa; 1.
DR PROSITE; PS0234; WVF.A; 1.
SQ SEQUENCE 1150 AA; 129876 MW; 37B75F687AFB573C CRC64;

Query Match 54.4%; Score 3045; DB 4; Length 1150;
Best Local Similarity 54.6%; Pred. No. 1.4e-182;
Matches 588; Conservative 172; Mismatches 286; Indels 30; G;

QY 7 LALTTLFQSLLLIGPSSEPFPSAVTIKSWDKMQEDLVTLAKTASGVNQLVDIYE
DB 44 LMLLLPLLELLAAGASAYSFPQOHTMQHWARKLEQVGVGVMRIFGVQOOLREIYK
QY 67 LYTVEPNNAQQLVETIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRWEDFASNEV
DB 104 LPRVQENEPQKLVKAGVAGDIESLLDRKQALKLADAAENFQKAHRWQDNKEEDI
QY 127 AKDDL--DPEKNDSPGSG--RIKPVFIEDANFGROIYSYQHAHVHPTDIYEGST
DB 164 AKADAEELDPESDEVERGSKASTLRIDPFIEDPNFKKNVSYAAVQIPTDIYKSGT
QY 182 ELNWTLSALDEVFKQNEEDPSLLWQVFGSATGLARYYPASPWVDNSRTNKNKIDLYD
DB 224 ELNWTLELVNFWENRQRDPTLLWQVFGSATGVTRYIPATPW---RAPKKIDLYD
QY 242 PWYIOGAASPDKMLILVDVSGSVSGLTLLKIRTSVSEMLETSLDSDDDFVNVASFNSN
DB 280 PWYIOGASSPKDMVIIVDVSGSVSGLTLLKMTSVCEMLDTLSDDDDYVNVASFNEK
QY 302 SCFQHLVQANVNNKVKLQDAVNNITAGITDYKKGSPFAPBQLNLYNVSRANCKI
DB 340 SCFTHLVQANVNNKVKFKAQVQWAKGTTGYKAGFEYAFDQIQNSNITRANCKM
QY 362 TDGGERAQEIEFNKYN-KDKKVRVFRFSVQGHNYRGPQIOMACENKGYIYETPSI
DB 400 TDGGERVQDVFEKTNWPNRTVTVFVSQGHNYDVTPLQMACANGYIFELPSI
QY 421 INTQBYLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGLPVFNITGOFENK
DB 460 INTQBYLDVLRPMVLGAKAKQVQWNTNYLDALGLVITGLPVFNITG--DGRK
QY 481 NQLILGVMGVDSLEDIKLTTPRTLCPNGYYPADIPNGVYLLHPNLPQENPKSQBI
DB 518 NQLILGVMGIDVALNDIKLTTPNTYILGANGYYPADIPNGVYLLHPNLPQNTNPRE
QY 541 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGT
DB 578 DFLDAELENDIKVEIRNKMIDGESGKTFRTLVKSQDERYIDKGNRTYTWTPVNGT
QY 601 ALVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGYTFIAPRDYCNM
DB 638 GLVLPYSFYIYKAKLEETITQARSKKGKMDSETLKPDPFESGYTFIAPREYCKI
QY 661 SDNNTFEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQK-NIKG
DB 698 SDNNTFEFLNFNEFIDRKTTPNPNPCNADLINRVLLDAGFTNELVQNYWSKQK-NIKG
QY 720 RFVVTDDGGITRVVPKEAGENQWNPETYEDSFYKRSLDNDNYFTAPYFNK-SGFGP
DB 758 VFAATDGGITRVVPKEAGENQWNPETYEDSFYKRSLDNDNYFTAPYFNK-SGFGP

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224 ELNWTALENVFMENRRQDPTLLMQVFGSATGVTRYYPATPW-----RAPKIDILYL
242 PWYIQAASPKDMLILVDVSGSVSLTKLIRTSVSEMLETLSDDDFVNVASFNSN
280 PWYIQAASSPKDMLILVDVSGSVSLTKLIRTSVSEMLETLSDDDFVNVASFNEK
302 SCFOHLVQANVRNKKVADKANNITAKITDYKKGFSFAPEQLLNVNVRANCKI
340 SCFTHLVQANVRNKKVFEAVQGMVAKGTTGYKAGFEYAFDQLQNSITRANCKM
362 TDGGEBAQELFNKYN-KDKKVRVERFSVGOHNYERGPIONMACENKGYEIEPSI
400 TDGGERVQDVEKKNWPNRVRVFTSVGOHNYDVTPLOMACANKGYEIEPSI
421 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYLDLDELGLVITGTLPVFNITGQFENK
460 INTQEYLDVLGRPMVLADGKAKQVQWNTNVYEDALGLVITGTLPVFNITGQFENK
481 NQLILGVMDVLSLEDKRLTPRTLCPNGYFAIDPNGYVLLHPNLOPNKPSQE
518 NQLILGVMDVLSLEDKRLTPRTLCPNGYFAIDPNGYVLLHPNLOPNKPSQE
541 DFLDAELENDIKVEIRNMIDGESGKERTLVKSODERYIDKGNRTYVTPVNGT
578 DFLDAELENDIKVEIRNMIDGESGKERTLVKSODERYIDKGNRTYVTPVNGT
601 ALVLPYTSFYIYKAKLETTITQAKSKKMKDSETLKPDNFEESGYTFIAPRYCN
638 GLVLPYTSFYIYKAKLETTITQAKSKKMKDSETLKPDNFEESGYTFIAPRYCN
661 SDNNTPELLNFEBIDRKTNNPNSCNADLNRVLLDAGFTNELVQVNSKQK-NIK
691 SDNNTPELLNFEBIDRKTNNPNSCNADLNRVLLDAGFTNELVQVNSKQK-NIK
720 RFVVTDCGIRTVPKKEAGENWQENPTYEDSFYKRSLDNDNYVFTAFYFNK-SGPG
751 VFAATDCGIRTVPKKEAGENWQENPTYEDSFYKRSLDNDNYVFTAFYFNK-SGPG
779 ---GIMYSKAVEIYIOGKLLKPAVVGKIDVNSWIENF-----TKTSIRDP--CAG
811 DTVGILVSTAVELSLGRRTLRPAVVGKIDVNSWIENF-----TKTSIRDP--CAG
826 -VCDCKNSDVMOCVILDDGGFLLMANHDDYTQIGRPFCEIDPSLMHLVNSIVY
870 CEMDCVNNEDLLCLVILDDGGFLLMANHDDYTQIGRPFCEIDPSLMHLVNSIVY
885 SYDYQSVCEPAAKQAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFP
930 SYDYQSVCEPAAKQAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFP
945 AVEMEDDDFTASLSKQSCITEQTQYFFDNDKSKPSGVLDGCGNSRIPHGEKLMNTN
990 ADPAEAEG-SPETRESSCVMKQTYFYFSGVNSYNAIIDCGNSRLFAOQLNTN
1005 MVESKGTCPDTRLLIOAEQTSQGNPCDMVKOPRYKGPVCFDNNVLEDDYDCG
1049 VAEKPLCSQCEAGRLQKETHSDGPEQCELQVRPRYRGRPHICFDYNATEDSDCG

RESULT 10
Q9EQG2 PRELIMINARY; PRT; 1156 AA.
ID Q9EQG2 PRELIMINARY; PRT; 1156 AA.
AC Q9EQG2 PRELIMINARY; PRT; 1156 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DB Voltage-dependent calcium channel alpha-2-delta-2 subunit.
GN CACNA2D2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX NCBI_TaxID=10090;
RN [1]

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IMVSKAVEIYIOGKLLKPAVVGKIDVNSWIENF-----TKTSIRDP--CAGP--- 825
ILVSTAVELSLGRRTLRPAVVGKIDVNSWIENF-----TKTSIRDP--CAGP--- 876
CKNSDVMOCVILDDGGFLLMANHDDYTQIGRPFCEIDPSLMHLVNSIVYFNK 884
CEVNNEDLLCLVILDDGGFLLMANHDDYTQIGRPFCEIDPSLMHLVNSIVYFNK 936
QSVCEPAAKQAGHRSAYVPSVADILQIGWATAAASILQOFLLSLTFPRLLE 944
QAACAPOPPGNLGAAPRGVFTVADFLNLAWMTSAAAWSLFQQLLYGLVHSWFQ 996
EDDDFTASLSKQSCITEQTQYFFDNDKSKPSGVLDGCGNSRIPHGEKLMNTLFI 1004
BAEG-SPETRESSCVMKQTYFYFSGVNSYNAIIDCGNSRLFAOQLNTNLLFV 1055
KGTCPDTRLLIOAEQTSQGNPCDMVKOPRYKGPVCFDNNVLEDDYDCG 1060
PLCSQCEAGRLQKETHSDGPEQCELQVRPRYRGRPHICFDYNATEDSDCG 1111

RELIMINARY; PRT; 1143 AA.

TrEMBLrel. 15, Created)
TrEMBLrel. 15, Last sequence update)
TrEMBLrel. 23, Last annotation update)
el, alpha 2/delta subunit 2.

(Human).
cazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
heria; Primates; Catarrhini; Hominidae; Homo.
06;

N.A.

C-(1999) to the EMBL/GenBank/DBJ databases.

N.A.

S. Marais E., Lacinova L.;
tribution and functional characterization of the calcium
2delta-2 subunit.*;
7; CAB86192.1; -.
004010; CAFE.
002035; VWF_A.
; CAFE; 1.
; vwa; 1.
7; VWA; 1.
234; VWF_A; 1.
43 AA; 129085 MW; 492556C9919A0CE5 CRC64;

arity 53.9%; Score 3017.5; DB 4; Length 1143;
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LTLFQSLIGPSSPEPPSAVITKSDVKMOEDLVTLAKTASGVNQLVDIYKQD 66
LPLLLPAAFCASAYSFPQHTMQHWRARLEQVDGVMRIFGGVQQLREIYKONRN 103
EPNNAROLVEIARDIEKLSNRKALVSLAEAEKVQAAHQWREDFASNEVYYN 126
QENEPQKLVKAVAGDIESLLDRKQVALKADAAENFQKARHWDNKEEDIVYD 163
L---DPEKNDSPEGSQ--RIKPVFIEDANEGROISYOHAAVHIPTDIYEGSTVLN 181
AELDDPSDEVERGSKASTURLFDIEPNFKNVYSYAAVQIPTDIYKGSTVLN 223
TSALDEVFKKNREDDPSLLWVFGSAGLARYYPASPDVNSRTPNPKIDLYVRRR 241

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3GDRVQDVPEKYNWPNRTVRVFTSVGOHNDVTPLOQWMACTNKGYYFIPSIGA 460
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 IQEYLDVLRPMVLGAKAKOVQWTVYVLDALGLVITGTLPVFNITGQFENKTN 482
 LILGVMGVDSLEDKRLTRFTLCPNGYFPAIDPNGYVLLHPLNLPKPKSOPV 538
 LILGVMGVDSLEDKRLTRFTLCPNGYFPAIDPNGYVLLHPLNLPKPKSOPV 540
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 LDLELENDIKVEIRNKMIDGESGKTRTLVKSODERYIDKGNRTYTWTPUNGTDY 600
 LDLELENDIKVEIRNKMIDGESGKTRTLVKSODERYIDKGNRTYTWTPUNGTDY 602
 VLPTYSFYIYKALEETITQARSKKGKMDSETLKPNNFESGYTFIAPRDYCNLD 658
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 AATDGGITRVYYPKEAGENWOENPEYEDSFYKRSIDNDNTVFTAPYFNK-SGPCAY 778
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 -GIMWSKAVEIYIOGKLLKPAVVGKIDVNSWIENF-----TKTSIRDP---CAGP 825
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 VDCCKRNSDMDCVILDDGGFLMANHDDYTNQIGRPFGEIDPMSLRHLNVSIVA 881
 EMDCEVNNEDLLCVLIDDGGFLVLSNQHWQDQVGRFSEFSEVDANLMLALYNSPYT 937
 YDQSVCEPGAAPQKQAGHRSAYVPSVADILQICWMTAAWSTLQOFLLSLTPPR 941
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 VESKGTCPDTRLLIQAEQ--TSQGNPDCMVQKPRYKGPVDFCDNNVLEDYDTC 1059
 AEPKLCQCEVGRLLQKETHCPADGPGQCELVQPRYRTGPHICFDYNATEDTSDC 1116
 60
 17
 RELIMINARY; PRT; 1148 AA.
 TREMBLrel. 23, Created
 TREMBLrel. 23, Last sequence update
 TREMBLrel. 23, Last annotation update
 el.
 (Mouse)
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 heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 090;
 N.A.
 6J; TISSUE-Retina;
 683; PubMed=12466651;
 nsorium,
 ome Exploration Research Group Phase I & II Team;
 the mouse transcriptome based on functional annotation of
 engh cDNAs.";
 3-573(2002).
 3; BAC1998.1; --.

SQ SEQUENCE 1148 AA; 129780 MW; 9B49FF0547F82851 CRC64;
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 Best Local Similarity 54.1%; Pred. No. 1.4e-180;
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 DB 45 LLLLPPLLLPLLTAPGASAYSFPQOHTMQHWRLEQEIQGVVQQLREI
 QY 65 QDLYTVPNNARQVLETAARDIEKLLSNRSKALVSLALEAEKQAAHQRWEDPASN
 DB 105 RNLFEVQENEPQKLEKVGAGDIESLLDRKQVQALRLADAENFOKAHRWQDNKEE
 QY 125 YNAKDDL---DPEKNDSEPGSQ--RIKPVIEDANFGQISYQHAHVHPTDIYEG
 DB 165 YDAKADAELODPESEDWERSKTSALRLDIEDFNKKNYSYTAQIETDIYKG
 QY 180 LNELNWTALDEVPKQREEDPSLLWQVGSATGLARYYPASVPWDSRTPNKIDL
 DB 225 LNELNWTALLENVFIENRRQDPTLLWQVGSATGVTTRYYPATPW---RAPKKIDL
 QY 240 RRPWYIOGASPKDMLTLVDVSGVSGTLKLRITSUSEMLETSLDSDDFYNVASFN
 DB 281 RRPWYIOGASPKDMLTLVDVSGVSGTLKLRITSUSEMLETSLDSDDFYNVASFN
 QY 300 DVSCFOHLVQANVRNKKVLDAVNNITAKGIDTYKGFSAFQQLLNYNVSRANCN
 DB 341 PVSCFTHLVQANVRNKKVKEAVQGVAKGTGYKAGFEAFDQLQNSNITRANCN
 QY 360 LFTDGGSEAEQIENKYN-KDKKRVRFPSVQGNHYRGPQIOWMACENKGYEIP
 DB 401 MFTDGGSDRVQDPEKKNWPNRTVRVFTSVGOHNDVTPLOQWMACTNKGYYFIP
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 QY 479 LKNQILIGVMGVDSLEDKRLTRFTLCPNGYFPAIDPNGYVLLHPLNLPKPKS
 DB 519 KKNQILIGVMGVDSLEDKRLTRFTLCPNGYFPAIDPNGYVLLHPLNLPKPKS
 QY 539 TLDPLDAELNIDIKVEIRNKMIDGESGKTRTLVKSODERYIDKGNRTYTWTPVN
 DB 579 TLDPLDAELNIDIKVEIRNKMIDGESGKTRTLVKSODERYIDKGNRTYTWTPVN
 QY 599 SLALVLPYFYIYKALEETITQARSKKGKMDSETLKPNNFESGYTFIAPRDY
 DB 639 SLGLVLPYFYIYKALEETITQARSKKGKMDSETLKPNNFESGYTFIAPRDY
 QY 659 KISDNTEFLNLFNEFIDRKTPNPNPCNADLINRVLLDAGFTNBLVQWNSKQK-N
 DB 692 NASDNTEFLNLFNEFIDRKTPNPNPCNADLINRVLLDAGFTNBLVQWNSKQK-N
 QY 718 KARFVTDGGITRVYYPKEAGENWOENPEYEDSFYKRSIDNDNTVFTAPYFNK-SG
 DB 752 LAVFAATDGGITRVYYPKEAGENWOENPEYEDSFYKRSIDNDNTVFTAPYFNK-SG
 QY 777 ES---GIMWSKAVEIYIOGKLLKPAVVGKIDVNSWIENF-----TKTSIRDP---
 DB 812 ENDTVGVLVSTAVELSGLRRLTRPAVVGKIDLEAWAEKFKVLASNRTHQDOPQKQC
 QY 826 ----VCDCKRNSDMDCVILDDGGFLMANHDDYTNQIGRPFGEIDPMSLRHLNVSIVA
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ikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
a H.;
the coding sequences of mouse homologues of KIAA gene;
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EKVAGDIESLLDRKVQALKELADAENFQKAHRWQDNIKEEDIMYDAKADAELDD 123
DSEPGSQ--RIKPVFIEDANFGQISVQHAAVHIPTDIYEGSTIVLHNLNWTSLD 190
DMERGKTSALRLDFIEDPNFKKNVSYTAVQIPTDIYKGSTVILHNLNWTSLALE 183
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LILVDVSGSVGLTLKIRTSVSEMLTSLDDDFNVVASFNNSNAQDVSCFOHLVQA 310
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LEDIKLTPRTFLPCNGYYFAIDPNGVYLLHPNLPQKNPKSQBPVTLLDFLDAELEN 549
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NSWIENF-----TKTSIRDP--CAGP---VCDCKRNSDVMDCVILDDGGFLMA 850
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February 20, 2004, 16:58:16

secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.
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 (without alignments)
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 3308 seqs, 96168682 residues
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 inimum Match 0%
 ximum Match 100%
 listing first 45 summaries
 [R:76:*
 pir1:*
 pir2:*
 pir3:*
 pir4:*
 the number of results predicted by chance to have a
 : than or equal to the score of the result being printed,
 ad by analysis of the total score distribution.

SUMMARIES

seq	Length	DB	ID	Description
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1.3	1091	2	A44147	calcium channel pr
1.1	1106	1	CHRB2	calcium channel pr
1.0	1091	2	T30256	calcium channel al
1.8	734	2	S44617	CS0C3.11 protein -
1.4	1148	2	T18770	probable calcium c
1.5	1450	2	C86880	hypothetical prote
1.5	886	2	S54355	inter-alpha-trypsi
1.3	885	2	S30350	inter-alpha-trypsi
1.1	1819	2	D97033	uncharacterized pr
1.9	889	2	JC5576	inter-alpha-trypsi
1.9	2706	2	T28155	variant-specific s
1.8	1984	2	A44396	P-type cation tran
1.8	575	2	D64998	hypothetical prote
1.8	918	2	E90542	lipoprotein [impor
1.8	680	2	A97331	membrane associate
1.8	1516	2	E71619	RAD2 endonuclease
1.8	2364	2	I40884	cytotoxin L - Clos
1.8	946	1	IYH02	inter-alpha-trypsi
1.8	1315	2	T28679	fibrinogen-binding
1.7	932	2	JC5953	inter-alpha-inhibi
1.7	1291	2	S46431	botulinum neurotox
1.7	1291	2	A49777	botulinum neurotox
1.7	420	2	S76691	hypothetical prote
1.7	1426	2	A99580	hypothetical prote
1.7	921	2	JC4625	inter-alpha-trypsi
1.7	1385	2	D89824	hypothetical prote
1.7	654	2	A69656	methyl-accepting c
1.7	1027	2	B90527	atp-binding protei

ALIGNMENTS

RESULT 1
 JH0565
 calcium channel alpha-2b chain precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug
 C:Accession: JH0565
 R:Williams, M.X.; Feldman, D.H.; McCue, A.F.; Brenner, R.; Velicelebi,
 Neuron 8, 71-84, 1992
 A:Title: Structure and functional expression of alphas, alpha2, and be
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 A:Residues: 1-1091 <WIL>
 A:Cross-references: GB:M76559; NID:G179761; PIDN:AAA51903.1; PID:G1797
 A:Experimental source: basal ganglia
 A:Note: Several conflicts are found between GenBank submission, author
 C:Comment: This protein is a subunit of the voltage dependent calcium
 C:Superfamily: calcium channel alpha-2 chain
 C:Keywords: glycoprotein; phosphoprotein
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-1067/Product: calcium channel alpha-2b chain #status predicted <C
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 F:91,142,250,625,817/Binding site: phosphate (Ser) (covalent) (by prot
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 F:501/Binding site: phosphate (Thr) (covalent) #status predicted
 F:833/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kina

Query Match	100.0%	Score 5599	DB 2	Length 1091
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1063	Conservative	0	Mismatches	0
Indels	0			

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 Db 121 EVVYNAKODLDEPKNDSEFGSRQIRKPVFIEDANFGQRQISYQAAVHIPTDIYEGS
 Qy 181 NELNWTSDALDEVKKNREDEPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLY
 Db 181 NELNWTSDALDEVKKNREDEPSLLQVFGSATGLARYYPASPWVDNSRTPNKIDLY
 Qy 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETSLDDDFVNVASFNS
 Db 241 RPWYIQGAASPKDMLILVDVSGVSGLTLLKIRTSVSEMLETSLDDDFVNVASFNS
 Qy 301 VSCFQHLVQANVRNKKVLDVANNITAKGITDYKKGFSFAFEQLLNVTNVRANCNK

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inter-alpha						
thoptry prc						
DNA-directe						
hypothetica						
methyl-acce						
hypothetica						
probable re						
incernalin						
probable pe						
hypothetica						
hypothetica						
cellulose 1						
fibronectin-						
ATP-depende						

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PTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRDYCNDLKI 660
PTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRDYCNDLKI 660
TEFLNLFNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720
TEFLNLFNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNIKGVKAR 720
DGGITRVYPKBAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
DGGITRVYPKBAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPGAYESGI 780
AVEIYIOGKLKPAVVGKIDVNSWIENTKTSIRDPKAGPVCDCRNSDVMDCVI 840
AVEIYIOGKLKPAVVGKIDVNSWIENTKTSIRDPKAGPVCDCRNSDVMDCVI 840
GFLLMANHDDYTNQIGRFFGIDPSLMHRLVNI SVYAFNKSVDYQSVCEPAAKPKQ 900
GFLLMANHDDYTNQIGRFFGIDPSLMHRLVNI SVYAFNKSVDYQSVCEPAAKPKQ 900
RSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
RSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTASLSKQ 960
EQQYFFNDNDSKPSGVLDCCGNCRI FHGEKLMNTNLI FIMVESGTCPCDTRLLI 1020
EQQYFFNDNDSKPSGVLDCCGNCRI FHGEKLMNTNLI FIMVESGTCPCDTRLLI 1020
TSDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
TSDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063

otein alpha-2 chain precursor - rat
dihydropyridine-sensitive L-type
m channel alpha-2 chain
norvegicus (Norway rat)
4 #sequence_revision 27-Jun-1994 #text_change 20-Aug-1999
7
H.; Lee, P.; King, R.G.; Chin, H.
Sci. U.S.A. 89, 3251-3255, 1992
expresses an alternatively spliced form of the dihydropyridine-sensit
: A44147; MUID:92228762; PMID:1314383
7
ary
RNA
<KIM>
: GB:M86621; NID:q203954; PIDN:AAA41088.1; PID:q203955
cium channel alpha-2 chain
m; glycoprotein; ion channel; transmembrane protein
96.3%; Score 5390; DB 2; Length 1091;
```

```
Best Local Similarity 95.8%; Pred. No. 7.1e-316;
Matches 1019; Conservative 24; Mismatches 19; Indels 2; C

QY 1 MAAGCLLALTUTLTFQSLIIGPSSEPPPPSVTIKSWVDKMOEDLVTLAKTAGVNC
DB 1 MAAGCLLALTUTLTFQSLIIGPSSEPPPPSVTIKSWVDKMOEDLVTLAKTAGVTC
QY 61 YEKQODLVYVPEPNARQIVETAARDIEKLNSRSKALVSLAEAKVQAAHQRREI
DB 61 YEKQODLVYVPEPNARQIVETAARDIEKLNSRSKALVSLAEAKVQAAHQRREI
QY 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGE
DB 121 EVVYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFGRQISYQHAHVHIPTDIYEGE
QY 181 NELNWTSALEDEVFKQNRDEDSLLWQVFGSATGLARYYPASFWVDNSRTPNKIDLI
DB 181 NELNWTSALEDEVFKQNRDEDSLLWQVFGSATGLARYYPASFWVDNSRTPNKIDLI
QY 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLI RTSVS EML ETLSDDDDFVNVASFNE
DB 241 RPWYIQGAASPKDMLILVDVSGSVGLTLKLI RTSVS EML ETLSDDDDFVNVASFNE
QY 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKGFSAPEQLLNNVSRANCKN
DB 301 VSCFOHLVQANVRNKKVLKDAVNNITAKGIDTYKGFSAPEQLLNNVSRANCKN
QY 361 FTDGGEERAQEI FNKYNDKKVRFVSFGHNYRGPIQWMAKNGKGYIPIGAIK
DB 361 FTDGGEERAQEI FNKYNDKKVRFVSFGHNYRGPIQWMAKNGKGYIPIGAIK
QY 421 INTQEYLDVLGRPMVLADGKAKOVQWNTVYLDALHGLVITGTLPVNITGPFENH
DB 421 INTQEYLDVLGRPMVLADGKAKOVQWNTVYLDALHGLVITGTLPVNITGPFENH
QY 481 NQLILGVMGVDVLSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLQPKNSQEI
DB 481 NQLILGVMGVDVLSLEDIKRLTFRFTLCPNGYYFAIDPNGYVLLHPNLQPKNSQEI
QY 541 DFLDALENDIKVEIRNKMIDEGSEKTPRTLKVSQDERYIDKGNRTYTWTPVNGI
DB 541 DFLDALENDIKVEIRNKMIDEGSEKTPRTLKVSQDERYIDKGNRTYTWTPVNGI
QY 600 LALVLPTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRDY
DB 600 LALVLPTYSFYIYKAKLEETITQARSKKGKMDSETLKPDPNFESGYTFIAPRDY
QY 660 ISDNNTPEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNIK
DB 660 ISDNNTPEFLNFEFIDRKTNNPNSCNADLINRVLLDAGFTNELVQNYWSKQNIK
QY 720 RFVYTDGGITRVYPKBAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
DB 720 RFVYTDGGITRVYPKBAGENWQENPETYEDSFYKRSLDNDNYVFTAPYFNKSGPG
QY 780 IMVSKAVEIYIOGKLKPAVVGKIDVNSWIENTKTSIRDPKAGPVCDCRNSDV
DB 780 IMVSKAVEIYIOGKLKPAVVGKIDVNSWIENTKTSIRDPKAGPVCDCRNSDV
QY 840 ILDDGGFLLMANHDDYTNQIGRFFGIDPSLMHRLVNI SVYAFNKSVDYQSVCEP
DB 840 ILDDGGFLLMANHDDYTNQIGRFFGIDPSLMHRLVNI SVYAFNKSVDYQSVCEP
QY 900 QGAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTA
DB 900 QGAGHRSAYVPSVADILQIGWATAAANSILOQFLLSLTFPRLLEAVEMEDDDFTA
QY 960 QSCITEQYQYFFNDNDSKPSGVLDCCGNCRI FHGEKLMNTNLI FIMVESGTCPCD
DB 960 QSCITEQYQYFFNDNDSKPSGVLDCCGNCRI FHGEKLMNTNLI FIMVESGTCPCD
QY 1020 IQABQTSIDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
DB 1020 IQABQTSIDGNPCDMVKQPRYKGPDPVCFDNNVLEDYTDGCGVS 1063
```

TSDGPDPCDMVKQPRYKRGPDVCFDNNVLEDTDCGGVS 1063

tein alpha-2 chain precursor - rabbit
dihydropyridine-binding protein, 140K
guinea pig (domestic rabbit)
#sequence revision 31-Mar-1992 #text_change 22-Jun-1999
A39518; A33409
A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.
3287-3293, 1991
Characterization of the dihydropyridine-sensitive calcium channel al
A39518; MUID:91131638; PMID:1847144

EMBL: M21948; NID:g164762; PIDN:AAA81562.1; PID:g164763
Lys, and deletion of 620-Ser were also found

A.H.; Kahl, S.D.; Vedvick, T.S.; Harpold, M.M.; Campbell, K.P.

3287-3293, 1991
Characterization of the dihydropyridine-sensitive calcium channel al
A39518; MUID:91131638; PMID:1847144

otein

ice represents the amino end of a glycosylated peptide that appears ad
and identical molecular weights (17K) following deglycosylation
lawkes, M.J.; Brush, K.; Cook, R.

120-7828, 1989
Composition of the purified dihydropyridine binding protein from skelet
A33409; MUID:90122765; PMID:2558713

try

otein

S', 46-47 <HAM>
ium channel alpha-2 chain
i: disulfide bond; glycoprotein; ion channel; membrane protein; phosph
al sequence #status predicted <SIG>
calcium channel alpha-2 chain #status predicted <MAT>
50,470,477,606,615,678,697,784,891,898,988,1001,1081/Binding site:

96.1%; Score 5380.5; DB 1; Length 1106;

arity 94.8%; Pred. No. 2.7e-315;

nservative 15; Mismatches 12; Indels 29; Gaps 4;

LLALTLTLTQSS--LLIGPSSEPPFPSPAVTIKSWVDKMQEDLVTLAKTASGVNQLV 58

PLAWTLTLQAWLILIGPSSEPPFPSPAVTIKSWVDKMQEDLVTLAKTASGVNQLV 60

CYQDLATVEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFA 118

CYQDLATVEPNNARQLVEIAARDIEKLLSNRSKALVSLALEAEKVQAAHQRDFA 120

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 178

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

AYYNAKDDLDPEKNDSEPGSQRIKPVFIEDANFORQISYQAAVHIPTDIYEGSTI 180

[illegible]

```

2y DPEKNDSPGSRQIKP---VFIEDANFGRIQSYQHAAVH----- 167
: : : : : : : : : : : : : : : : : : : : : : : : :
2b NNESSQRETVSOLKQDSQLAFSPNFGIKASFNDLAQNYENISPEYRQDETGLSP 240
: : : : : : : : : : : : : : : : : : : : : : : : :
2y IPTDIYEGSTIVLHNLWTSALDEVFKKQREDDPSLLHQVFGSATGLARYYPASFW 223
: : : : : : : : : : : : : : : : : : : : : : : : :
2b IPT-----GNTTVVHQGNNSF-----SSQMDGVNSWN--GEATNLSNYSIEYAG 287
: : : : : : : : : : : : : : : : : : : : : : : : :
2y -----SRTPNKIDLY-DVRRRPWYIQGAASPKMDLILVDVSGSVSGLTLK 270
: : : : : : : : : : : : : : : : : : : : : : : : :
2b VDFALRYKAKETETFGLYDVLYNRGN---VQNPVKPVDIVLVIDMSGMOGAKET 344
: : : : : : : : : : : : : : : : : : : : : : : : :
2y SVSEMLETLSD---DFNVV--ASFNSNAQDVSCFQHLVQANVRNKKVLKD----A 321
: : : : : : : : : : : : : : : : : : : : : : : : :
2b GVSDFLSTIQNTAVADYVNVGIVGYSSPGNTVGTASGYITVPI--DKVSSSHVKS 402
: : : : : : : : : : : : : : : : : : : : : : : : :
2y TA---KGTIDYKGFSAFAPOLLNYSRANCKLIMLFTDGGHRAQRIENKYNK 378
: : : : : : : : : : : : : : : : : : : : : : : : :
2b LAQFSGTFTQLGLRKGTML---EQSSNQKQMLMTDG---VPTFSYKYN 455
: : : : : : : : : : : : : : : : : : : : : : : : :
2y R--VRFPSVGQHNTERG---PIQ---MMACENKGYIYEI-----PSIGAIRINTQE 425
: : : : : : : : : : : : : : : : : : : : : : : : :
2b DNVIYQGSFAERDEPGNTSKIQSPYVKDINGSGSNIEIRDTWAATLGEABISQBE 515
: : : : : : : : : : : : : : : : : : : : : : : : :
2y LGRPMWLAGD-----KXQVQWNTVYLDALGLVITGLTPVFNITGQFE 474
: : : : : : : : : : : : : : : : : : : : : : : : :
2b HTLGIQLNGDGSYLSQBEVKSRTSLIATTLGYQDANSAN-----DITDYLK 565
: : : : : : : : : : : : : : : : : : : : : : : : :
2y -----LKNQILGVMDVSVLEDIKRLTPFTLCPNGYYPALDPNGYVLLHPN 526
: : : : : : : : : : : : : : : : : : : : : : : : :
2b VLSRFNTITNGLIDPLGAQFEYKTK-----FETSVG----- 604
: : : : : : : : : : : : : : : : : : : : : : : : :
2y NPKSQEPVTLDFLDALENDIKVIRKMDGESCKETFTLVKSQDERYIDKGNR 586
: : : : : : : : : : : : : : : : : : : : : : : : :
2b -----EDSIDNLTPTKINEKGLSISNLNI--GKQEQVQHIVQVRLNFTETDPTNY 653
: : : : : : : : : : : : : : : : : : : : : : : : :
2y ---TWTPVNGT--DYSALVLPYSPFYIKAKLE-----ETITQARSKK 627
: : : : : : : : : : : : : : : : : : : : : : : : :
2b NGETTLTP--NGSNPDKNVNFVPSAKSGSINGLTLEKQWLNSENIPENVELLIGRR 712
: : : : : : : : : : : : : : : : : : : : : : : : :
2y DSE-----TLKPDNFEESGYTFIAPRDYCNLKI SDNTEFLNFEIDRKTPNN 682
: : : : : : : : : : : : : : : : : : : : : : : : :
2b SSWTKVTYTLKEDDEWTSOLENLPKYSILGEEFYIEIKDEIVLN--SEIYDWITIGE 771
: : : : : : : : : : : : : : : : : : : : : : : : :
2y ADLNRVLLD---AGFTNELQVNYWQKQNIKGKXARFVVYTDGGITRVYPKEAGE 738
: : : : : : : : : : : : : : : : : : : : : : : : :
2b IANIEKPLQLIKTSNHDNEPLSEVEFVLKNSQGEIDKAVTN-----EKGE 822
: : : : : : : : : : : : : : : : : : : : : : : : :
2y ENPTYEDSFYKRSLDNDNYYFTAPYFNKSGPGAYESGIMVSK-----AVEIYIQ 791
: : : : : : : : : : : : : : : : : : : : : : : : :
2b KTRILNYGEEYQLHEIKSPGHSLEGPKIKT---EFENGQPIIKVYDGEQIALDEHYN 879
: : : : : : : : : : : : : : : : : : : : : : : : :
2y KPAVVGIKIDVNSWIENFTKTSIRDPCAGPCVDCRNSDVMDCVILD-----DG-- 844
: : : : : : : : : : : : : : : : : : : : : : : : :
2b S---LNTINDIN--VEEF-----RNSVTIDKRAVDSEKLDGAV 917
: : : : : : : : : : : : : : : : : : : : : : : : :
2y LMANHDYTNQIGRFFGEIDPSLMRHLWNISVYAFNKSVDYQSVCEPAAPKQAG 903
: : : : : : : : : : : : : : : : : : : : : : : : :
2b QIESVDDELTLQKPL--EITNNLLPGL-----YALQESVSPNGYVRDDEV 964
: : : : : : : : : : : : : : : : : : : : : : : : :
2y SAYVPSVADILQIGWATAAWSILQOFL-----LSLTF- 939
: : : : : : : : : : : : : : : : : : : : : : : : :
2b VKFNGSIVAIGSEG-----IDIPLDENESGKGLVINEENGDLHLTLIFY 1015
: : : : : : : : : : : : : : : : : : : : : : : : :
2y PRLLAEVEMEDDDFTASLSKQSC-ITEQTYFFDNDN-----KSPFGLVDCNCRSRI 990
: : : : : : : : : : : : : : : : : : : : : : : : :
2b PPLQLEVDKIDDDTSLAGVSPFLTRLGKASTSDSVKRNISFDRILKTFN--NE 1073
: : : : : : : : : : : : : : : : : : : : : : : : :
2y KL--MNTNL 1001
: : : : : : : : : : : : : : : : : : : : : : : : :
2b TALKSNL 1085
: : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 8
S54355
inter-alpha-trypsin inhibitor heavy chain 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Fet
C:Accession: S54355
R:Chan, P.; Rialler, J.L.; Raguenes, G.; Salier, J.P.
Biochem. J. 306, 505-512, 1995
A:Title: The three heavy-chain precursors for the inter-alpha-inhibitor
A:Reference number: S54353; MUID:95194326; PMID:7534067
A:Accession: S54355
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-886 <CRA>
A:Cross-references: EMBL:X70393; NID:G95635; PIDN:CAA49843.1; PID:565
C:Superfamily: inter-alpha-trypsin inhibitor complex component II

Query Match 3.5%; Score 194.5; DB 2; Length 886;
Best Local Similarity 19.9%; Pred. No. 0.0013;
Matches 185; Conservative 138; Mismatches 347; Indels 261; G

QY 27 FPSAVTIKSWVDKMQEDIATLAKTAGVNLQVDIYEKYQDLYTVPEPNARQLVEIF
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 98 YPGNVKEVAQKQYKAVSQGTAG---LVKASGRKLEKFTVSVNVVAAGSKVTF
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 EKLISNRSKALVSLALEAEKVQAAHQRDPASNEVVVYNAKDDLDPEKNDSEPG
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 154 EELL-KRNGKGYEVLKVPKQLVRHFEID-----AHIFEP--
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 147 PVFIEDANFGRIQSYQHAAVHIPTDIYEGSTIVLHNLWTSALDEVFKQREDDPS
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 GISMLDAB-----ASFITNDL-LGSALTQSF-----
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 207 VFGSATGLARYYPASPMVDNSRT--PNKID-----LYDVRRRP--
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 215 -----SGKKGHVSPKSLDQORSCPTCTDSLLNGDFTIVDVNRESQGVQVNGY
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 ---QG--AASPKMDLILVDVSGSVSGLTKLIRTSVSEMLETSLDDDFVNVASFNSN
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 270 PAPQGLPVVPKNIIVFVIDVSGSMGRKIQTQREALLKILDDVDKEDDYLNFILFST-
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 302 SCFO-HLVQANVRNKKVLKQAVNNITAKGITYDKKGFSAFAPQLLNINVSAN--
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 327 TTWKDHLVQATPANLKBKAKTFVKNIHQDSMTNINDGLLKGIEML---NKAREHTV
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 355 NKIIMLFTDG---GEBAQEIFNKYNK--DKKVRVRFVSQGHNYERGPQIOWMAC
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 384 TSIILMLTDGANTGESRPEKIQENVRNAGKGFPLYNLGFQ--NNLNVNFEETLAL
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 409 YYPEIPSGAIRINTQBYLDVLGRPMVLGADKAKQVQWNTVYLDALBGL--VITG
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 443 LARRIYEDSDANLQGFYEAVANPLL-----TNVEVEYPENAILDLTRN
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 467 PNIITQGFENKLNKQLILGVMDVSVLEDIKRLTPFTLCPNGYYPALDPNGYVL
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 492 F-----YDG-----SEIVAGRLVDRNMDN-----FKADYKGHGA
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 527 LQPNKPSQEPVTLDFLDALENDIKVIRKMDIDGESGEK--TFRTLKVSQDERY
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 524 ----DLTFTFEVDMEEMDAALK-----EGYIFGDYIERLMAYLTIEQLLEKRX
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 585 NRTYTWTPVNGTDYSLA--LVLPITYSFYIKAKLEETITQARSKGKWKDQSET---
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 573 DEKENIT-AREALDLSLVKVFVTPLTSMVVTKPEDNEDQTSIADNAGEAEFAETTM
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 638 PDNFEESGYTFIAPRDYCNLKI SDNTEFLNFEIDRKTPNNPSCNADLNVRV
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 632 TQSSQSPFYV-----DGDPHFIIQI-----PGKNDISCFNI
: : : : : : : : : : : : : : : : : : : : : : : : :
QY 698 GFTNELQVNYWQKQNIKGKXARFVVYTDGGITRVYPKEAGENWQENPETYEDSPYK
: : : : : : : : : : : : : : : : : : : : : : : : :
Db 669 GTVLRLLIQD-----PVT--GIT-VTGQIIIGD-----K
: : : : : : : : : : : : : : : : : : : : : : : : :

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3. 0 3. 0 5. 0

; A; ; S; ; D; ; A; ; B; ;
 ; E;

1. M_1
 2. M_2

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 $\bar{C}; \bar{D}; \bar{u}; \bar{t}; \bar{R};$

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$$\begin{aligned} & \text{; T:} \\ & \text{; Re} \end{aligned}$$

25

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25

RECEIVED: 1977

5: 25

24. 25.

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inc

Re:

253

 $\frac{1}{2} \quad 0 \quad \frac{1}{2}$

0.5

9

FS1
FS0
nLE
; A₁
; S₁
; D₂
; A₂
; B₂

 $\mu; \nu; \kappa; \lambda;$;Mc
;Re
;U

; Br
; Re

$$; \text{M}; ; \text{R}; ; \text{C}$$
[illegible] $\frac{1}{2}, \frac{1}{3}, \frac{1}{4}$

MC Re Co

1992

$$; \mathcal{D}C \quad ; \mathcal{M}C \quad ; RE$$

1. 11. 1971

2000

11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 841. 842. 843. 844. 845. 846.

;
; R;
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W: 100

$$\begin{array}{l} \text{Re} \\ \text{Ac} \\ \text{Mc} \end{array}$$

[illegible]

| | | | | | | |
|---|------|------------|--------------|------------|--------------|---------------------------------|
| Qy | 605 | PTYFYIKAKL | BETTIOARSKGK | MOSETLKP | DNPFESGYTTFI | APRDYCNLDLKI |
| Db | 871 | QOYSIY | -----EIN- | ----- | ----- | -----DYNLSIGI |
| | | | | | | |
| Qy | 665 | TEFLINFE | TRDRTKPNP | NSCNADLINR | VLLDAGFTN | ELVQNYWSKOKNIKGVKAR |
| Db | 899 | TENITYIN | LNLIKSSVFN | AS----- | DIQTKV | -----NALISVGYEIN |
| | | | | | | |
| Qy | 725 | DGGITRVY | PKAENMOEN | PETVEDSFY | KRSISLNDN | VYVFTAPYFNKSGPGAYESGI |
| Db | 949 | SLIGITGV | ----- | ----- | ----- | -----TKENIIFINTYIKE--GOYFDLT |
| | | | | | | |
| Qy | 785 | AVEI | ----- | YIQ----- | GKLLKPA | VGVIKIDVNSWIENTKTSTRDPCAGPVCDDK |
| Db | 981 | SVLEEK | EYAEYKITS | GK----- | AVVG----- | -----DYTKVGIKDVTENIAYIN |
| | | | | | | |
| Qy | 835 | VMDK | 838 | | | |
| Db | 1027 | LQNC | 1030 | | | |
| | | | | | | |
| RESULT 11 | | | | | | |
| JC5576 | | | | | | |
| inter-alpha-trypsin inhibitor heavy chain 3 - golden hamster | | | | | | |
| C:Species: Mesocricetus auratus (golden hamster) | | | | | | |
| C:Date: 23-Sep-1997; sequence revision 23-Sep-1997 #text_change 17-Mar | | | | | | |
| C:Accession: JC5576; PC4486 | | | | | | |
| R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohara, H. | | | | | | |
| J. Biochem. 122, 71-82, 1997 | | | | | | |
| A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy | | | | | | |
| sin inhibitor heavy chain family. | | | | | | |
| A:Reference number: JC5574; MUID:97420688; PMID:9276673 | | | | | | |
| A:Accession: JC5576 | | | | | | |
| A:Molecule type: mRNA | | | | | | |
| A:Residues: 34-53;443-475;509-526 <NA2> | | | | | | |
| A:Cross-references: DBU;D89287 | | | | | | |
| A:Experimental source: liver | | | | | | |
| A:Accession: PC4486 | | | | | | |
| A:Molecule type: protein | | | | | | |
| A:Residues: 34-53;443-475;509-526 <NA2> | | | | | | |
| C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy cha | | | | | | |
| that the complexes play important role for pancreatic cancer. | | | | | | |
| C:Superfamily: inter-alpha-trypsin inhibitor complex component II | | | | | | |
| F:236-239,664-865/Disulfide bonds: #status predicted | | | | | | |
| Query Match 2.9%; Score 164.5; DB 2; Length 889; | | | | | | |
| Best Local Similarity 23.2%; Pred. No. 0.082; | | | | | | |
| Matches 66; Conservative 56; Mismatches 112; Indels 51; G | | | | | | |
| Qy | 202 | SLMQVFG | SATGLARYYP | ASPWNDSRT | -PNKID----- | LYDVRRL-PWIIQ |
| Db | 211 | SALTQSF | GKGHVSKPS | ---LDQQR | SCPTCTSL | NGDPTFIYVDVNR |
| | | | | | | |
| Qy | 249 | ----- | ASPKDM | LILVDVSG | VSGLTGLK | LIRTSVSEMLETSLD |
| Db | 268 | YFVHF | PAQGLPVVP | PKNIVF | VIDISGS | NAGRKIQQTRVALLKILDDMKQDDYLNFI |
| | | | | | | |
| Qy | 297 | NAQVSC | FQHLVQAN | VNRKKVL | KDAVN | NIITAKGITDYKKGFSFAFEQLM---- |
| Db | 328 | GV---- | TTWK | SDLSVQAT | PANLEEAR | TFTVRSISDQGM |
| | | | | | | |
| Qy | 353 | NCNKI | MLFTDG---- | GEERAQ | EIKFNKY | KDKKRVFRFVSQGHNVERGPIQMAA |
| Db | 386 | STSI | IML-TD | GANTGES | RPSKIQEN | VRKALIEGRFPLNLGFGNNLUNYFL |
| | | | | | | |
| Qy | 408 | GYYYE | IPSIGAIR | INTQEV | LDVLGR | PMVLADKAKQVQWNTNYVID 452 |
| Db | 445 | GVAR | RIYEDS | DANLQ | OGFVEE | VANPLL-----TNVEVE 478 |
| | | | | | | |
| RESULT 12 | | | | | | |
| T28155 | | | | | | |

IAISRLKKKFSISCLCPHKINAGQINTWVFDKGT-TLTENNLOFIGHTQKKNK 547
 LDLDLAELENDIKVEIRNKMIDGESGKFTFLVKSQDERVIDKGNRTYTTPVNG 595
 -DFHIK-----EMNTSYIHSKDDMIHNK----- 577
 LALVLPYFYIYKAKLBETTQAKSKYKGMKD-----SETLKPDPFESSG 645
 -----SIISYYIYKNNKMLTSSK-KKSIITKERSNPLVQTIKSLKLDHYIKKK 627
 APDYCNLDKISDNN-TEFLN-----FNEF--IDRKTNNPSCNADLINRVLLD 696
 TNNYCNLDHLINDSCSSYLNSSETKDAYCEYNDH-----LCD-----INKNMD 678
 NELQNYMSKOKIKGVKARFVVDGGITRVYKPEAGENQENPETYBDSYKRS 756
 NELMGYSKNELMGKTIKNELM-----GKYSKNEL 712
 YVFTAPYKSGPGAYESGIMVSKAVEIYIOGKLLKPAVG-----IKIDVNSWI 810
 ---MGYSKNELMGKYSKNELMGKYSKNELMGKTIKNQGVDTNIYH 765
 KTSIRD-PCAGPVCDCRNSDVMDCV-----ILDDGGFLMANHDDYTNQIGRF--- 862
 NDYNDYPCD---YNCNNDYTHRLEVHNKNSFNIPPEKNSYNNISEHIKI 822
 -----FGEIDPMLRHLVNSVAF-----NKSYDYQ 889
 LFEALACCHTLKSVNNKIMGVDLILMFNTCDMLNNSFIIEKKKNSYDFQ 882
 PGAPKOGAGHRSAYVSADILQIGWATAAANSILOQFLLSLTFPRLLBAVEME 949
 -DGNKTGANDERCHLNN-----NLVSYNLIKRF----- 912
 TASLSKOSCIETEOTYFPDNDKS 977
 QSLQMSVIVKST-YGNNDNN 937

in b2270 - Escherichia coli (strain K-12)
 7 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 8
 Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
 au, B.; Shao, Y.
 1462, 1997
 ate genome sequence of Escherichia coli K-12.
 : A64720; MUID:97426617; PMID:9278503
 3
 ary; nucleic acid sequence not shown; translation not shown
 VA
 <BLAT>
 : GB:AE000317; GB:U00096; MID:g1788605; PIDN:AC75330.1; PID:g1788606;
 cce: strain K-12, substrain MG155
 2.8%; Score 157.5; DB 2; Length 575;
 arity 21.6%; Pred. No. 0.11;
 onservative 93; Mismatches 206; Indels 105; Gaps 25;
 ARQLVETAEADIEKLSNRKALVSLAEKVOAHQWREDFASNEVYVYNAKD 130
 KESQOQOPSTFTQOVLAAQQAIAK---EAEQSA---AKALAAQOQVQOYSDKQA 75
 KND-----SPGSRIRKPVIEDANFGROISYQHA---VHIPTDI 172
 QEAFTPARAKAKATHIANGPARYOQF---DNPVKQAQNPATFSLDVTGS 132
 TVVINE-----LNWTSALDVEFKKNEEDPSLLMQVGSATGLARY 218
 RFNLQGLPPPPDAVRVEIVNYPSPDWDI--KDKQSIPASKPIPFAMRYELA--- 187

QY 219 PASPWVDSRTPNKIDLYDVRRRPWIYIOGAASPKDMLILVDVSGS-VSGLTKLH
 Db 188 PA-PW-NQRTLLKVLIDKDKSEELPAS-----NLVFLIDTSGSMISDERPLI
 QY 278 EMLTSLDDDDFFNVASFNSNAQDVSCFOHLVQANVRNKKVLKADVNNITAKGITD
 Db 242 LLVTELREQDNIAIVTYAGDSRIA-----LPSISGSHKAEINAAITSDLDAGSTNC
 QY 338 SFAPOLLNVNVRANCNKIIMLFTDG-----GERRAQEIFNKYKNDKKVRFRE
 Db 297 ELAVQOATK-GFIKGINR-ILLATDGDVNFVIGIDDPKSIEMVKKQRESGVTLSTE
 QY 392 HNYRGPQIOMACENKGYEIPISGAIIRINTQBYLDVLRPMVL--AGDKAKQVC
 Db 355 SNYNEAMVRIADVCGNGNSYDITLS-----EAQKVLNSEMQLLITVAKQVKAQIE
 QY 446 WTNVYLDALGLVITGLPVFNITGQFENKTNLKNQILGVMGVD-VSLEDI---
 Db 411 WYTEY---RQIG-----YE-----KQLRVEHFNNNDVNDAGDIGAC
 QY 502 PRFTLCPNGYVFAIDPNGYVLLHNLQPKPKSOS 536
 Db 448 LLELTNGQKASIDKLRYA--PNKLAKSDKTKE 480

RESULT 15
 E90542
 lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug
 C:Accession: E90542
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissc
 Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathog
 A:Reference number: A99512; MUID:21267165; PMID:111353084
 A:Accession: E90542
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-918 <KUR>
 A:Cross-references: GB:AL445566; PID:g14089658; PIDN:CAC13418.1; GSPDB
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYPU_2450
 A:Genetic code: GSC3

Query Match 2.8%; Score 156.5; DB 2; Length 918;
 Best Local Similarity 20.0%; Pred. No. 0.26; Mismatches 229; Indels 161; G
 Matches 122; Conservative 99;
 QY 305 QHLVQANVRNKKV---LKDANNITAKGITYKGFSAFQQLNLYNVRANCNK
 Db 91 KRILPSNVNENLDFNSLKLITKNTLIGKNTPKNYTVAFSIDPN-SVENASADN
 QY 361 FTGGERAEAEIENKYNKKV---RVFRFSVGOHNYRGPQIOMACENKGYEIE
 Db 146 -TDG-----SNIIIVSLKDKNGVLEKVKFIT-----GLLSEL
 QY 418 AIRINTQBYLDVLRPMVLADGKAKQVNTNVYLDALGLVITGTLP-----
 Db 182 DQMLK-----VDVPKNENILASSIVEEQTNE-----KISLTQGRKVPSTFDITKY
 QY 468 NITGQFENKTNLKNQILGVMG-----VDVSLEDIKR--LTPRFTL-CPNGYVFA
 Db 233 HVLSHDDKGLAIRVSLSAKSTKSKDPDYTTIEGFKQSFLEDRISLAKAQVYNTK
 QY 519 GYVLLHNPLOPKPKSQEPVTLDFLAELENDIKVEIRNKMIDGESGKFTFLVKE
 Db 292 --TIKSLQLLPSSASSED--KLVLSAYDISVPDGLKFNFSFEAKQGT-----
 QY 579 RYTDKGNRTYTTPVNGTDSLALVLPYFYIYKAKLBETTQAKSKYKGMKDSE
 Db 339 ---DKGVLYTFLYQINGTRTRTEEVKLDIOTFNIIKRYLDETILKIDSV--VLKENS!

